

IOCVS
2nd Edition
2026
Conference

The 2nd International Online Conference on Veterinary Sciences

7-9 September 2026, online



Program and Abstract Book

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The 2nd International Online Conference on Veterinary Sciences

7-9 September 2026 | Online



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Ms. Nichaporn Khongthung
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Welcome from the Chair

Dear Colleagues,

It is our great pleasure to welcome you to the **2nd International Online Conference on Veterinary Sciences (IOCVS 2026)**, which will take place online on **7–9 September 2026**. This event is organized by the open access MDPI journal Veterinary Sciences (ISSN: 2306-7381; Impact Factor: 2.7; CiteScore: 3.9).

Following the successful first edition, IOCVS 2026 returns with a sharpened focus on **global health challenges at the human–animal–environment interface**. This year's conference will highlight cutting-edge research and foster cross-disciplinary exchange through three key themes:

S1. One Health Approaches to Emerging Zoonotic Threats;
S2. Surveillance and Epidemiological Modelling at the Human–Animal–Environment Interface;
S3. Antimicrobial Resistance and Food Safety: A One Health Perspective.

Our goal is to provide an engaging platform that bridges research and practice, encourages collaboration across disciplines, and inspires innovative solutions to safeguard animal and human health alike.

We warmly invite the community to join us in shaping this exciting event. Together, let us engage in meaningful discussions, share innovative research, and address pressing global challenges at the intersection of veterinary science, public health, and environmental health.

For details on oral and poster submissions, please see the *Instructions for Authors* on the conference website.

Your support and contributions are essential to the success of this event, and we look forward to welcoming you to IOCVS 2026.



Prof. Dr. Patrick Butaye
Conference Chair

1. Department of Pathobiology,
Pharmacology and Zoological
Medicine, Faculty of Veterinary
Medicine, Ghent University,
Merelbeke, Belgium
2. Department of Infectious
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Jockey Club College of Veterinary
Medicine and Life Sciences, City
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veterinary sciences

Veterinary Sciences (ISSN 2306-7381) is an international and interdisciplinary scholarly open access journal. It publishes original research articles, reviews, communications, and short notes that are relevant to any field of veterinary sciences, including prevention, diagnosis and treatment of disease, disorder and injury in animals. There is no restriction on the maximum length of the papers. Our aim is to encourage scientists to publish their experimental and theoretical research in as much detail as possible. Full experimental details and/or method of study, must be provided for research articles. Articles submitted that involve subjecting animals to unnecessary pain or suffering will not be accepted, and all articles must be submitted with the necessary ethical approval (please refer to the Ethical Guidelines for more information).

Journal Webpage: <https://www.mdpi.com/journal/vetsci>

Session Chairs



Prof. Dr. Beibei Li

Shanghai Veterinary Research
Institute, Chinese Academy of
Agricultural Sciences,
Shanghai 200241, China



Prof. Dr. Chengming Wang

Department of Pathobiology,
College of Veterinary Medicine,
Auburn University,
Auburn, AL 36849, USA



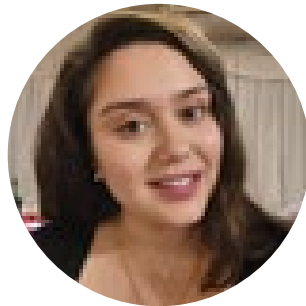
Prof. Dr. Francesco Mira

Department of Agricultural,
Food and Forest Science,
University of Palermo,
Palermo, Italy



Prof. Dr. Ruichao Li

Jiangsu Co-Innovation Center
for Prevention and Control of
Important Animal Infectious
Diseases and Zoonoses,
College of Veterinary Medicine,
Yangzhou University,
Yangzhou, China, Institute of
Comparative Medicine,
Yangzhou University, China



Prof. Dr. Vanessa Silva

University of Trás-os-Montes
and Alto Douro,
Vila Real, Portugal



Prof. Dr. Vincent L. Bels

Department of Veterinary
Medicine, Università degli Studi
di Teramo, 64100 Teramo, Italy

Plenary Speaker



Prof. Dr. Patrick Butaye

1. Department of Pathobiology, Pharmacology and Zoological Medicine, Faculty of Veterinary Medicine, Ghent University, Merelbeke, Belgium
2. Department of Infectious Diseases and Public Health, Jockey Club College of Veterinary Medicine and Life Sciences, City University of Hong Kong, Hong Kong, China

Professor Patrick Butaye is STEM-professor at City University's Jockey Club College of Veterinary Medicine and Life Sciences. Patrick graduated with a degree of Veterinary Medicine from Ghent University in 1994. In 2000, he obtained his PhD from the same university. Following this, he worked as Senior researcher and head of division at the former Veterinary and Agrochemical Research institute in Brussel until 2015. In 2006, he became Adjunct Professor at Ghent University and still holds that position. In 2015, he started a Professorship at Ross University School of Veterinary Medicine, whereafter in 2023, he started at City University of Hong Kong. He is also senior research fellow at the One Health Research Foundation, Miramar Florida. Patrick is or has been member of several national and international advisory committees and expert panels and has been ad hoc expert on a multitude of occasions. These include the European Food Safety Authority (EFSA), World Health Organization (Who), Pan American Health Organisation (PAHO), Food and Agriculture Organisation (FAO), Belgian Food safety authority (FAVV), ... He is member of the Executive board of the European Study Group on Veterinary Microbiology (ESGVM), as part of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID). He has been member of several project review panels worldwide. Patrick was in the organising and/or scientific committee of several national and international conferences, including but not limited to ARAE, ICOHAR, ECVI, Belgian Wildlife Disease Society,... Patrick is Editor in Chief of the journal Veterinary Sciences (MDPI), member of the Editorial Board of BMC Veterinary Research and Editor for PlosOne and Associate Editor for Frontiers in Antimicrobials, Resistance and Chemotherapy as well as Guest Editor for Frontiers in Veterinary Science.

Keynote Speakers



Prof. Dr. Chengming Wang

Department of Pathobiology, College of Veterinary Medicine, Auburn University, Auburn, AL 36849, USA

Dr. Chengming Wang is a Professor and Director of the Molecular Diagnostic Laboratory in the Department of Pathobiology at the Auburn University College of Veterinary Medicine, USA. He earned his DVM from Anhui Science & Technology University and an MS in Veterinary Preventive Medicine from Nanjing Agricultural University. He later received a PhD in Biomedical Sciences from Auburn University. Dr. Wang served as an Assistant Professor at the Ross University School of Veterinary Medicine, after which he joined the College of Veterinary Medicine at Yangzhou University as a Jiangsu Specially Appointed Professor. His research focuses on antimicrobial resistance, molecular diagnostics, and vector-borne pathogens of zoonotic importance. He has authored more than 190 peer-reviewed publications and has secured research funding from major federal agencies including the USDA, FDA, and NIH, as well as the National Natural Science Foundation of China.



Prof. Dr. Giovanni Franzo

Department of Animal Medicine, Production and Health (MAPS), University of Padua, Legnaro, Italy

Prof. Giovanni Franzo graduated in Veterinary Medicine from the University of Padua in 2011 and earned a PhD in Veterinary Sciences in 2015, focusing on viral molecular epidemiology. He also holds a Master's degree in Biostatistics and Clinical Epidemiology, with research on the application of machine learning to predict infectious disease outcomes in companion animals. Since completing his degree, he has worked on the development and validation of molecular diagnostic techniques and application of different sequencing approaches for viral characterization, microbiome analysis, and metagenomics, with a particular focus on data processing and interpretation. His research centers on the molecular evolution of animal viruses, leveraging biostatistics, bioinformatics, and artificial intelligence to investigate their epidemiology and dynamics and to improve disease control and diagnostics. He is a Diplomate of the European College of Veterinary Microbiology and has authored more than 200 scientific publications.



Prof. Dr. Leyi Wang

College of Veterinary Medicine, University of Illinois, Urbana, Illinois, USA

Dr. Leyi Wang is an Associate Professor of Veterinary Clinical Medicine and Virology Section Head of Veterinary Diagnostic Laboratory, College of Veterinary Medicine at University of Illinois at Urbana-Champaign. Dr. Wang has been in the clinical diagnostic virology field for 13 years. His research interests include diagnostic assay development and validation, animal coronavirus identification and surveillance, and new pathogen discovery. He has co-authored 120 peer reviewed articles and 8 book chapters and edited two versions of Animal Coronaviruses book. He is the co-inventor for two US patents. He serves as editorial boards for several journals including Associate Editor of Veterinary Vaccine, Academic Editor of Transboundary and Emerging Diseases, Advisory Board of Veterinary Microbiology, Editorial Board of Virologica Sinica, Viruses, COVID, Medicine, Scientific Reports, Journal of Veterinary Diagnostic Investigation, Animal Diseases, and World Journal of Virology. As an Editor-in-Chief, he is currently editing a book of Veterinary Virology of Domestic and Pet Animals in the series of Major Reference Works at Springer Nature. Dr. Wang's significant contribution to the field is that he participated in first identification of variant PEDV, deltacoronavirus in diarrhetic pigs, novel sparrow deltacoronavirus, new Bottlenose dolphin coronavirus, SARS-CoV-2 in zoo animals (tiger, snow leopard, fishing cat, binturong, coatimundi, and mandrill), bovine-like coronavirus in Indonesian tapir, bovine kobuvirus, and bovine boosepivirus.



Prof. Dr. Ruichao Li

Jiangsu Co-Innovation
Center for Prevention and
Control of Important
Animal Infectious Diseases
and Zoonoses, College of
Veterinary Medicine,
Yangzhou University,
Yangzhou, China; Institute
of Comparative Medicine,
Yangzhou University, China

Dr. Ruichao Li is a Professor and PhD supervisor at the College of Veterinary Medicine, Yangzhou University. He is a PI of the Jiangsu Collaborative Innovation Center for Prevention and Control of Important Animal Epidemics and Zoonoses. He received a PhD in Biological Science from The Hong Kong Polytechnic University. Currently, his research focuses on the development of genomic source-tracing technologies for drug-resistant bacteria and the research of their emergence and transmission mechanisms. Over the past years, he has published more than 200 SCI papers in prestigious journals such as Lancet Microbe, Nature Communications, Science Bulletin, ISME Journal, etc. He has been consecutively listed in Elsevier's World's Top 2% Scientists (2023-25) with papers cited more than 5000 times and has presided over more than 10 research projects. He currently serves as an editorial board member of Veterinary Sciences.

Invited Speakers



Dr. Marta Canuti

Department of Veterinary
and Animal Sciences,
University of Copenhagen,
1870 Frederiksberg, Denmark



Assoc. Prof. Mashkoor Mohsin

Institute of Microbiology,
University of Agriculture
Faisalabad,
Faisalabad, Pakistan



**Prof. Dr. Somporn
Techangamsuwan**

Center of Excellence in Animal
Virome and Diagnostic
Development (CE-AVDD),
Department of Pathology,
Faculty of Veterinary Science,
Chulalongkorn University,
Bangkok, Thailand



Dr. Xuemei Yang

School of Life Science,
Nanjing University, China



Prof. Dr. Yi Yang

College of Veterinary Medicine,
Yangzhou University,
Yangzhou, China

Rising Star Researcher Speakers



Assoc. Prof. Heng Li

School of Basic Medical
Sciences, Soochow University,
Jiangsu, China



Dr. Zsófia Lanszki

National Laboratory of Virology,
University of Pécs,
Pecs, Hungary

Program Overview

IOCVS 2026	Day 1 7 September 2026	Day 2 8 September 2026	Day 3 9 September 2026
Morning	08.30 (CEST) Session 3. Antimicrobial Resistance and Food Safety: A One Health Perspective (Part I)	09.00 (CEST) Session 2. Surveillance and Epidemiological Modelling at the Human–Animal–Environment Interface (Part I)	09.00 (CEST) Session 1. One Health Approaches to Emerging Zoonotic Threats (Part I)
Afternoon	13.00 (CEST) Cont. Session 3. Antimicrobial Resistance and Food Safety: A One Health Perspective (Part II)	14.00 (CEST) Cont. Session 2. Surveillance and Epidemiological Modelling at the Human–Animal–Environment Interface (Part II)	15.00 (CEST) Cont. Session 1. One Health Approaches to Emerging Zoonotic Threats (Part II)

IOCVS Program

7th September 2026 (Monday)

Session 3. Antimicrobial Resistance and Food Safety: A One Health Perspective (Part I)

Time: 8:30 (CEST) / 2:30 (EDT, New York) / 14:30 (CST, Asia, Beijing)

Time In CEST	Speaker	Title
8:30–8:35	Prof. Dr. Patrick Butaye Welcome from the Event Chair	
8:35–8:40	Prof. Dr. Beibei Li Welcome from the Session Chair	
8:40–9:20	Prof. Dr. Patrick Butaye Plenary Speaker	Antimicrobial resistance and One Health, what can we conclude about the past and current status?
9:20–9:40	Dr. Xuemei Yang Invited Speaker	Evolutionary Mechanism and Antibacterial Strategies of Highly Virulent and Resistant <i>Klebsiella pneumoniae</i>
9:40–9:55	Assoc. Prof. Heng Li Rising Star Researcher Speaker	Pork, Pathogens, and Globalization: How Modern Pig Farming Fuels the International Transmission of <i>Salmonella</i>
9:55–10:10	Muhammad Shoalb Oral Speaker	Global genomic analysis revealed first emergence of mcr-10.1 carrying <i>Enterobacter cloacae</i> ST1 clone from retail pork in Jiangsu, China
10:10–10:25	ShuHui Zhang Oral Speaker	Crisaborole resensitizes KPC-producing Gram-negative bacteria to carbapenems
10:25–10:40	Zulquernain Halder Oral Speaker	Beyond common serotypes: Genomic characterization of diverse avian pathogenic <i>Escherichia coli</i> associated with broiler colibacillosis in Pakistan
10:40–10:55	Romay da Costa Oral Speaker	Antibacterial, antioxidant and hemolytic properties of <i>Prunus persica</i> leaf extracts against <i>Staphylococcus</i> isolates from dogs of Angola
10:55–11:10	GiIndya Bhagya Lakshmi Oral Speaker	Cracking the Shell: Genomic Insights into Antimicrobial-Resistant <i>Escherichia coli</i> on Retail Eggs in the United Arab Emirates
11:10–11:25	Mulugeta Bekele Oral Speaker	Integrating AI, Machine Learning, and Geospatial Technologies for One Health Management of Emerging Zoonoses: Distributed Surveillance and Communication Solutions for Antimicrobial Resistance and Food Safety

Session 3. Antimicrobial Resistance and Food Safety: A One Health Perspective (Part II)

Time: 13:00 (CEST) / 7:00 (EDT, New York) / 19:00 (CST, Asia, Beijing)

Time In CEST	Speaker	Title
13:00–13:05	Prof. Dr. Ruichao Li Welcome from the Session Chair	
13:05–13:35	Prof. Dr. Ruichao Li Keynote Speaker	Transmission and Evolutionary Characteristics of Carbapenem-Resistant <i>Enterobacteriaceae</i> from the One Health Perspective
13:35–13:55	Assoc. Prof. Mashkoor Mohsin Invited Speaker	Antimicrobial Usage and Resistance Dynamics in Commercial Poultry Farms in Pakistan
13:55–14:10	Joab de Mello Oliveira Oral Speaker	Genotypic and Phenotypic Characterization of <i>Listeria Monocytogenes</i> Reveals Challenges to Sanitization Efficacy in Brazilian Food Industries
14:10–14:25	Aman Ullah Khan Oral Speaker	Comparative Phytochemical Profiling and Therapeutic Efficacy of <i>Syzygium aromaticum</i> and <i>Cinnamomum cassia</i> Extracts against Colistin-Resistant <i>Escherichia coli</i> of Poultry Origin

14:25–14:40	Elisana Julek Oral Speaker	Environmental Variation in the Physicochemical and Microbiological Profile of Melipona mondury Honey in Eastern Paraná
14:40–14:55	Muhammad Tahir Khan Oral Speaker	Molecular Epidemiology and Dissemination of Extended-Spectrum Beta-Lactamases (ESBL)-producing Escherichia coli of European Wildlife: A Systematic Review and Meta-Analysis
14:55–15:10	Catarina Freitas Oral Speaker	Genomic Characterization of Multidrug-Resistance mecC-MRSA in Portuguese Rabbit Production
15:10–15:35	Flash Poster Presentation (5 mins per person)	Yuting Ma Prevalence, Antimicrobial Resistance, and Genomic Analysis of Yersinia enterocolitica from Livestock Farms in Qinghai, China Caio Vidal Detection of Antibiotic Residues in Raw Bovine Milk and Environmental Risks Associated with Improper Disposal: A One Health Approach Mahdis Mahdavi Molecular Detection, Antimicrobial Resistance Profiling, and Genetic Diversity of Campylobacter jejuni and Campylobacter coli Isolated from Urban Backyard Poultry, Companion Animals, and Environmental Samples: A One Health Approach in Peri-Urban Regions Mohammad Manian High Prevalence of Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Producing Escherichia coli in Equine Uterine Infections: A One Health Concern Margarita Terentjeva Antimicrobial resistance in Salmonella Enteritidis and Typhimurium isolates from laying hens in Latvia

8th September 2026 (Tuesday)

Session 2. Surveillance and Epidemiological Modelling at the Human-Animal-Environment Interface (Part I)

Time: 9:00 (CEST) | 3:00 (EDT, New York) | 15:00 (CST, Asia, Beijing)

Time in CEST	Speaker	Title
9:00–9:05	Prof. Dr. Francesco Mira Welcome from the Session Chair	
9:05–9:25	Prof. Dr. Somporn Techangamsuwan Invited Speaker	Following Viral Fingerprints: How Wildlife Pathology Reveals Emerging Disease Threats
9:25–9:55	Prof. Dr. Giovanni Franzo Keynote Speaker	What Viral Genomes Reveal: Decoding the Epidemiology and Evolution of Animal Viruses
9:55–10:10	Zhou Ziyao Oral Speaker	Analysis of Viruses Carried by Wild Animal Feces in the Wolong Nature Reserve
10:10–10:25	Dr. RENU Oral Speaker	Emerging and Re-Emerging Bluetongue Virus Serotypes in Indian Ruminants: A Systematic Review
10:25–10:40	Abdul Kabir Oral Speaker	Knowledge, Attitudes, and Practices of Livestock Stakeholders for Risk-Based Control of Peste des Petits Ruminants in the Pakistan-Afghanistan Transboundary Region
10:40–10:55	Md. Nazmul Islam Oral Speaker	Prevalence of Neospora caninum Antibodies and Associated Risk Factors in Dairy Herds in Bangladesh
10:55–11:10	Reza Fayaz Oral Speaker	Epidemiological Status of Linguatula serrata Infection among Domestic Ruminants in Northwestern Iran: A Systematic Review and Meta-analysis
11:10–11:25	Parisa Ghazanfaripannah Oral Speaker	Animal Reservoir Hosts of Zoonotic Visceral Leishmaniasis in Iran: A Systematic Review and Meta-Analysis
11:25–11:40	Adjlane Nouredine Oral Speaker	Surveillance of Varroa destructor in Honey Bees: A One Health Approach and Epidemiological Modelling
11:40–11:55	Moses Adriko Oral Speaker	Spatial-Temporal Risk Mapping and Epidemiological Modeling of Bovine Fascioliasis in Uganda: A One Health Surveillance Framework at the Livestock, Snail, and Water Interface (IOCVS 2026)

Session 2. Surveillance and Epidemiological Modelling at the Human-Animal-Environment Interface (Part II)

Time: 14:00 (CEST) | 8:00 (EDT, New York) | 20:00 (CST, Asia, Beijing)

Time in CEST	Speaker	Title
14:00–14:05	Dr. Giovanna Liguori Welcome from the Session Host	
14:05–14:25	Dr. Marta Canuti Invited Speaker	Amdoparvoviruses of terrestrial carnivores: virus evolution and transmission patterns between and within wildlife and farms
14:25–14:40	Dr. Zsófia Lanszki Rising Star Researcher Speaker	Genome-scale evolution of canine distemper virus
14:40–14:55	Roberto Bava Oral Speaker	The peregrine falcon (Falco peregrinus) as a sentinel species for environmental contamination at the human-animal-environment interface
14:55–15:10	Valeria Blanda Oral Speaker	Zoonotic pathogens in fallow deer (Dama dama) from Sicily (Southern Italy): implications for wildlife-livestock-human interface
15:10–15:25	Joab de Mello Oliveira Oral Speaker	Machine Learning for Microbiological Risk Assessment of Animal-Derived Foods: A Systematic Review Focusing on Predictive Model Validation
15:25–15:40	Muhammad Numan Oral Speaker	Molecular profile and B-cell epitope mapping of trypsin inhibitor-like proteins of Hyalomma anatolicum and Rhipicephalus linnaei as potential anti-tick vaccine candidates

15:40–15:55	Polya Avramova Oral Speaker	Environmental and organ distribution of copper in Cervids from regions with different levels of human activity
15:55–16:10	Sunday Olaogun Oral Speaker	Clinical, haematological and biochemical features associated with foot rot infection in sheep in Oyo State, Nigeria
16:10–16:25	Martina Karasová Oral Speaker	Epidemiological Surveillance of Babesia gibsoni in Slovakia: Transmission Routes and Modelling Risk in High-Risk Dog Breeds
16:25–16:50	Flash Poster Presentation (5 mins per person)	Mikulas Kálnoky Evaluation of a Mobile Flow Cytometer as a Rapid Tool for Environmental Hygiene Monitoring in Broiler Farms Mohammad Derogar Jahromi Dogs as Sentinels for Emerging Human Infectious Diseases: A Systematic Review of One Health Surveillance Opportunities Parichehr Ebrahimi Shahabadi The One Health role of interplay between canine parvovirus and Gram-negative bacterial translocation in sepsis and multi-organ failure in dogs Tamas Petrovic Veterinary Abortion Surveillance as an Epidemiological Tool: A Seven-Year Study in South Bačka and Srem, Serbia (2019–2026) Gianmarco Ferrara Detection of PBFDV, APyV and AdV in captive pet birds in Sicily, Italy

9th September 2026 (Wednesday)

Session 1. One Health Approaches to Emerging Zoonotic Threats (Part I)

Time: 9:00 (CEST) | 3:00 (EDT, New York) | 15:00 (CST, Asia, Beijing)

Time in CEST	Speaker	Title
9:00–9:05	Prof. Dr. Vittorio Sarchese Welcome from the Session Chair	
9:05–9:25	Prof. Dr. Yi Yang Invited Speaker	Critical Amino Acids Play a Regulatory Role in Bovine Leukemia Virus Replication
9:25–9:40	Syeda Hamid Oral Speaker	Antimicrobial Resistance in Pathogenic Bacteria from Endangered Fish: A One Health Approach to Emerging Zoonotic Threats
9:40–9:55	Dikshya Paudel Oral Speaker	Seroprevalence of Avian Influenza Viruses (H5N1 and H9N2) Among Poultry Workers and Live Bird Market Vendors in Asia: A Systematic Review and Meta-Analysis
9:55–10:10	Touran Tahmasbi Oral Speaker	Hematologic Mycoplasma Infection in Four Persian and British Cats: Clinical and Laboratory Findings
10:10–10:25	Debel EFA Oral Speaker	Community knowledge, attitudes and practices related to cystic echinococcosis in Ethiopia: implication for control
10:25–10:40	Mustafa Sadek Oral Speaker	Prevalence and characterisation of ESBL- and MCR-1-harboring multidrug-resistant Escherichia coli in raw milk cheese and chicken carcasses in Egypt: Algal Extracts as a Potential Control Strategy
10:40–10:55	Paola Galluzzo Oral Speaker	Characterisation of the microbiome and resistome in the loggerhead sea turtle (Caretta caretta) in the Mediterranean basin
10:55–11:10	Adriana Cuevas Domínguez Oral Speaker	Integrated approach to Brucella ceti infection in stranded Mediterranean dolphins
11:10–11:25	Gabrielle Beckford Oral Speaker	Evaluating Veterinary Stakeholder Readiness for Standardized Clinical Terminologies to Improve Surveillance and One Health Collaboration

Session 1. One Health Approaches to Emerging Zoonotic Threats (Part II)

Time: 15:00 (CEST) | 9:00 (EDT, New York) | 21:00 (CST, Asia, Beijing)

Time in CEST	Speaker	Title
15:00–15:05	Prof. Dr. Chengming Wang Welcome from the Session Chair	
15:05–15:35	Prof. Dr. Chengming Wang Keynote Speaker	The Hidden Impact of Chlamydia spp.: A One Health Perspective on Human and Animal Health
15:35–16:05	Prof. Dr. Leyi Wang Keynote Speaker	Detection and Characterization of Zoonotic Pathogen Potential Using Traditional Diagnostic Approaches with State-of-the-Art Technology
16:05–16:20	Gil Firmino Sanfins Couto Oral Speaker	Illegal wildlife trade and zoonotic spillover risk at human–animal–environment interfaces: a systematic review
16:20–16:35	Marta Arias-Mosquera Oral Speaker	Protective assessment of oral immunization against genotype II using a new ASFV live attenuated vaccine prototype in wild boar
16:35–16:50	Tomas García Ramírez Oral Speaker	Maternal, colostrum management, and environmental factors associated with clinical signs of neonatal disease in calves from Yolombó, Antioquia, Colombia: a pilot study with a One Health approach
16:50–17:05	Valeria Rodríguez Villavicencio Oral Speaker	Antimicrobial resistance in horses in Mexico from a One Health perspective
17:05–17:20	Blítrus Inuwa Oral Speaker	Active Circulation of Middle East Respiratory Syndrome Coronavirus at the Camel-Human-Environment

		Interface in Nigeria: Evidence from One Health Surveillance
17:20–17:45	Flash Poster Presentation (5 mins per person)	Ewelina Szacawa Detection of Bovine Tuberculosis in Animals Using Interferon-Gamma Release Assays and Its Public Health Relevance in the One Health Approach Farshad Shahkhah Toxoplasma gondii in Feline Populations: A Systematic Review of Hematological and Biochemical Markers with a One Health Perspective on Zoonotic Risk Assessment Nate Brown Surveillance for influenza A virus H5-specific antibodies in Canada Geese (Branta canadensis) in Pennsylvania Marija Ivaškienė Development and Evaluation of Organic Acid-Based Hydrogels for Antifungal Treatment of Companion Animal Dermatophytes: A One Health Perspective Philippe Sessou Epidemiological study of canine and human rabies in southern Benin: A retrospective analysis (2012–2017)

Poster List

Submission ID	Author	Title
Session 1. One Health Approaches to Emerging Zoonotic Threats		
Sciforum-194420	Asmaa Nasr; Mustafa Ozan Atasoy; Mohammed A. Rohaim; Waqas Khokhar; Nikki Copeland; Christopher C. Broder; Muhammad Munir*	Effectiveness of N6-methyladenosine (m6A) and Innate Immunity as Barriers to the Emergence of Cedar Henipavirus in Roussettus aegyptiacus Cells
Sciforum-194469	Ewelina Szacawa*; Nina Kozieł; Monika Krajewska-Wędzina; Agnieszka Kuś; Krzysztof Szulowski	Detection of Bovine Tuberculosis in Animals Using Interferon-Gamma Release Assays and Its Public Health Relevance in the One Health Approach
Sciforum-188046	Francesca Gucciardi*; Antonina princiotta; Silvia Scibetta; Valeria Blanda; Paola Galluzzo; Sergio Migliore; Ettore Napoli; Santina Di Bella; Annalisa Guercio; Giuseppa Purpari	HEPATITIS E VIRUS IN WILDLIFE: AN EMERGING HEALTH RISK
Sciforum-194320	Haniyeh Amirinezhad; Sina Rouzmehr; Arya Heidari; Marziyeh Saki; Farshad Shahkhah*	Toxoplasma gondii in Feline Populations: A Systematic Review of Hematological and Biochemical Markers with a One Health Perspective on Zoonotic Risk Assessment
Sciforum-194670	Kimia Azami; Soroush Partovi Moghaddam*	One Health Pharmacotherapy of Zoonotic Giardiasis in Dogs and Cats: A Systematic Review
Sciforum-194258	Mahsa Tavangar*; Seyyed Sattar Tohidifar; Masoud Ghorbanpoor; Mahdi Salimi	Salmonella Surveillance in Wild Raptors: Evidence from Wildlife Rehabilitation Centers in Iran
Sciforum-185600	Marija Ivaškienė*; Smiltė Verbickaitė; Zoja Miknienė; Modestas Žilius	Development and Evaluation of Organic Acid-Based Hydrogels for Antifungal Treatment of Companion Animal Dermatomycoses: A One Health Perspective
Sciforum-194621	mary jananeh*; Touran Tahmasbi; Leyla Roshani; Samin Shariati majd; Fazel Shirzad	SUCCESSFUL GS ANTIVIRAL THERAPY IN A JUVENILE CAT WITH NEUROLOGICAL AND OCULAR FELINE INFECTIOUS PERITONITIS: A CASE REPORT
Sciforum-190119	Maryam Kermanshahian*; Tara Marzban	Artificial Intelligence for Chest Radiography in Tuberculosis Detection Across Humans and Animals: A Systematic Review of One Health Diagnostic Applications
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Sciforum-189127	Saba Asghari Bejestani; Hannah Behtaji; Mohammad Shahraki*	A Systematic Review of Methicillin-Resistant Staphylococcus aureus (MRSA) Surgical Site Infections in Companion Animals and Their Human Contacts: A One Health Perspective
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Sciforum-187625	Sakineh Khanamani Falihatipour; Atefeh - Heidar ammameh*	Plant Secondary Metabolites as Adjuvants to Restore Tetracycline Efficacy Against Multidrug-Resistant Zoonotic Escherichia coli
Sciforum-194181	Sakineh Khanamani Falihatipour; Atefeh - Heidar ammameh*	Florfenicol Pharmacokinetics and Pharmacodynamics in Food-Producing Animals: A Systematic Review
Sciforum-188097	Lidia Pansera, Irene Ricci, Caterina Ellen Culoma, Ettore Napoli	Systematic Review on the Use of Natural Products for Ectoparasite Control in Ruminants

Session 1. One Health Approaches to Emerging Zoonotic Threats

sciforum-192116: *De Novo* Discovery of Dual Hantavirus G_c/G_n Inhibitors Using a General-Purpose Generative AI

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Background: Hantaviruses cause severe zoonotic hemorrhagic fevers with limited treatment options. Targeting the viral envelope glycoproteins G_c and G_n remains a priority. This study integrates a general-purpose generative AI (DeepSeek) with molecular docking to design and optimize novel ligands aiming for dual inhibition.

Methods: Novel SMILES strings were generated using DeepSeek, filtered for Lipinski compliance and low toxicity (SwissADME), and checked for novelty via PubChem. SMILES were converted to 3D structures using the SMILES to SDF/Mol Online Converter (FYIcenter.com). Ligands were docked into Hantavirus G_c (PDB: 5LJZ) and G_n (PDB: 5OPG) using Schrödinger Glide XP, with ribavirin and favipiravir as controls. Initial docking scores were inferior to controls, prompting AI-guided SMILES refinement and re-docking.

Results: Against G_c, the best refined ligand (FYI-CoreB-2) achieved a docking score of -5.251, outperforming favipiravir (-4.262) and ribavirin (-3.596). Against G_n, FYI-CoreB-3 scored -9.220, markedly superior to both controls. Several CoreB and CoreA variants showed enhanced binding relative to reference drugs, confirming successful refinement.

Conclusion: We provide preliminary evidence that general-purpose generative AIs like DeepSeek, alongside specialized drug-design AIs, can be effectively used for de novo inhibitor design. Our workflow produced novel ligands with improved predicted binding affinity to both Hantavirus G_c and G_n, achieving dual-target inhibition and yielding promising candidates for in vitro validation.



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sciforum-194258: *Salmonella* Surveillance in Wild Raptors: Evidence from Wildlife Rehabilitation Centers in Iran

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Introduction: *Salmonella* is a leading zoonotic pathogen worldwide. Wildlife species can act as silent reservoirs, disseminating the pathogen through environmental contamination and posing indirect risks to livestock and public health. Among wildlife, raptors are particularly valuable bio-sentinels; their position as apex predators and high spatial mobility expose them to pathogens across multiple trophic levels. Despite their epidemiological relevance, data on raptor-associated *Salmonella* in Iran remain scarce. This study investigated *Salmonella* occurrence in wild raptors admitted to wildlife rehabilitation centers in Isfahan and Chaharmahal va Bakhtiari provinces, Iran.

Methods: A total of 68 samples (59 cloacal swabs and 9 fecal samples) were collected from 59 raptors of multiple species upon admission, before any feeding or therapeutic intervention. All samples underwent bacterial culture following standard *Salmonella* isolation protocols: pre-enrichment in TSB, parallel selective enrichment in Selenite F and RVS broths, and plating on XLD agar. Suspicious colonies were subcultured on nutrient agar to screen for swarming motility before biochemical confirmation (MRVP, urease, SIM, Simon's citrate, and TSI). A subset of 50 samples was additionally analyzed by PCR to enhance diagnostic sensitivity.

Results: Four suspicious colonies were recovered across all 68 cultured samples; none fulfilled the biochemical criteria for *Salmonella*. Among the 50 samples analyzed by PCR, one fecal sample from a Golden Eagle (*Aquila chrysaetos*) tested positive, while the paired cloacal swab from the same individual was negative, indicating a PCR-based *Salmonella* occurrence of 2%.

Conclusions: These findings suggest that culture alone may underestimate *Salmonella* occurrence in wildlife, underscoring the value of complementary molecular detection in surveillance programs. Furthermore, fecal samples appeared more sensitive than cloacal swabs in *Salmonella* detection. Although overall occurrence was low, *Salmonella* detection in a Golden Eagle, an apex predator, signals active pathogen circulation in the ecosystem and highlights a zoonotic risk at the wildlife–environment interface, reinforcing the value of raptor-based One Health surveillance.



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sciforum-194320: *Toxoplasma gondii* in Feline Populations: A Systematic Review of Hematological and Biochemical Markers with a One Health Perspective on Zoonotic Risk Assessment

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Introduction: *Toxoplasma gondii* is an obligate intracellular zoonotic parasite, with felines as its definitive host, playing a pivotal role in transmission to humans and other animals. This systematic review aimed to investigate the associations between hematological and serum biochemical markers in cats infected with *Toxoplasma* and to assess their implications for public health.

Methods: A systematic search was conducted in accordance with PRISMA guidelines across PubMed, Scopus, Web of Science, and Google Scholar for studies published between January 2020 and December 2025. Inclusion criteria included observational, case-control, and cross-sectional studies that examined hematological and biochemical parameters in cats with specific anti-*Toxoplasma* antibodies (IgG and IgM). Data on complete blood count, biochemical profile, and inflammatory factors were extracted.

Results: Of the 1,324 studies identified, 38 met the inclusion criteria. The synthesized findings indicate that cats with acute *Toxoplasma* infection (IgM-positive) frequently presented with lymphopenia (reported in 65% of cases), mild neutrophilia (42%), and thrombocytopenia (38%). In the chronic phase, relative lymphocytosis and mild eosinophilia were the most commonly observed hematological changes. Biochemically, moderate elevations in liver enzymes (ALT and AST) were recorded in 47% of cases, and increased total protein (attributable to hyperglobulinemia) in 35% of cases. However, due to the inherent heterogeneity among the included observational studies, these pooled percentages should be interpreted with caution and are presented as descriptive summaries rather than definitive meta-analytical estimates.

Conclusion: From a One Health perspective, integration of routine hematological and biochemical markers with serological status may offer valuable supportive information for the clinical monitoring of feline toxoplasmosis. Nevertheless, the available evidence does not conclusively support the use of these nonspecific markers as a direct early warning system for predicting oocyst shedding, which primarily occurs during the acute phase of primary infection and is not directly determined by IgG titers or secondary hematological changes.



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sciforum-194281: A Systematic Review of the Molecular Epidemiology, Phylodynamics, Genetic Diversification, and Regional Dissemination of GI-23 Infectious Bronchitis Virus in Iran and the Middle East

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Introduction: Infectious bronchitis virus (IBV) remains one of the most challenging viral pathogens impacting the poultry industry worldwide. Among circulating genotypes, GI-23 (Variant 2/IS-1494-like) has become the predominant lineage in Iran and the Middle East. Its ongoing circulation, genetic diversification and variation raises its regional dissemination risks and vaccine ineffectiveness problems.

Methods: This systematic review was conducted according to PRISMA guidelines to evaluate the Relevant studies published between 2015 and 2025 were retrieved from PubMed, Scopus, Web of Science, and Google Scholar. Studies reporting molecular characterization, sequencing, phylogenetic analyses, recombination, or vaccine-related findings of GI-23 IBV in Iran and Middle Eastern countries were included and systematically analyzed.

Results: This review demonstrated that GI-23 considers as a dominant IBV lineage in the Middle East for nearly two decades. In Iran, the prevalence of GI-23 reached nearly 70% among characterized isolates between 2015 and 2017. Partial S1 gene analyses revealed high nucleotide identities (99.31–100%) among Iranian and Middle Eastern GI-23 isolates. Eastern GI-23 isolates, supporting ongoing transboundary circulation. Otherwise, phylogenetic studies identified substantial genetic heterogeneity within the lineage, with approximately 11–13% divergence between major Variant-1 and Variant-2 groups. Iranian isolates were predominantly assigned to the GI-23.2 sublineage and shared 95–97% similarity with previously reported Iranian variants. Molecular evolutionary analyses estimated a substitution rate of approximately 4.3×10^{-3} substitutions/site/year. Multiple amino acid substitutions and insertion/deletion events within S1 hypervariable regions were demonstrated, including 7–11 substitutions in HVR3 of Variant-2 strains. Recombination involving GI-23, GI-13, and GI-19 lineages was also reported. Circulating Iranian GI-23 strains showed only 82.64% nucleotide identity with H120 and 4/91 vaccine strains.

Conclusions: High nucleotide identity among Iranian and Middle Eastern GI-23 isolates suggests a close epidemiological and genetic relationship. Continuous molecular surveillance and genotype-matched vaccination strategies is essential for disease control in the Middle East.



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sciforum-194378: Active Circulation of Middle East Respiratory Syndrome Coronavirus at the Camel-Human-Environment Interface in Nigeria: Evidence from One Health Surveillance

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Background

Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is one of the coronaviruses of greatest concern for global public health. MERS-CoV remains on the World Health Organization watch list because of its pandemic potential. The primary reservoir for MERS-CoV is the dromedary camel (*Camelus dromedarius*), with over 80% of the global population residing in Africa, yet surveillance remains critically limited. With growing human-animal interactions and the rising demand for camel meat and dairy products, understanding the zoonotic exposure risks, particularly among high-risk occupational groups, is critical for global health security. This study, therefore, investigated MERS-CoV exposure and its active circulation at the animal-human-environment interface in Nigeria, using One Health surveillance.

Methods

Between 2024 and 2025, nasopharyngeal swabs and blood samples (n = 479 each) were collected from dromedary camels at slaughter. Plasma samples (n = 272) were collected from abattoir workers. Environmental swabs (n = 38) were collected from abattoir hard surfaces. Serum and plasma samples were screened for MERS-CoV antibodies using camel- and human-specific commercial ELISA and virus neutralization tests (VNT). Swab samples were screened by RT-qPCR to detect MERS-CoV RNA, followed by whole-genome sequencing of positive samples.

Results

Evidence of MERS-CoV was detected across animal, human, and environmental samples. Among camels, seropositivity was 75.78%, with 91.33% (137/150) of the randomly selected samples confirmed by VNT. Viral RNA was detected in 13.9% of camel samples. In abattoir workers, seropositivity was 9.56%, with viral RNA in 2.20% of plasma samples. Environmental testing showed 2.63% MERS-CoV RNA from abattoir surfaces. Whole-genome sequencing positioned Nigerian MERS-CoV strains with those from Ethiopia and others in Clade C.

Conclusion

In Nigeria, MERS-CoV subclinical circulation is under-reported. This finding provides evidence of asymptomatic human infection and environmental contamination likely from camel saliva or excretions, and points to ongoing silent spillover. This highlights the need for strengthened biosecurity measures for camel handlers, continued genomic surveillance, and expanded integrated surveillance in the livestock population.



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sciforum-188130: Beyond the Eye: *Sarcocystis* Infections in Lithuanian Cattle (*Bos taurus*) and Horses (*Equus ferus caballus*)

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Sarcocystis are protozoan parasites with a mandatory two-host life cycle involving carnivores as definitive hosts and herbivorous or omnivorous animals as intermediate hosts. These parasites are of considerable veterinary and public health importance due to their widespread occurrence in livestock and their relevance to food safety. In cattle, three species are recognized as zoonotic or potentially foodborne (*Sarcocystis hominis*, *Sarcocystis heydorni*, and *Sarcocystis bovifelis*), and there have been sporadic reports of human food poisoning cases suspected to be associated with consumption of infected meat, including cases speculated to involve *Sarcocystis bertrami* from equine sources.

The present study aimed to investigate the occurrence and species diversity of *Sarcocystis* in cattle and horses in Lithuania using both microscopic and molecular approaches. Tissue samples were collected from cattle heart and diaphragm muscles, and from horses' masticatory, cheek, and masseter muscles. All samples were examined microscopically for the presence of sarcocysts, and molecular analyses were performed to identify species richness within each investigated host.

Microscopic examination revealed the presence of sarcocysts in multiple muscle tissues of both host species. Molecular characterization confirmed the presence of distinct *Sarcocystis* species. In horses, *Sarcocystis bertrami* was identified, while in cattle, *Sarcocystis cruzi* and *Sarcocystis bovifelis* were detected.

These findings contribute to the understanding of *Sarcocystis* distribution in Lithuanian livestock and highlight the importance of combined microscopic and molecular diagnostic approaches for accurate species identification. The results also provide relevant data for veterinary parasitology and food safety.



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sciforum-187741: Bridging the Knowledge–Practice Gap in Tick Prevention: A One Health based Study among Companion Animal Owners in Kerala, India

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Background:

Tick-borne diseases represent an increasing threat at the human–animal–environment interface, particularly in tropical regions such as Kerala, India. Despite close human–pet interactions, evidence on how pet owners perceive and respond to tick-borne risks remains limited. This study adopted a One Health–oriented Knowledge, Attitude, and Practice (KAP) approach to identify gaps that may undermine effective tick control.

Methods:

A cross-sectional survey was conducted among 405 pet animal owners using a structured, pre-validated questionnaire. KAP scores were computed using standardized criteria. Associations between socio-demographic variables, veterinary engagement, and preventive practices were examined using chi-square tests and multivariable logistic regression.

Results:

While 58.3% of respondents demonstrated good knowledge and 76.0% expressed positive attitudes toward tick control and zoonotic risk, only 37.0% reported good preventive practices. Awareness of zoonotic transmission was high (82.1%); however, misconceptions regarding year-round tick occurrence persisted. A knowledge–practice gap was identified. Receipt of information from veterinarians emerged as the strongest predictor of good practices (adjusted OR = 2.71; p 0.001), exceeding the influence of education and attitudes. Respondents showed strong support (88.1%) for inter-sectoral collaboration, reflecting receptiveness toward One Health strategies.

Conclusions:

This study indicates that high awareness and favorable attitudes do not translate into effective tick-prevention behavior. The findings emphasize the role of veterinarians as behavioral change agents and highlight the need to move beyond awareness-based interventions toward practice-focused strategies. By demonstrating a knowledge–practice disconnect in high-risk tropical setting, this study provides evidence to support integrated tick-borne disease control policies.



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sciforum-193154: Clinical Assessment and Outcomes of Wildlife Rescued during Reservoir Filling of a Small Hydropower Plant in Paraná, Brazil

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Reservoir filling for small hydropower plants (SHPs) leads to rapid environmental changes that directly affect wildlife, increasing the demand for rescue and clinical intervention. This study aimed to describe the clinical assessment and management of wild animals rescued from the water, adrift during the filling of an SHP reservoir in the state of Paraná, Brazil, emphasizing species distribution, clinical findings, and outcomes. Rescues were conducted using a support boat, and animals were transported to a field station for triage and evaluation. A total of 100 animals were examined, including reptiles from the families Colubridae, Gekkonidae, and Amphisbaenidae, and one bird from the family Hirundinidae. Clinical evaluation included palpation of the coelomic cavity and spine, body condition scoring, inspection for injuries, assessment of mucous membranes and cloaca, and measurement of respiratory rate and, when feasible, heart rate (via Doppler in reptiles and auscultation in the avian patient). Neurological assessment in reptiles was based on the righting reflex. In the bird, it included posture, balance, and response to stimuli. The avian patient required tranquilization due to dyspnea during handling. Among the rescued animals, reptiles accounted for 99% of cases, with a predominance of amphisbaenians, particularly *Leposternon microcephalum* (69%) and *Amphisbaena cf. mertensii* (26%), while *Leptotyphlops sp.*, *Oxyrrhopus guibei*, *Erythrolamprus poecilogyrus*, and *Hemidactylus mabouia* each represented 1% of cases. The only avian species recorded was *Pygochelidon cyanoleuca*. Most animals were in good clinical condition, with no severe abnormalities, and the righting reflex was preserved in the majority of reptiles, indicating adequate neurological function. Thermal support using heating pads was essential for stabilization, especially in reptiles presenting lethargy or hypothermia. All animals showed favorable recovery and were successfully released. These findings highlight the effectiveness of immediate clinical assessment and supportive care in wildlife rescue operations and reinforce the importance of standardized protocols in mitigating the impacts of environmental disturbances.



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sciforum-189039: One Health-Based Modelling of H5N1 Clade 2.3.4.4b Spillover Risk in Urban and Peri-Urban Interfaces

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Avian Influenza H5N1 clade 2.3.4.4b has caused widespread global outbreaks since 2020, with increasing transmission to mammalian hosts, including dairy cattle, domestic cats, and wildlife species. Urban and peri-urban environments may act as important interfaces for viral spread because of dense human and animal populations, backyard poultry keeping, and expanding wildlife contact. This study applied a One Health framework to assess spillover risk and develop an integrated epidemiological prediction model.

A systematic review was conducted according to PRISMA guidelines using data retrieved from PubMed, Web of Science, Scopus, GISAID, WOA H WAHIS, and WHO databases between 2020 and 2026. Integrated datasets included surveillance records, genomic sequences, climate variables (ERA5), land-use information (Copernicus), and wastewater monitoring reports. A hybrid framework integrating compartmental transmission modelling with machine learning-based hotspot prediction was developed to evaluate spillover dynamics and early warning capacity. Model performance was assessed using k-fold cross-validation and retrospective comparison with outbreaks reported during 2024–2025.

Peri-urban areas with high backyard poultry density (>5 units/ha) and proximity to water bodies (1.5 km) were significantly associated with increased spillover risk (OR = 3.87; 95% CI: 2.64–5.68; $p = 0.001$). Integration of wastewater and community-based surveillance data improved predictive performance (AUC = 0.91; sensitivity = 87%) compared with conventional surveillance approaches. The framework also showed potential to identify high-risk periods approximately 5–7 weeks earlier than routine reporting systems. Climate variability and land-use change were identified as major predictors of viral persistence and spillover probability.

These findings support the importance of integrated One Health surveillance strategies for improving outbreak preparedness, early warning capacity, and risk mitigation in urban and peri-urban settings.



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sciforum-194621: SUCCESSFUL GS ANTIVIRAL THERAPY IN A JUVENILE CAT WITH NEUROLOGICAL AND OCULAR FELINE INFECTIOUS PERITONITIS: A CASE REPORT

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Introduction: Feline infectious peritonitis (FIP) is a fatal, multisystemic disease primarily affecting young cats, often presenting with neurological and ocular manifestations. **Background & Objectives:** Cases involving the nervous and ocular systems historically carry a poor prognosis due to limited treatment options. This report aims to describe the clinical presentation, diagnostic findings, and successful management of neurological and ocular FIP using GS antiviral therapy in a juvenile cat. **Methods:** A 5-month-old spayed female domestic shorthair cat presented with periorbital icterus and a “sitting with open pelvis” posture. Abdominal ultrasonography revealed free fluid, while laboratory tests showed a markedly reduced albumin-to-globulin ratio of 0.1. Neurological examination identified signs consistent with central nervous system involvement. The cat was treated with GS antiviral therapy and monitored over 31 days, with repeated clinical and laboratory assessments. **Results:** Following treatment, neurological deficits and ocular abnormalities gradually resolved and were completely absent by day 31. The cat regained normal behavior, activity, and overall health. No adverse effects were observed during therapy. Follow-up confirmed sustained recovery, highlighting the potential of GS antiviral therapy for severe FIP cases. **Conclusion:** GS antiviral therapy can achieve complete recovery in young cats with neurological and ocular FIP. Early recognition of clinical signs, timely diagnosis, and prompt antiviral intervention are crucial for favorable outcomes. This case supports the efficacy of GS antiviral agents in managing complex FIP and emphasizes the importance of early therapeutic strategies in veterinary practice.



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sciforum-194399: Surveillance for influenza A virus H5-specific antibodies in Canada Geese (*Branta canadensis*) in Pennsylvania

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Wild waterfowl serve as reservoirs for low pathogenic (LP) avian influenza viruses (AIV), maintaining a diversity of viral subtypes; however, infection with the H5 subtype has historically been uncommon in most species. This has changed with the emergence of H5N1 highly pathogenic (HP) AIV in North America during 2021–2022, substantially altering AIV ecology in wild birds.

Prior to H5N1 HPAIV's emergence in North America, Canada geese (*Branta canadensis*) exhibited high exposure to H5 LPAIV relative to other waterfowl. During 2009–2012, 24% (20–28%) of Canada geese sampled in Pennsylvania during June had antibodies to AIV nucleoprotein (NP). Though antibodies to multiple hemagglutinin subtypes were detected, the most common was H5.

To assess changes in AIV exposure following H5N1 HPAIV's introduction, blood samples from Canada geese throughout Pennsylvania were collected in June 2025, with antibodies to AIV NP detected in 33% of the geese. Among NP-seropositive samples, 52% had H5 antibodies. Of these, 48% reacted to a North American H5 LPAIV antigen, 18% to a Eurasian H5 HPAIV antigen, and 14% to both antigens. Additionally, among samples positive to both H5 antigens, 75% had Eurasian H5 antibody titers that were equal or higher than North American.

These results indicate that Canada geese in Pennsylvania are exposed to H5N1 HPAIV, although seroprevalence remains lower than that associated with historic North American H5 LPAIV. Collectively, these findings improve understanding of H5 AIV exposure and immunity in Canada geese and clarify the role of this species in the evolving epidemiology of H5N1 HPAIV.



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sciforum-194611: Title: Hematologic Mycoplasma Infection in Four Persian and British Cats: Clinical and Laboratory Findings

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Introduction: Hematotropic Mycoplasma species are recognized as causative agents of hemolytic anemia and leukocytosis in cats. **Objectives:** Hematotropic Mycoplasma species are recognized as causative agents of hemolytic anemia and leukocytosis in cats. Clinical signs are often nonspecific, including vomiting, diarrhea, and lethargy, which can mimic gastrointestinal disorders or toxin exposure. Early detection through specialized diagnostic tests is critical to optimize therapeutic outcomes. This report describes clinical presentation, laboratory findings, and treatment responses in four cats under a single caretaker. **Methods:** Four Persian and British cats, aged 2–5 years, were referred for vomiting with hematemesis and diarrhea. Physical examination revealed mild dehydration and pale mucous membranes. Complete blood count with differential (CBC diff) and specialized cytology were performed to identify hematologic parasites. Supportive care included fluid therapy and targeted antibiotic therapy (Choice antibiotic) over 2–3 weeks. **Results:** CBC revealed leukocytosis ($>27,000/\mu\text{L}$) and evidence of hemotropic parasites on blood smear, suggestive of Mycoplasma infection. Following supportive therapy and antibiotic treatment, repeated CBC and differential showed normalization of white blood cell counts and absence of hemotropic parasites. Clinical signs resolved completely. **Conclusion:** Hematotropic Mycoplasma infection should be considered in cats presenting with vomiting, diarrhea, and leukocytosis. Prompt diagnosis using CBC differential and cytology, followed by supportive and antibiotic therapy, leads to favorable outcomes. Early recognition avoids misdiagnosis and enhances treatment efficacy.



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sciforum-193188: Transcriptome-Driven Repurposing for Chikungunya Virus: A Connectivity Map Approach

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Introduction: Chikungunya virus (CHIKV) causes recurrent outbreaks worldwide with no approved antiviral therapy available. Drug repurposing offers a rapid and cost-effective alternative to de novo drug development. This study aimed to identify existing approved drugs that can reverse or mimic a protective gene expression signature induced by immunomodulatory compounds in CHIKV-infected cells.

Methods: A gene expression profile was derived from CHIKV-infected cells treated with cAIMP (a STING agonist) or scleroglucan (a Dectin-1 agonist), dataset GeoNCBI GSE197744. The resulting significant gene signature was uploaded to the Connectivity Map platform (www.clue.io). Drugs with a high connectivity score (TAS > 0.8 and TAG > 0) were selected as candidates for repurposing.

Results: The analysis yielded five drugs with transcriptional signatures matching the input profile: everolimus (mTOR inhibitor), afatinib (EGFR/HER2 inhibitor), ponatinib (multi-kinase inhibitor), PHA-848125 (dual CDK/tropomyosin receptor kinase inhibitor), and brefeldin-A (protein transport inhibitor). These compounds are predicted to induce a cellular state like that produced by cAIMP/scleroglucan in infected cells.

Conclusions: The four identified drugs represent mechanistically diverse candidates that could potentially suppress CHIKV replication or modulate host immunity. Further in vitro and in vivo validation is required to confirm their antiviral efficacy. However, this computational approach demonstrates a rapid and unbiased strategy for repurposing approved drugs for emerging viral diseases, such as Chikungunya.



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sciforum-193161: Wildlife Rescue and Ophthalmic Trauma in a *Rhinella* sp. Toad during Small Hydropower Plant Construction in Southern Brazil: A One Health Perspective

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Wildlife rescue operations conducted during environmentally licensed infrastructure projects provide important opportunities for animal welfare, biodiversity conservation, and wildlife health surveillance within a One Health framework. Amphibians, such as *Rhinella* spp. toads are widely distributed throughout Brazilian territory and are vital species for insect pest control, soil aeration, and recognized as sensitive indicators of environmental change and ecosystem health. This group is particularly vulnerable during activities at construction sites, where heavy machinery accidents can inflict in physical injuries. Reports describing clinical management in free-ranging *Rhinella* remain scarce. This report describes veterinary assessment and treatment of a juvenile male *Rhinella* sp. (20 g) rescued during activities at a small hydropower plant construction site in Paraná, Brazil. The toad was found active and vocalizing upon capture during backhoe activity. During clinical examination, hyphema was detected in the left eye, washed with sterile 0.9% NaCl saline solution. Treatment included topical dexpanthenol ophthalmic gel (50 mg/g, BID), morphine (35 mg/kg, 0.07 mL), enrofloxacin (10 mg/kg SID, 0.01 mL), vitamin B complex, and 0.9% NaCl saline (0.1 mL) administered SQ. After 24 h of monitoring it showed favorable clinical recovery, considered fit for release at a designated release area according to the project's Environmental Basic Plan guidelines. This report highlights the challenges of providing veterinary care to injured wildlife in field settings where infrastructure and diagnostic resources are limited. It also demonstrates the importance of rapid clinical assessment and access to essential medications for the successful rehabilitation of rescued amphibians. Beyond individual patient outcomes, wildlife rescue programs associated with environmental licensing generate valuable information on species occurrence, health status, and anthropogenic threats affecting local fauna. Within a One Health perspective, the clinical evaluation of rescued amphibians contributes to environmental monitoring and biodiversity conservation, supporting the identification of ecological disturbances that may ultimately influence wildlife population health and ecosystem resilience.



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sciforum-188094: A chimeric vaccine based on peptides from salivary serpins for tick control

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The cattle tick *Rhipicephalus microplus* causes significant economic losses to the livestock industry, underscoring the need for the development of effective control methods. Vaccination with tick antigens has been proposed as a promising strategy to induce a protective immune response, especially using tick salivary antigens, which play important roles in modulating the host immune response. It was previously demonstrated by our research group that three serpins (RmS-3, RmS-6 and RmS-17) are present in the saliva of the cattle tick *Rhipicephalus microplus* and are secreted during feeding, where they act by interfering in the host immune response. In addition, antibodies raised against these serpins are able to neutralize their inhibitory functions. More recently, we identified neutralizing epitopes for RmS-17 using an *in vitro* approach. Based on these results, we developed a cost-effective strategy to identify neutralizing epitopes by combining epitope prediction algorithms with the spatial localization of the epitopes within the serpin structure. This strategy was applied to RmS-3 and RmS-6, and peptides were synthesized based on the predicted epitopes. Rabbits were immunized with these peptides to generate antisera against the respective peptides. Purified IgG was then used in a neutralization assay for RmS-6, which demonstrate that anti-p1RmS-6 neutralized rRmS-6 activity by 48%, anti-p3RmS-6 by 22% and a combination of both antibodies by 25%. Assays for RmS-3 are still ongoing. Based on the peptides identified for the three serpins, a chimeric protein it will be developed and evaluated for their capacity to generate a protective immune response against tick infestations.



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sciforum-189127: A Systematic Review of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Surgical Site Infections in Companion Animals and Their Human Contacts: A One Health Perspective

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Background

Methicillin-resistant *Staphylococcus aureus* (MRSA) is one of the most important antibiotic-resistant pathogens. Surgical site infection (SSI) after surgery in companion animals is a veterinary therapeutic challenge, posing a potential zoonotic threat to animal owners and veterinary personnel. This systematic review aimed to investigate the epidemiology, resistance patterns, and evidence of interspecies transmission of MRSA in SSI of companion animals and their human contacts from a One Health perspective.

Methods

According to the PRISMA 2020 guidelines, a systematic search was conducted in the PubMed/MEDLINE, Web of Science, Scopus, and Google Scholar databases for studies published between January 2019 and December 2025. Eligible studies included observational designs (cohort, case-control, cross-sectional), case reports, and case series that reported concurrent MRSA surgical site infection in dogs or cats and at least one human contact (owner or veterinary staff). The resulting methodological heterogeneity is explicitly addressed in the interpretation of the findings.

Results

Of the 1,247 articles found, 18 studies met the inclusion criteria. The prevalence of MRSA in companion animal SSI ranged from 2.4% to 18.7%. The most important risk factors included previous hospitalization, previous antibiotic therapy, and orthopedic surgery with implants. In 12 studies (66.7%), MRSA strains isolated from animal SSIs and human contact were identical in molecular typing (SCCmec type IV and spa types t011 and t034), indicating cross-species transmission. Resistance to clindamycin (72%), erythromycin (68%), and tetracycline (55%) was common, while all isolates were susceptible to vancomycin and linezolid. In 5 studies, asymptomatic veterinary personnel were carriers of MRSA, and the same strain was found in the SSI of the animal they operated on.

Conclusion

Integrating preoperative MRSA screening, which suggests probable interspecies transmission, implementing infection control protocols in veterinary hospitals, and coordinating with the human health system are recommended as key One Health strategies to reduce MRSA antibiotic-resistant zoonoses.



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sciforum-188024: Analysis of immunogenic interactions among recombinant antigens in experimental multicomponent vaccines against ticks

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Ticks are obligate ectoparasites that are associated with pathogen transmission and economic losses in the cattle industry. In Brazil, there is only one available vaccine against *Rhipicephalus microplus* based on a single antigen (Bm86), which has variable efficacy (0–51%) influenced by factors such as tick population and geographical region, highlighting the need for alternative vaccine approaches. This study evaluated the immunogenic interaction among three recombinant proteins from *R. microplus*, previously evaluated individually for their immunogenicity (neprilysin, inositol monophosphatase and scoloptoxin 14-like) whether different antigen proportions could influence the antibody response in experimental cocktail formulations. The recombinant proteins were expressed separately in *Escherichia coli* strain BL21 (DE3) Star, purified using urea, and quantified. Vaccine formulations containing different concentrations of the three proteins were formulated and emulsified in Montanide ISA 61 VG adjuvant with shared antigen ratios to assess potential immunogenic interactions. New Zealand White rabbits (n = 1 per group) were subcutaneously immunized with three doses administered at two-week intervals. Avidity and antibody levels for each antigen were evaluated by indirect ELISA from blood samples collected before first dose, after each dose and fifteen days following the third dose. The results indicate potential interactions among the antigens under the tested conditions, while the antibody response profile may support a two-dose vaccination regimen in future studies. Avidity test suggest that all formulations induced the production of antibodies with similar avidity against the three antigens, regardless of their proportions. The recombinant protein inositol monophosphatase exhibited lower antibody levels compared to other antigens, implying that adjustments in antigen proportion could be required to achieve a balanced humoral response. These findings support further investigation into the combined use of the three antigens for broader immunological coverage against *R. microplus*, and the present preliminary data are now guiding an ongoing experiment with four rabbits per group.



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sciforum-188184: Antimicrobial resistance in horses in Mexico from a One Health perspective

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Antimicrobial resistance is one of the main threats to global health in the 21st century, as it decreases the effectiveness of antibiotics in both human and veterinary medicine, with direct implications for public health, food safety and the environment. Furthermore, the WHO and the OIE note that over 70% of emerging infectious diseases in humans are of zoonotic origin, highlighting the role of animals in the transmission of resistant pathogens. In this context, equines are of particular importance due to their close interaction with humans in various activities, which facilitates the cross-species transmission of resistant zoonotic bacteria. However, despite its epidemiological and public health significance, the information available on antimicrobial resistance in horses remains limited in Mexico, even though the country has the world's second-largest horse population. Against this backdrop, the aim of this study was to identify the bacteria present in horses in central Mexico and to determine their antimicrobial resistance profiles.

To this end, rectal swabs were collected from horses exhibiting clinical signs of enteric disease. The samples were processed using bacterial culture, followed by antimicrobial susceptibility testing against eleven antibiotics commonly used in humans and animals, in accordance with the guidelines established by the CLSI.

This study analysed 30 equine samples, from which various zoonotic enterobacteria were isolated, mainly *Escherichia coli*, *Salmonella* spp. and *Klebsiella* spp. Furthermore, phenotypic profiles revealed high levels of resistance to antimicrobials commonly used in veterinary and human medicine; as, in more than 80% of the isolated strains, susceptibility to antimicrobials was less than 50%, whilst 51% showed resistance to three or more families of antibiotics, classifying them as multidrug-resistant, with β -lactams, tetracyclines and sulphonamides being the least effective against these strains. These findings support the 'One Health' approach, which recognises antimicrobial resistance as an interconnected problem affecting human, animal and environmental health.



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sciforum-176612: Antimicrobial Resistance in Pathogenic Bacteria from Endangered Fish: A One Health Approach to Emerging Zoonotic Threats

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Introduction:

Emerging antimicrobial resistance (AMR) in aquatic ecosystems poses significant threats to biodiversity, particularly for endangered fish species. Pathogenic bacteria, such as *Aeromonas*, are increasingly recognized as reservoirs of resistance, yet their role in the context of endangered species remains underexplored. Understanding the pathogenic potential and resistance profiles of *Aeromonas* is critical for the development of effective conservation strategies and the protection of both animal and human health. This study aims to investigate the occurrence and antimicrobial resistance of *Aeromonas* in endangered fish species, with a focus on the zoonotic potential and implications for One Health.

Methods:

Aeromonas was isolated from various organs of endangered fish species from the Tarim River and identified using molecular techniques. The isolates were evaluated for antimicrobial susceptibility, focusing on tetracyclines and fluoroquinolones. Genomic analyses were performed to identify resistance genes and virulence factors linked to pathogenicity and zoonotic transmission.

Results:

All isolates were confirmed as *Aeromonas*. The bacteria exhibited significant multidrug resistance, particularly to tetracyclines (38 genes) and fluoroquinolones (28 genes). Other antibiotic classes, including macrolides, peptide antibiotics, and cephalosporins, also showed notable resistance. Genomic analysis revealed the presence of virulence genes related to bacterial adherence, motility, and host invasion, suggesting zoonotic potential.

Conclusions:

This study highlights the emerging threat of AMR in *Aeromonas* species from endangered fish, emphasizing the need for a One Health approach to monitor and manage resistance in aquatic environments. The findings underscore the importance of integrating AMR surveillance into conservation efforts to mitigate risks to both wildlife and human health.



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sciforum-187654: Application of Nanobiosensors in the Diagnosis of Leishmaniasis in Humans with a One Health Approach: A Systematic Review

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Introduction

Rapid and accurate detection of Leishmaniasis is essential to interrupt transmission and prevent epidemics of this fatal zoonotic disease. This systematic review aims to study the types of nanobiosensors developed for the detection of Leishmaniasis, and to analyze their diagnostic performance in a One Health context.

Methods

This systematic review was conducted according to the PRISMA guidelines. PubMed, Scopus, Web of Science, and Google Scholar databases were searched for articles published in English between January 2018 and December 2025 with the keywords nanobiosensor, *Leishmania*, Leishmaniasis, gold nanoparticles, electrochemical nanosensors, DNA sensor, One Health, detection in reservoir animals, and environmental detection. Three reviewers were involved in screening and data extraction. Of the 187 articles found, 22 original articles with inclusion criteria, including the development of a nanobiosensor for the detection of Leishmaniasis and reporting performance parameters with applicability in low-resource settings, were included in the final analysis.

Results

Based on this systematic review, six main categories of nanobiosensors have been developed for highly accurate detection of Leishmaniasis. Gold nanoparticle-based sensors (gene sensors and lateral flow assays) detect trace amounts of parasite DNA with sensitivity far superior to traditional methods like microscopy and ELISA. Graphene-based electrochemical sensors are portable and ideal for field use, while quantum dot sensors enable simultaneous detection of multiple pathogens in endemic areas. Aptamer-based sensors (chitosan-carbon dot nanocomposite) act like synthetic antibodies to accurately identify parasite surface proteins with excellent specificity. Electrochemical immunosensors using magnetic-carbon nanocomposites can precisely detect antibodies in patient serum, effectively solving the problem of differential diagnosis of visceral leishmaniasis from clinically similar diseases such as malaria and typhoid fever.

Conclusion

Nanobiosensors have demonstrated high diagnostic accuracy for leishmaniasis in a One Health context; however, challenges such as standardization, scalability, cost-effectiveness, regulatory approval, and implementation in resource-limited settings must be addressed.



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sciforum-187574: Application of Nanomedicines in the Control of Gastrointestinal Helminths in Dogs and Cats with a One Health Approach: A Systematic Review

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Objective and introduction

Gastrointestinal helminths (GIH) in dogs and cats, including *Toxocara canis*, *Toxocara cati*, *Dipylidium caninum*, and *Echinococcus granulosus*, are important causes of zoonosis. The present study evaluates nanomedicines as a novel strategy to enhance anthelmintic efficacy and reduce dosage, supporting zoonotic disease control under the One Health framework.

Methods

This systematic review followed the PRISMA guidelines. PubMed, Scopus, Web of Science, and Embase were searched from January 2020 to April 2026 using keywords related to nanoparticles, nanomedicines, anthelmintics, dogs, cats, major zoonotic helminths, One Health, and zoonoses, in English only. Eligible studies included *in vitro*, *in vivo*, and clinical studies. Two independent reviewers performed screening and data extraction. Risk of bias was assessed using the SYRCLE's RoB tool for animal studies and the Joanna Briggs Institute checklists for *in vitro* and clinical studies.

Results

Analysis of the 21 included studies showed that lipid nanocarriers, polymeric nanoparticles (such as chitosan and PLGA), and nanoemulsions can significantly increase the bioavailability of anthelmintic drugs. Nanodelivery of drugs, while protecting the active ingredient from enzymatic degradation in the gastrointestinal tract, increases drug absorption via transcytotic mechanisms and reduces the effective dose required. Praziquantel nanoformulation has shown greater anthelmintic activity against *Toxocara canis*, *Toxocara cati*, *Dipylidium caninum*, and *Echinococcus granulosus*. Ivermectin-containing nanoparticles have also increased drug stability in the digestive environment and reduced neurotoxicity. Regarding One Health, reducing drug dosage and frequency of administration leads to reduced release of chemical compounds into the environment and protection of the ecosystem.

Conclusion

Nanomedicines demonstrate promising anthelmintic efficacy and reduced toxicity in predominantly experimental studies, but clinical evidence remains limited. The translation of nanomedicines into routine veterinary practice is currently hindered by challenges such as scalability, cost, safety standardization, and regulatory gaps, which must be addressed before integrating nanomedicines into One Health-based zoonoses control programs.



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sciforum-190119: Artificial Intelligence for Chest Radiography in Tuberculosis Detection Across Humans and Animals: A Systematic Review of One Health Diagnostic Applications

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Background/Objective: Tuberculosis (TB) is one of the most important global zoonoses, affecting millions of human and animal cases annually. Chest radiography (CXR) is a key screening tool in human medicine, and in recent years, deep learning-based artificial intelligence (AI) algorithms have been developed for automated interpretation of CXR. This systematic review aimed to assess the current status of AI in chest radiography for TB diagnosis in humans and animals.

Methods: This study was conducted according to the PRISMA 2020 guidelines. A systematic search was conducted in PubMed/MEDLINE, IEEE Xplore, arXiv, Web of Science, and Scopus databases for studies published between January 2020 and March 2026. Inclusion criteria included original studies (excluding reviews and commentaries) that used deep learning algorithms (such as convolutional neural networks – CNN) to detect tuberculosis from chest radiographs in humans (any age) or animals (domestic and wild mammals).

Results: 23 studies met the inclusion criteria. In human studies, the mean area under the receiver operating characteristic curve (AUC) for diagnosing TB from CXR with AI was reported to be between 0.94 and 0.98, which was comparable to or better than that of human radiologists. In animal studies, the detection accuracy was lower (AUC: 0.76 to 0.85), mainly due to the lack of training data volume and anatomical differences between species (chest wall thickness, heart size, vascular pattern). The most important barriers to cross-species translation were the lack of a standardized and labeled database of animal images, the diversity of animal species and body size, and differences in radiographic protocols.

Conclusion: Artificial intelligence in the diagnosis of TB from chest radiographs in humans has reached a high level of maturity, but its application in animals is very limited and nascent. Transfer learning from human to animal models represents a promising strategy to fill this gap.



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sciforum-193503: Assessment of Oxidative Stress in Clinical Bovine Leukosis and Asymptomatic Seropositive Cattle

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Introduction: Bovine leukemia virus (BLV), a retrovirus, causes enzootic bovine leukosis, a chronic infectious disease in cattle worldwide. BLV establishes persistent infection by integrating proviral DNA into the host genome, targeting B-lymphocytes. Beyond its oncogenic potential, BLV infection is linked to immune dysfunction, reduced productivity, and poses a major challenge in bovine health management. Oxidative stress is associated with the pathogenesis of many infectious diseases, but its role in clinical and subclinical BLV infection has not been sufficiently described.

Methods: We investigated oxidative stress parameters in 30 BLV seropositive cattle: 15 asymptomatic seropositive and 15 with clinical bovine leukosis. Blood was collected from the jugular vein, and serum was stored at -70°C. Total antioxidant capacity (TAC), superoxide dismutase (SOD), glutathione peroxidase (GPx), and malondialdehyde (MDA) levels were measured using commercial ZellBio (Germany) kits. Statistical comparisons were performed between asymptomatic seropositive and clinically affected groups.

Results: SOD activity differed significantly between groups ($P = 0.0001$), with higher levels in asymptomatic seropositive cattle. TAC was also higher in asymptomatic seropositive cattle. MDA and GPx were higher in clinically affected animals, though not statistically significant ($P > 0.05$).

Conclusions: BLV infection correlates with host oxidative status, particularly antioxidant defense mechanisms. Altered SOD activity suggests a potential role in early intracellular antioxidant responses to BLV infection in cattle. Oxidative stress dynamics may offer new avenues to understand BLV pathogenesis from a One Health perspective.



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sciforum-187974: Bioinformatics methods for managing drug resistance in zoonotic gastrointestinal helminths of pets with a One Health approach: A Systematic Review

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Introduction

The widespread use of chemical anthelmintics has led to the emergence of drug resistance in zoonotic gastrointestinal helminths of pets, including *Toxocara canis*, *Toxocara cati*, *Ancylostoma caninum*, and *Dipylidium caninum*. This systematic review aims to investigate the application of bioinformatics methods to identify molecular mechanisms of resistance in domestic animal gastrointestinal helminths with a One Health approach.

Methods

This systematic review was conducted according to the PRISMA guidelines. PubMed, Scopus, Web of Science, and Google Scholar databases were searched for articles published between January 2016 and December 2025. Inclusion criteria was original studies that used bioinformatics methods to study drug resistance in gastrointestinal parasites of dogs and cats. Of the 162 articles found, 35 eligible articles were included in the final analysis.

Results

Bioinformatics methods have contributed to the management of drug resistance in three main areas. First, whole genome sequencing and phylogenetic analysis have identified resistance-associated mutations in drug target genes, including the tubulin gene and the glutamate-gated chloride channel genes in various parasite species. Second, molecular docking has successfully predicted and quantified the effect of specific mutations (such as the Phe200Tyr substitution in tubulin) on reducing drug affinity for the target protein. Third, virtual screening of natural compound libraries (including flavonoids, alkaloids, and terpenoids) has led to the identification of novel molecules that are capable of binding to the mutated and defective site and can be used as alternative or auxiliary options.

Conclusion

From a One Health perspective, bioinformatics methods, including whole genome sequencing, molecular docking, virtual screening, and molecular epidemiological modeling, play a key role in the sustainable management of zoonotic parasites by reducing unnecessary use of chemical drugs, extending the lifespan of existing drugs, and preventing the spread of resistance alleles to the human population and the environment.



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sciforum-194635: Can Canine Papillomavirus Be Oncogenic in Humans? A Bioinformatics Assessment of E6 Oncoprotein–p53 Interaction Across Host Species

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Background: Papillomaviruses are typically host-specific and non-zoonotic, but sporadic reports suggest possible canine papillomavirus transmission to humans. This raises the question: could canine papillomavirus exert oncogenic effects in humans? The E6 oncoprotein promotes carcinogenesis by degrading the tumour suppressor p53. Whether canine E6 can interact with human p53 is unknown.

Objectives: To evaluate the potential oncogenicity of canine papillomavirus E6 oncoprotein in humans through comparative sequence analysis, structural prediction, and molecular docking with human p53.

Methods: E6 sequences from human and canine papillomaviruses were retrieved from NCBI. Phylogenetic analysis (MEGA) identified closest human–canine E6 pairs. Three-dimensional structures were predicted with ColabFold and refined with PyMOL. Molecular docking against human p53 chain A was performed using HawkDock. Binding free energy (ΔG) and residue-level interactions were analysed for the top three models.

Results: Human and canine E6 protein sequences shared 30% amino acid similarity. Canine E6 was shorter and lacked one functional motif. Docking revealed $\Delta G = -52$ kJ/mol for human E6–human p53 versus $\Delta G = -36$ kJ/mol for canine E6–human p53, indicating weaker binding. In human E6, 48% of human p53 binding sites mapped to p53 residues 100–140; in canine E6, 39% mapped to residues 150–200, with no binding sites in the 100–140 region, suggesting a distinct and likely less effective interface.

Conclusions: While a ΔG of -36 kJ/mol indicates measurable binding between canine E6 and human p53, the substantially reduced binding affinity, low sequence similarity, absence of a key functional motif, and altered p53 binding site distribution collectively suggest that canine papillomavirus E6 oncoprotein is unlikely to exert significant oncogenic activity in humans through the p53 degradation pathway. However, alternative oncogenic mechanisms cannot be excluded. Further in vitro and in vivo investigations are warranted to fully characterise the zoonotic oncogenic potential of canine papillomavirus.



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sciforum-194411: Canine Transmissible Venereal Tumor as a One Health-Relevant Model of Contagious Cancer: A Case of Combined Vincristine and Exosome-Based Immunotherapy

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Background: Canine Transmissible Venereal Tumor (CTVT) is a unique clonally transmissible cancer. Although not zoonotic, its contagious nature makes it a valuable comparative model for host-tumor immune interactions within the One Health framework. This case report evaluates the clinical outcome of combining vincristine chemotherapy with immunotherapy using exosomes derived from macrophage-like monocytes primed with CTVT tumor lysate in a severely debilitated patient.

Methods: A six-year-old, 20-kg, female mixed-breed dog was referred to the University of Tehran's Veterinary Hospital with severe cachexia, a 13 × 20 cm genital mass, and a history of starvation-induced malnutrition. Diagnosis was confirmed via cytology and histopathology; baseline imaging showed no metastasis. The treatment protocol included six weekly doses of vincristine and three subcutaneous injections of patient-derived monocyte exosomes primed with CTVT lysate at two-week intervals. Exosomes were isolated after 24-hour incubation of monocytes with tumor lysate and characterized using scanning electron microscopy (SEM), dynamic light scattering (DLS/Zeta), and NanoDrop analysis. Intensive nutritional support was provided throughout the hospitalization.

Results: The combined approach resulted in marked tumor necrosis and a significant volume reduction to approximately 4 × 6 cm. Parallel to tumor regression, the patient's body weight increased by 10 kg, reflecting successful cachexia reversal and recovery from malnutrition. No systemic or local toxicity was detected based on longitudinal hematological, biochemical, and ultrasonographic monitoring.

Conclusion: The combination of vincristine and monocyte-derived exosomes, supported by intensive nutritional management, was associated with substantial tumor regression and clinical recovery. However, given the limitations of a single-case report, these findings remain preliminary and necessitate validation through larger controlled studies to confirm therapeutic efficacy. From a One Health perspective, utilizing transmissible animal tumors in comparative oncology offers valuable insights into fundamental cancer biology, immune evasion, and host-tumor co-evolution, ultimately contributing to translational biomedical research while enhancing animal welfare.



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sciforum-194659: Characterisation of the microbiome and resistome in the loggerhead sea turtle (*Caretta caretta*) in the Mediterranean basin

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Loggerhead sea turtles (*Caretta caretta*) are considered sentinel species for investigating the anthropogenic impacts on the marine environment within a *One Health* framework. Longitudinal sampling of rehabilitating individuals at C.Re.Ta.M. (National Reference Center for the welfare of marine turtles) provides an opportunity to assess temporal changes in gut microbial communities.

Fecal samples were collected from 20 *Caretta caretta* individuals at admission (T0) and after one month of rehabilitation (T1) to investigate gut microbiome during the rehabilitation. Genomic DNA was used to amplify and sequence the V3–V4 region of the 16S rRNA gene. In addition, the resistome was assessed by PCR at admission.

Overall, microbial community structure remained stable over time, with no consistent cohort-wide shift. However, genus-level analyses revealed individual-specific trajectories driven by changes in the relative abundance of dominant taxa. Specifically, age class specific patterns were observed. Juveniles showed an increase in *Clostridium_sensu_stricto_1* (0.47 ± 0.98 ; 6.02 ± 9.41) and a decrease in *Fusobacterium* (3.37 ± 3.92 ; 0.80 ± 1.02) from T0 to T1. Conversely, subadults showed a decrease in *Bacteroides* (8.17 ± 4.78 ; 4.35 ± 2.89) and *Clostridia_vadinBB60_group* (8.78 ± 7.07 ; 2.46 ± 2.61). Microbiome dynamics differed between age classes, and curved carapace length (CCL) was significantly associated with both the direction and extent of compositional changes ($p = 0.044$), suggesting size-dependent microbial dynamics. Although no linear association between microbiome and resistome emerged across the entire cohort, an exploratory extreme-tercile comparison indicated higher within-host turnover in individuals with higher resistome levels ($p = 0.0428$). Among the antibiotic classes analyzed, the highest resistance levels were observed against tetracyclines (80%) and β -lactams (75%).

These findings indicate that the gut microbiome of *Caretta caretta* remains stable during rehabilitation while exhibiting size-dependent compositional changes. Integrating microbiome and resistome analyses may support health assessment and environmental surveillance.



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sciforum-180468: Community knowledge, attitudes and practices related to cystic echinococcosis in Ethiopia: implication for control

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Background: Cystic echinococcosis (CE), caused by *Echinococcus granulosus*, is a parasitic zoonosis of major public health and economic importance. Ethiopia is among the most endemic countries, yet baseline data on community knowledge, attitudes and practices are scarce. Addressing these issues are essential to reduce transmission, mitigate economic and public health impacts, and align national strategies with the WHO 2030 roadmap in combating neglected tropical disease and the Sustainable Development Goals.

Methods: We conducted a cross-sectional survey of 310 randomly selected participants across different regions of Ethiopia using a Research Electronic Data Capture administered questionnaire. The survey primarily included farmers; however, veterinarians, educators, abattoir workers, and others were also represented. Knowledge was assessed using ten binary questions while attitudes and practices were evaluated using 11 and 13 items, respectively. Data were analysed using descriptive statistics and chi-square tests in R software, and multiple correspondence analysis (MCA) was applied to identify latent KAP profiles in relation to education level.

Results: Farmers constituted the largest proportion (54.2%, n = 168), followed by veterinarians (20.3%), abattoir workers and butchers (11.6%). Dog ownership was common, and most livestock were grazed on open pasture. Only 11.0% (n = 35) of respondents demonstrated good knowledge of CE, the majority of whom were veterinarians, while 56.0% (n = 174) had limited knowledge. Furthermore, only 22.6% of respondents exhibited a positive attitude toward CE, whereas 54.2% displayed a negative attitude. Safe practices were observed in only 2.6% of respondents, while 71.3% reported risky practices. Education was strongly associated with greater awareness and safer practices. MCA revealed **heterogeneous behavioural profiles across the study population**.

Conclusion: These findings highlight entrenched knowledge gaps and behaviours that perpetuate CE endemicity in Ethiopia, reflecting both cultural practices and structural constraints. Addressing this burden will require coordinated One Health interventions that combine culturally tailored health education with regular dog deworming, improved abattoir services and surveillance, safe slaughter practices and better household hygiene.



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sciforum-192930: Curcumin vs. *Toxoplasma gondii*: A Network Pharmacology and Molecular Docking Blueprint for Anti-Parasitic Target Identification

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Introduction: Toxoplasmosis is a disease caused by *Toxoplasma gondii* and affects nearly one third of the world population. Current therapies cannot eradicate chronic tissue cysts and have serious side effects. Several studies confirmed that curcumin, the active compound in turmeric, may have anti toxoplasmosis activities. However, its exact molecular targets are not still discovered.

Methods: We used network pharmacology to identify common targets between curcumin and host responses to *T. gondii* in human. A protein protein interaction network was constructed by STRING and the key hub proteins were identified using Cytoscape. Molecular docking of curcumin with the ATP binding pocket of AKT1 was performed using Schrödinger Glide in extra precision (XP) mode.

Results: The overlap resulted in 27 common proteins, three of which demonstrated the highest level of connectivity: AKT1, MMP9, and TNF. AKT1 was chosen as the most suitable target for docking due to its biological relevance and safety. Curcumin bound favorably to AKT1 with the best pose achieving a docking score of -4.412 kcal/mol and an E model of -59.380 kcal/mol. The review of preclinical evidence confirmed that curcumin and its nanoformulations decrease tachyzoite and brain cyst loads, modulate inflammation and oxidative stress, and also improve survival rates in animal models.

Conclusions: Curcumin is a safe, multi target agent that has shown promising anti-toxoplasmosis effects in both acute and chronic phases. In this study, AKT1 is identified as one of the best key host directed targets. In combination with conventional drugs or advanced delivery systems, curcumin may resolve the limitations of existing therapies.



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sciforum-175849: Detection of Bovine Tuberculosis in Animals Using Interferon-Gamma Release Assay and Its Public Health Relevance in the One Health Approach

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Introduction: The World Health Organization (WHO) describes One Health as an approach that integrates human, animal, and ecosystem health in order to control diseases. The *Mycobacterium tuberculosis* complex (MTBC) includes *M. tuberculosis*, responsible for human tuberculosis, and *M. bovis/caprae* - primarily cause bovine tuberculosis, and can also infect humans (zoonotic tuberculosis). The Interferon-Gamma Release Assay used in humans demonstrates immune sensitization to infection with MTBC. The IFN- γ is used in animals to determine sensitization directed against *M. bovis/caprae*. The test is usually performed together with other elements of bovine tuberculosis control programmes, such as tuberculin skin tests. The aim of this study was to evaluate the usefulness of the interferon-gamma release assay (IFN- γ) for the detection of bovine tuberculosis in selected animal species and to assess its significance for public health within the One Health framework. **Methods:** The IFN- γ test was used in this study. The test is adequate for intended use according to WOAH Terrestrial Manual it's approved for use in cattle, goats, and camelids. Bison are phylogenetically closely related to cattle, and evidence indicates that this assay, is also applicable to bison, as supported by the obtained results. **Results:** In 2025, a total of 68 animals (including alpacas, European bison, cattle, and camels) were tested for IFN- γ release using the Bovigam test (Thermo Fisher Scientific). Among the tested samples, six European bison originating from a showing pen in the Podkarpackie Province and one cow from the Zachodniopomorskie Province tested positive for bovine tuberculosis, representing 8.8% of positive samples (6/68). **Conclusions:** The results indicate that this test is adequate and suitable for the early detection of bovine tuberculosis in cattle and other described animal species. After receiving positive results, appropriate decisions regarding animal management can be made in order to reduce the potential risk of infection transmission to humans.



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sciforum-194469: Detection of Bovine Tuberculosis in Animals Using Interferon-Gamma Release Assays and Its Public Health Relevance in the One Health Approach

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Introduction: The World Health Organization (WHO) describes One Health as an approach that integrates human, animal, and ecosystem health in order to control diseases. The *Mycobacterium tuberculosis* complex (MTBC) includes *M. tuberculosis*, responsible for human tuberculosis, and *M. bovis/caprae* - primarily cause bovine tuberculosis, and can also infect humans (zoonotic tuberculosis). The Interferon-Gamma Release Assay used in humans demonstrates immune sensitization to infection with MTBC. The IFN- γ is used in animals to determine sensitization directed against *M. bovis/caprae*. The test is usually performed together with other elements of bovine tuberculosis control programmes, such as tuberculin skin tests. The aim of this study was to evaluate the usefulness of the interferon-gamma release assay (IFN- γ) for the detection of bovine tuberculosis in selected animal species and to assess its significance for public health within the One Health framework. **Methods:** The IFN- γ test was used in this study. The test is adequate for intended use according to WOAH Terrestrial Manual it's approved for use in cattle, goats, and camelids. Bison are phylogenetically closely related to cattle, and evidence indicates that this assay, is also applicable to bison, as supported by the obtained results. **Results:** In 2025, a total of 68 animals (including alpacas, European bison, cattle, and camels) were tested for IFN- γ release using the Bovigam test (Thermo Fisher Scientific). Among the tested samples, six European bison originating from a showing pen in the Podkarpackie Province and one cow from the Zachodniopomorskie Province tested positive for bovine tuberculosis, representing 10.3% of positive samples (7/68). **Conclusions:** The results indicate that this test is adequate and suitable for the early detection of bovine tuberculosis in cattle and other described animal species. After receiving positive results, appropriate decisions regarding animal management can be made in order to reduce the potential risk of infection transmission to humans.



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sciforum-185600: Development and Evaluation of Organic Acid-Based Hydrogels for Antifungal Treatment of Companion Animal Dermatophytes: A One Health Perspective

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Introduction

Dermatophytosis caused by *Microsporum canis* is a common zoonotic skin infection in pets, often requiring prolonged treatment due to persistence in keratinized tissues. Its zoonotic nature highlights its importance within the One Health framework, as infected animals may contribute to transmission to humans. Organic acids represent promising antifungal agents due to their biocompatibility and mechanisms of action. Hydrogel systems may enhance topical drug delivery by enabling controlled release and improved retention. This study aimed to evaluate the antifungal activity of selected organic acids and to assess the physicochemical and antifungal properties of acid-based hydrogel formulations.

Methods

Ethanol-based solutions of gallic, coumaric, ferulic, and cinnamic acids (0.31–5%) were tested against *M. canis* using the agar well diffusion method. Cinnamic acid demonstrated the highest antifungal efficacy, which led to its selection for incorporation (0.5%) into hydrogel formulations containing poloxamer 407 and hydroxyethylcellulose with varying polymer ratios. Hydrogels were characterized by pH measurement and rheological analysis. Antifungal activity was evaluated using the same diffusion method. In vitro release studies were performed using a modified Franz diffusion cell system.

Results

Cinnamic acid demonstrated the highest antifungal activity, with inhibition zones increasing from 35.6 ± 1.7 mm (0.31%) to 73.2 ± 13.8 mm (5%). All hydrogel formulations retained antifungal activity against *M. canis*, producing ~17 mm inhibition zones, indicating diffusion limitations within the polymer matrix. Rheological analysis showed formulation-dependent viscosity (73.1–311.5 Pa·s at 35 °C), and all hydrogels had slightly acidic pH (4.81–4.92). In vitro, $34.8 \pm 3.3\%$ of cinnamic acid was released over 5 hours, suggesting a diffusion-controlled release profile.

Conclusions

Cinnamic acid demonstrated strong antifungal activity and retained its efficacy when incorporated into hydrogel systems, enabling controlled release. These findings indicate that cinnamic acid is a promising candidate for topical antifungal therapy, while poloxamer 407/hydroxyethylcellulose hydrogels may serve as a platform for prolonged local antifungal drug delivery.



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sciforum-187983: Development of an HR2-Derived Fusion Inhibitor Against Canine Coronavirus; in vitro and in silico approaches

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Introduction: Zoonoses are infectious diseases transmitted from animals to humans and pose a significant global public health threat due to our close contact with animals. Approximately two-thirds of emerging infectious diseases in humans originate from animals, including Ebola, avian influenza, COVID-19, and hantavirus. Among coronaviruses, Canine coronavirus (CCoV), an alphacoronavirus, causes mild enteritis in dogs and other carnivores; however, its high recombination rate has led to hypervirulent strains with increased pathogenicity and potential for cross-species transmission. Recently, a novel CCoV strain, CCoV-HuPn-2018, was identified in patients with pneumonia in Malaysia, Haiti, and Vietnam, highlighting the zoonotic potential of CCoV-like viruses, although their epidemiological implications remain under investigation.

Aim: Innovative solutions are needed from a One Health perspective to address growing challenges. In this study, to prevent or block CCoV replication, we designed a fusion-inhibiting peptide derived from the heptad repeat domain (HRC) of the CCoV S glycoprotein, a crucial region for membrane fusion and viral infection.

Material and methods: *In vitro* TCID₅₀ antiviral assays, cell-cell fusion assays, and Real-Time PCR, together with *in silico* analyses and molecular dynamics simulations, were conducted to evaluate the peptide's interaction with the S protein fusion core.

Results: At non-toxic concentrations (3–50 µM), the peptide effectively blocked S protein-mediated fusion and markedly reduced live-virus infection *in vitro* at 35 and 25 µM, respectively. Molecular detection showed a dose-dependent reduction in gene expression of the S glycoprotein. These results were supported by molecular docking and dynamics simulations, which revealed that the peptide, mimicking the HR2 region, binds strongly to the HR1 region, thereby hindering viral protein binding and fusion.

Conclusion: Overall, these results provide a strong foundation for developing peptide-based treatments to inhibit CCoV fusion and replication.

Additional research is needed to examine the chemical properties of the peptide and its safety in animal models.



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sciforum-187951: Diversity and Zoonotic Potential of *Anaplasma* spp. in Domestic Animals and Their Associated Ticks in Sicily: A One Health Perspective

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Introduction

Tick-borne pathogens of the genus *Anaplasma* are of increasing concern within the One Health framework because of their impact on animal and human health. Sicily is a Mediterranean hotspot for vector-borne diseases due to its climate, biodiversity, and animal movements; however, data on the circulation of *Anaplasma* spp. in domestic animals and associated ticks remain limited. Dogs, equids, and cats can serve as sentinels of pathogen circulation. This study investigated the occurrence and diversity of *Anaplasma* spp. in these hosts and their ticks in Sicily.

Materials and Methods

Between 2024 and 2025, a molecular survey was conducted in the Sicilian provinces of Palermo, Messina, Siracusa, Agrigento, Trapani, and Catania. Samples were collected throughout all seasons. Blood samples from dogs (n=719), equids (n=273), and cats (n=84), together with ticks collected from the same animals (dogs: n=327; equids: n=32; cats: n=14), were analyzed. Ticks were identified as *Rhipicephalus sanguineus*, *Ixodes ricinus*, and *Haemaphysalis punctata*. DNA was extracted and screened by PCR targeting the 16S rRNA gene; positive amplicons were sequenced.

Results

Anaplasma DNA was detected in 6/719 canine blood samples (0.83%; 95%CI: 0.31–1.81%) and 3/327 dog ticks (0.92%; 95%CI: 0.19–2.66%). All equine blood samples were negative, whereas 1/32 ticks from equids tested positive (3.13%; 95%CI: 0.08–16.22%). In cats, positivity was detected in 1/84 blood samples (1.19%; 95%CI: 0.03–6.46%) and 1/14 ticks (7.14%; 95%CI: 0.18–33.87%). Sequencing identified *A. bovis*, *A. phagocytophilum*, *A. ovis*, and *A. platys*. Given the low number of positives and wide confidence intervals, these findings should be interpreted cautiously.

Conclusions

The detection of multiple *Anaplasma* species, including the zoonotic pathogen *A. phagocytophilum*, demonstrates their circulation in Sicily and suggests active host-tick transmission cycles. These preliminary findings highlight the need for integrated One Health surveillance to better understand transmission dynamics and support control strategies in Mediterranean ecosystems.

Funding: Italian Ministry of Health, Project IZSSI03/23RC.



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sciforum-188159: Drug repurposing of farnesyltransferase inhibitors as novel anthelmintics for the treatment of larval cestodiasis

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Introduction: Larval cestodiasis are caused by parasitic helminths of the class Cestoda, whose metacestode larvae infect host tissues and cause neglected diseases such as echinococcosis and cysticercosis. Current treatments are limited because available drugs are mainly parasitostatic and require prolonged administration at high doses, often causing severe side effects. In this context, drug repurposing represents a promising strategy for the development of more effective anthelmintics. The mevalonate pathway, essential for isoprenoid synthesis in eukaryotes, is conserved in cestodes, except for the cholesterol biosynthesis branch. Within this pathway, farnesyltransferase (FTase) emerges as a potential therapeutic drug. **Objectives:** This study evaluated the potential of the FTase inhibitors Tipifarnib and Lonafarnib for the treatment of larval cestodiasis against the model cestode *Mesocostoides corti*. **Methods:** amino acid sequences of FTase α and β subunits from parasitic helminths and their hosts were identified and used for phylogenetic analyses. *Ab initio* 3D models of *M. corti* FTase subunits were generated, followed by molecular docking analyses with Tipifarnib. In addition, *in vitro* assays with *M. corti* larvae were performed to evaluate anthelmintic activity. **Results:** FTase α and β subunit sequences from 53 helminth species and their hosts were recovered. The β subunit showed greater structural conservation. Structural modeling of *M. corti* FTase revealed high similarity to the human enzyme. Molecular docking analyses indicated that Tipifarnib binds to catalytic site of FTase, potentially blocking substrate access. *In vitro* assays demonstrated strong anthelmintic activity. Lonafarnib induced morphological damage in parasites within 24 h, whereas Tipifarnib caused complete parasite mortality within 48 h. **Conclusions:** These findings support FTase as a promising target for the repurposing of its inhibitors as novel anthelmintic agents. Future studies exposing parasites to Tipifarnib and Lonafarnib will be conducted to generate samples for proteomic analyses and to further investigate their mechanisms of action.



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sciforum-194420: Effectiveness of N6-methyladenosine (m6A) and Innate Immunity as Barriers to the Emergence of Cedar Henipavirus in *Rousettus aegyptiacus* Cells

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The Egyptian fruit bat (*Rousettus aegyptiacus*) is a pteropodid bat closely related to *Pteropus alecto*, the natural reservoir of the pathogenic henipaviruses Nipah virus and Hendra virus. Cedar virus (CedPV) is a less pathogenic henipavirus that is used as a model to study the pathogenesis of Nipah and Hendra viruses due to its genetic and phylogenetic relatedness. N6-methyladenosine (m6A) is an important cellular RNA modification and regulates the replication of many viruses through cellular proteins that add (writers), remove (erasers), and recognise (readers) this modification on RNA. Innate immunity constitutes the primary arm of host defence against viral infection.

In this study, a recombinant Cedar virus expressing green fluorescent protein (rCedPV-GFP) and transcriptomic analyses were used to investigate whether m6A modification and innate immunity act as effective barriers to CedPV emergence and replication in *R. aegyptiacus* cells. Infection of *R. aegyptiacus* cells with rCedPV-GFP resulted in abortive infection, with the virus unable to be passaged in bat cells. However, the virus was able to adapt to *R. aegyptiacus* cells using Vero E6 cells, but not BHK-21 cells, despite both cell lines supporting high viral titers. RNA-seq analysis revealed adaptive mutations in CedPV replication genes, particularly in the polymerase gene and its nucleocapsid template, but not in the immune-evasion gene. Nevertheless, gene expression profiling of infected *R. aegyptiacus* cells showed limited suppression of the interferon response. In contrast, m6A machinery exhibited modest upregulation, with the writer protein METTL3 showing the greatest increase in expression. Overexpression of METTL3 strongly inhibited CedPV replication. However, evidence of viral hijacking of METTL3 was observed through the translocation of the protein from the nucleus to the cytoplasm following the viral infection. These findings establish m6A and innate immune responses as important barriers to CedPV infection and replication in *R. aegyptiacus* cells.



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sciforum-188178: Epidemiological study of canine and human rabies in southern Benin: A retrospective analysis (2012–2017)

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Rabies is a significant zoonotic disease triggered by a lyssavirus from the Rhabdoviridae family. In human cases, domestic dogs are responsible for 99% of transmissions, and the virus is invariably fatal once clinical symptoms manifest. Although control initiatives have been launched in several major cities across Benin, the disease remains endemic, and comprehensive epidemiological data continues to be scarce. This study aimed to evaluate the effectiveness of rabies control efforts in Abomey-Calavi, Cotonou, and Ouidah. A retrospective survey from 2012 to 2017 was conducted, analyzing data from 17 veterinary clinics and four health centers specializing in animal bite treatment. Of the 900 biting dogs identified, only 770 were placed under veterinary surveillance, with 53 confirmed cases of canine rabies. During the same period, 1,436 dog bites were recorded in health centers, leading to 287 clinical cases of human rabies and subsequent deaths. Men were more frequently affected (55.22%), and children aged 1 to 14 years accounted for 45.89% of the bite victims. The incidence of human rabies in Cotonou dropped from 4.86 per 100,000 inhabitants in 2013 to 1.44 in 2017, whereas in Abomey-Calavi, it rose sharply from 4.57 to 16.71. In Ouidah, the incidence rates remained largely unchanged. These findings highlight that rabies persists as a critical public health challenge in Benin, requiring urgent and enhanced eradication measures to be implemented



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sciforum-194714: Evaluating Veterinary Stakeholder Readiness for Standardized Clinical Terminologies to Improve Surveillance and One Health Collaboration

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Introduction

Veterinary medicine currently lacks widespread adoption of standardized clinical terminology systems, limiting efficient data sharing across the industry, veterinary clinics, diagnostic laboratories, public health agencies, and academic institutions. In contrast, human healthcare systems use standardized terminologies to support interoperability, surveillance, and large-scale health data integration. Furthermore, these systems are commonly supported by regulations and governmental agencies. Despite the development of the Veterinary Extension of SNOMED CT in the United States, veterinary clinical documentation and data exchange remain fragmented across practice types and software platforms. This study uses the state of Minnesota, USA, as a case study to evaluate veterinary stakeholders' awareness, readiness, and perceived barriers related to adopting standardized clinical terminologies to strengthen veterinary surveillance and One Health coordination.

Methods

A cross-sectional mixed-methods study was conducted. The study population included veterinary stakeholders across multiple sectors, including private clinical practice, academia, diagnostic laboratories, public health, pharmacy services, and veterinary electronic medical record (EMR) software companies. Surveys targeted veterinarians and other veterinary personnel involved in clinical documentation. Semi-structured interviews were conducted with additional veterinary industry stakeholders to further explore implementation challenges, interoperability concerns, perceived benefits, and opportunities related to standardized terminology adoption.

Results

Preliminary findings showed variable awareness and readiness regarding standardized veterinary terminologies across stakeholder groups. Commonly perceived barriers included limited training opportunities, EMR system constraints, workflow disruption concerns, financial and personnel resource limitations, and inconsistent documentation practices.

Conclusions

Standardized veterinary clinical terminologies have the potential to strengthen veterinary informatics and surveillance capacity. Implementation may facilitate more efficient data aggregation, data analysis, and support earlier detection of zoonotic threats and antimicrobial resistance patterns. Standardized datasets may also improve support for artificial intelligence and predictive analytics in veterinary surveillance and One Health decision-making.



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sciforum-187958: Feed-associated *Clostridium perfringens* enterotoxemia in cattle: toxin detection in organ and feed samples during clinical field investigations

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Clostridium perfringens represents an important cause of sudden death and acute disease in cattle. Although diagnostic investigations focus on organs or intestinal contents collected from animals, field experience suggests that feed management may play a central role in the occurrence of clostridial problems at farm level. In the clinical investigations considered in this study, sampling was triggered by sudden death or clinical signs compatible with clostridiosis. The diagnostic approach was extended to feed matrices and management-related risk factors, with particular attention to feed storage, preservation, and distribution. To evaluate and compare the detection patterns of *C. perfringens* toxins, an ELISA commercial kit was used to test 52 field samples collected during diagnostic investigations and monitoring activities. The dataset included 34 animal organ samples (kidney, spleen, liver, intestine, lung, and heart) and 18 food/feed samples. Samples were tested for the presence of alpha, beta, and epsilon toxins, as well as *C. perfringens* antigen. Toxin detection was more frequent in food/feed matrices (55.6%) compared to organ samples (32.4%). Epsilon toxin showed the most pronounced matrix-associated difference, being detected significantly more often in food/feed matrices (44.4%) than in organ samples (11.8%) ($p = 0.014$). This finding suggests that *C. perfringens* may complete its life cycle and fully activate its metabolic and toxigenic potential within feed prior to ingestion by the host. Among food matrices, unifeed samples showed a 53.3% overall toxin positivity rate. In organs, toxin positivity was most frequently observed in kidney (44.4%), lung (50.0%), and spleen (37.5%), predominantly involving beta and epsilon toxins, while liver samples were consistently toxin-negative. A farm-specific autogenous vaccine will be prepared from outbreak-associated *C. perfringens* isolates recovered from clinically affected animals. Strains will be selected on the basis of culture results and PCR detection of toxin genes, ensuring inclusion of beta- and epsilon-toxin antigens that are absent from commercial vaccines targeting alpha toxin alone.



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sciforum-188063: Genetic Characterization of *Dermacentor* sp. and Associated *Anaplasma bovis*, Infesting Small Ruminants in Pakistan

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Ticks are hematophagous ectoparasites and important vectors of pathogens affecting animal and human health. Species of the genus *Dermacentor* infest a wide range of mammalian hosts, including small ruminants; however, information on their occurrence and genetic diversity in Pakistan remains limited. The present study aimed to morphologically and molecularly characterize *Dermacentor* ticks collected from small ruminants in Balochistan, Pakistan, and to screen them for *Anaplasma* species. A total of 35 ticks were collected and morphologically identified as *Dermacentor* sp. Female ticks showed an oval, brownish-red body with an ornamented scutum, well-developed spiracles, and distinct coxal spurs, while male ticks exhibited an oval body with a strongly ornamented scutum having distinct grooves and punctations, with festoons and lateral eyes at the level of coxa II. Genomic DNA was extracted and subjected to PCR amplification of mitochondrial 16S rDNA and *cox1* genes for tick characterization, while *Anaplasma* spp. were screened using 16S rDNA. BLAST analysis of the obtained 16S rDNA and *cox1* sequences revealed the highest similarity (98.42% and 97.45%, respectively) to *Dermacentor pavlovskyi* reported from China. Phylogenetic analyses based on both markers placed the Pakistani *Dermacentor* sequences in a clade closely related to *D. pavlovskyi*. Furthermore, *Anaplasma* 16S rDNA sequences detected in *Dermacentor* ticks showed 100% identity with *Anaplasma bovis* and clustered with corresponding reference sequences in the phylogenetic tree. The findings provide molecular evidence of a *Dermacentor* lineage closely related to *D. pavlovskyi* and the presence of *A. bovis* DNA in *Dermacentor* ticks from Balochistan, highlighting the need for broader sampling and additional genetic markers to clarify the taxonomic status, distribution, and pathogen associations of *Dermacentor* ticks in Pakistan.

Keywords: *Dermacentor* sp.; *Anaplasma bovis*; tick; Pakistan



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sciforum-191199: Hepatic Oxidative Stress Response to Folate Supplementation in Diabetic Rats

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Background: Diabetes mellitus is associated with multiple metabolic disturbances, particularly in the liver, where oxidative stress plays a major role in the development of hepatic dysfunction. Folate, a water-soluble B vitamin with antioxidant properties, may attenuate diabetes-induced oxidative damage through modulation of antioxidant defense mechanisms and homocysteine metabolism.

Materials and Methods: Eighteen male Wistar rats (200 ± 20 g) were randomly divided into three groups ($n=6$): control, streptozotocin (STZ)-induced diabetic, and folate-treated diabetic groups. Diabetes was induced by intraperitoneal injection of STZ (55 mg/kg). Folate was administered intraperitoneally at a dose of 15 mg/kg/day for 4 weeks. Fasting blood glucose (FBS), serum alanine aminotransferase (ALT), aspartate aminotransferase (AST), hepatic malondialdehyde (MDA), superoxide dismutase (SOD) activity, and total antioxidant capacity (TAC) were evaluated. Statistical analysis was performed using one-way ANOVA followed by Dunnett's post hoc test.

Results: Folate treatment resulted in mild improvements in body weight, FBS, ALT, and AST levels in diabetic rats; however, these changes were not statistically significant compared with untreated diabetic animals. Hepatic MDA and TAC levels remained largely unchanged, while SOD activity showed a slight but non-significant increase following folate administration.

Conclusion: Folate supplementation exhibited limited yet potentially supportive effects on hepatic oxidative stress parameters in diabetic rats. Although statistical significance was not achieved, the observed trend toward improved antioxidant status suggests a possible protective role of folate in diabetes-associated hepatic dysfunction. Further investigations with larger sample sizes, extended treatment durations, and varying dosages are warranted to better clarify its therapeutic potential.



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sciforum-188046: HEPATITIS E VIRUS IN WILDLIFE: AN EMERGING HEALTH RISK

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INTRODUCTION

Hepatitis E virus (HEV) represents a serious public health problem and is one of leading cause of viral hepatitis worldwide, primary transmitted through contaminated water or food. HEV is a small, positive-sense, non-enveloped, single-stranded RNA virus belonging to the Hepeviridae family HEV genotypes 1 and 2 are restricted to humans, while genotypes 3 and 4 infect humans, pigs, and other animal species. Domestic pigs remain the main reservoir of human infection globally, but in recent years, wild animals have been shown to play a crucial role in HEV ecology. This has important implications for food safety and poses a potential zoonotic risk for hunters. In this study, we assessed the presence of HEV in fallow deer and wild boars in Sicily.

METHODS

In the period 2024-2025, 242 samples (liver, intestine, spleen) were collected from 116 wild ungulate animals (51 wild boars, 65 fallow deers). The presence of the HEV genome in the organs was investigated using Real-time RT-PCR, which targets the ORF3 gene (*Macaluso et al. 2021*) HEV positive samples were sequenced by nested RT-PCR targeting the ORF2 gene. The sequences were analyzed to determine the genotypes by BLAST analysis and using the HEV Typing Tool 0.1 ([http:// www.rivm.nl/mpf/typingtool/hev/](http://www.rivm.nl/mpf/typingtool/hev/))

RESULTS

The organs of 6/51 wild boars tested positive for HEV (11.76%) with a Ct value ranging from 21.69 to 42.73 (positive samples should have a Ct ≤ 44). Only two samples with a Ct ≤ 23 could be sequenced, one liver and one spleen from two different animals. Sequence analysis revealed that the samples belonged to unclassifiable genotype 3 strains, as the sequences could not be assigned to any HEV subtype identified to date. All fallow deer samples tested negative for HEV.

CONCLUSIONS

The detection of HEV in wild boars confirms their role as a reservoir, contributing to the maintenance and transmission of the virus between wild animals and humans. The identification of HEV in game offal highlights a possible public health risk linked to the consumption of raw or undercooked wild boar meat, with important implications for food safety. These finding underscore the need to raise awareness among at-risk groups (hunters, game processing worker and consumers) through public communication campaigns. Such measures are particularly relevant in light of the region's ancient hunting traditions and the implementation of selective culling programs through which wild boar meat enters the food chain.



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sciforum-191549: Histopathological and Ki-67 Immunohistochemical Evaluation of Macrophage-Derived Extracellular Vesicles Loaded with 4T1 Tumor Lysate in Prophylactic and Therapeutic Murine Breast Cancer Models

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Background: Extracellular vesicles (EVs) derived from macrophages have emerged as promising carriers for tumor-associated antigens in cancer immunotherapy. This study evaluated the prophylactic and therapeutic efficacy of macrophage-derived EVs loaded with 4T1 breast cancer cell lysate in a murine breast cancer model and explored their translational relevance from a One Health perspective.

Methods: RAW264.7 macrophages were stimulated with lipopolysaccharide (LPS) and passively loaded by overnight incubation with 4T1 tumor cell lysate prior to EV isolation. Female BALB/c mice received antigen-loaded EVs either prophylactically (three injections before tumor challenge) or therapeutically after tumors became palpable. A control group received free 4T1 tumor cell lysate without EVs. Tumor growth, survival, histopathological alterations, lung metastasis, and Ki-67 expression were evaluated.

Results: Prophylactic EV administration markedly inhibited tumor growth compared with the control group (day 35 tumor volume: 0.0543 vs. 24.8 mm³, $p = 0.001$). Ki-67 expression was significantly reduced from 29% in controls to 14% in the prophylactic group ($p = 0.001$). Histopathological examination demonstrated fewer mitotic figures, reduced nuclear pleomorphism, and no histologically detectable metastatic foci in the examined lung sections of prophylactically treated mice. Therapeutic administration produced intermediate pathological improvement. Although survival was higher in the prophylactic group, the difference was not statistically significant.

Conclusions: Macrophage-derived EVs loaded with 4T1 tumor lysate significantly suppressed tumor growth and proliferation and reduced histological evidence of pulmonary metastasis, particularly when administered prophylactically. These findings support further investigation of antigen-loaded EVs as a translational strategy for comparative oncology and One Health, where naturally occurring cancers in animals and experimental murine models can provide insights relevant to human breast cancer.



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sciforum-187899: Illegal wildlife trade and zoonotic spillover risk at human–animal–environment interfaces: a systematic review

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Abstract: The illegal wildlife trade (IWT) is increasingly recognized as a driver of zoonotic disease emergence, creating high-risk interfaces between wildlife, humans, and domestic animals. This systematic review synthesized evidence on zoonotic pathogens associated with IWT and examined how trade-related conditions influence transmission and spillover risk. Primary studies investigating zoonotic pathogens, antimicrobial resistance (AMR), or transmission risks in wildlife involved in illegal trade were included. Studies not related to wildlife trade or lacking pathogen-related outcomes were excluded. A comprehensive search of databases (e.g., PubMed, Scopus, Web of Science) was conducted up to March 16th, 2026. Risk of bias was assessed using the Mixed Methods Appraisal Tool, and results were narratively synthesized due to heterogeneity in study designs and outcomes. A total of 21 studies were included, covering diverse taxa and geographic regions. Zoonotic pathogens, including *Salmonella* spp., *Escherichia coli*, and parasites, were consistently detected in trafficked wildlife. Higher pathogen prevalence was observed in animals exposed to stressors such as capture, transport, and captivity, as well as in anthropized environments. AMR was frequently reported, indicating microbial exchange between humans, domestic animals, and wildlife. However, while pathogen presence and conducive conditions for transmission were well documented, direct evidence of spillover events was limited. The evidence base is constrained by predominantly cross-sectional designs, small and non-representative samples, and variability in diagnostic methods. Overall, the findings support a One Health perspective, identifying IWT as a potential amplification pathway for zoonotic pathogens. Strengthened surveillance, improved biosecurity, and integrated policies are needed, alongside longitudinal and standardized research to understand transmission dynamics better.



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sciforum-186561: Immunoprotective Evaluation of Scoloptoxin SSD14, Inositol Monophosphatase, and Neprilysin Against Ticks Infestation

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Ticks are hematophagous arthropods and potential vectors of numerous tick-borne pathogens affecting both animals and humans. Globally, synthetic acaricides remains primary strategy for controlling tick infestations, however their prolong use poses challenges including resistance development and environmental contaminations. Herein, three candidate antigens including scoloptoxin SSD14, inositol monophosphatase and neprilysin antigens were immunologically characterized as anti-tick vaccine. Using *In-silico* bioinformatics tools, these *Rhipicephalus microplus* proteins were selected as a vaccine candidates based on physiochemical analyses and epitope prediction. The DNA fragments encoding these proteins were cloned into pET-32a(+) expression vectors, transformed into *Escherichia coli* BL-21 star for recombinant protein expression. Rabbits were subcutaneously immunized using 100 µg of each purified protein emulsified in oil adjuvant, and the control group received only adjuvant. The bioinformatic analyses of these proteins revealed the presence of several immunogenic epitopes which could be useful in a vaccine against ticks. Biological parameters including weight and number of fully engorged female ticks, egg laying, egg fertility, nymphal molting rate, and antibody level were statistically analyzed using Student t-test and one-way ANOVA. In vivo assessment demonstrated that all three antigens reduced tick parameters, the scoloptoxin SSD14 statistically decreased adult female egg laying up to 16%, and egg fertility decreased by 37%, with an overall vaccine efficacy of 47%. Inositol monophosphatase statistically reduced the number of adult females up to 23%, egg laying in adult females up to 11%, and larval hatching decreased by 40%, accounting for 59% total vaccine efficacy. Neprilysin statistically reduced the nymph numbers to 40%, larval hatching up to 41%, with overall vaccine efficacy of 64%. These findings highlight the potential of these antigens in the development of anti-tick vaccine.



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sciforum-187599: Integrated approach to *Brucella ceti* infection in stranded Mediterranean dolphins

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Introduction:

Brucella ceti is an emerging zoonotic pathogen causing neurological, reproductive, and systemic disease in cetaceans, representing a public health concern due to increasing humans-marine mammals interactions. Despite growing reports worldwide, critical gaps persist in cetacean-specific diagnostics and identification of genomic markers for epidemiological tracing. This study addresses these limitations to advance disease understanding in cetaceans.

Methods:

Thirty cetaceans with suspected *Brucella* infection stranded along the western Mediterranean coast (2011- 2021) were investigated combining bacteriological culture, qPCR, histopathology, and serological testing via a commercially available blocking ELISA, to assess diagnostic strategies for epidemiological surveillance and phylogenetic understanding. Whole-genome sequencing (WGS) assessed genetic diversity and phylogenetic relationships among circulating strains.

Results:

B. ceti infection was confirmed in nearly half of the investigated dolphins by culture and qPCR, with minor discrepancies underscoring their complementary utility. Culture remained the gold standard, while qPCR provides a valuable screening tool. Infection was detected exclusively in striped dolphins (*Stenella coeruleoalba*), consistent with their elevated susceptibility in the Mediterranean Sea.

A commercial blocking ELISA, originally developed for terrestrial livestock, was validated for cetaceans, using panels from culture-positive and brucellosis-free dolphins, achieving 100% diagnostic specificity and filling a key gap in marine brucellosis serology.

Two circulating sequence types, ST26 and ST49, were identified, clustering with Mediterranean strains from Spain and Italy. SNP analysis revealed minimal variation between isolates from the same animal, whereas comparisons between different animals showed both closely related and divergent strains, contributing to a genomic reference dataset for future epidemiological SNP thresholds.

Histopathological examination revealed lesions exclusively in the CNS, with no reproductive or osteoarticular findings reported.

Conclusions:

This study demonstrates the superiority of an integrated multi-method approach for marine brucellosis surveillance. Validation of blocking ELISA for cetaceans and genomic characterization

of circulating strains represents significant advances for wildlife health monitoring and zoonotic risk management.



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sciforum-173309: Isolation & Characterization of Bacteria, Fungi and Parasites from Infected Migratory Birds (Kokkare Belluru Pelicans)

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Pelicans (*Pelecanus*) are described as highly susceptible to a range of infections due to low immunity and unhealthy environments, with avian infections posing challenges to their life cycle and linked ecological systems. The study focuses on the most common infections, listing Botulinum, Aspergillosis, Helminths, Nematode (Ringworm), and Arthropod parasitic infections as key concerns. This framing highlights the breadth of potential pathogens that can affect pelicans and the importance of understanding their impacts on health and ecological balance.

To detect these pathogens, researchers collected pelican fecal matter and used plating techniques on Agar-Agar, Potato Paste, and Sheep Blood Agar, incubating at 25°C and then characterizing colonies by morphology. Fungal identifications involved mycelial studies with teased mounts stained by lacto phenol cotton blue (LPCB), and identifications followed guidelines proposed by Larone (1976) and Al-Doory (1980). Bacterial identification employed Gram staining (crystal violet, Gram's iodine, 90% alcohol, and safranin) as described by Hans Christian Gram. In addition, water samples were plated to identify microbes, and molluscs—an occasional pelican prey item—were collected and examined with bacterial staining. The analysis extended to the pelican food chain context, noting that their diet of molluscs, arthropods, and even maggots can influence the parasitic associations observed.

Among the findings, *Fusarium*-associated mycotoxin was identified, specifically Deoxynivalenol (DON), indicating a fungal toxin linked to the infections observed. The study concludes that further work is needed to elucidate the mechanisms and roles of these pathogens in pelican pathogenesis. Overall, the work documents multiple pathogens in pelicans using culture- and microscopy-based approaches and underscores the need for additional research to clarify the pathogenesis and ecological implications of these infections.



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sciforum-194672: Isolation of *Yersinia enterocolitica* in *Caretta caretta* nesting sites along the western coast of Sicily

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The loggerhead sea turtle (*Caretta caretta*) is the only sea turtle species known to nest along the Sicilian coast. Given its vulnerability and the constant threats posed by human activities, monitoring these nesting sites is crucial for conservation efforts. Adopting a One Health approach, this study evaluated the presence of zoonotic bacteria in unhatched eggs, sand, and seawater from three *C. caretta* nests located along the western coast of Sicily, to assess the potential impact of these bacteria on animal and environmental health

Two hundred unhatched eggs, sand from the nests and seawater in front of the nests were analyzed from three nests located along coast of Trapani (Sicily, Italy). Samples were plated on selective and differential agar media and incubated at 37°C for 24h.

The identification of isolated strains was carried out with the biochemical APIØ system. Microbiological analyses showed that *Yersinia enterocolitica* was present in all nesting sites and in all the samples analyzed. This zoonotic pathogen was found both as the only contaminant and in combination with other bacteria, such as *A. hydrophila*, *B. cereus*, *V. parahaemolyticus* and *E. coli*.

The presence of *Y. enterocolitica* in sea turtle nests was associated with embryonic mortality due to its ability to penetrate the pores of the shell under specific environmental conditions of humidity and temperature. The isolation of this pathogen suggests that it may play a role in the reproductive success of *C. caretta* in this area. The isolation of *Y. enterocolitica* from sand and seawater could indicate a source of environmental or anthropogenic contamination. The coastal areas of Sicily are often subject to anthropogenic pressures. Understanding the interaction between these zoonotic pathogens and the nest microenvironment is essential for developing conservation strategies aimed at mitigating embryonic mortality and protecting this vulnerable species along the Sicilian coast.



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sciforum-188137: Lizards as an unconventional model to evaluate the effects of contaminants on soil organisms.

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Soil is the Earth's upper layer that sustains plant life, hosts an extraordinary biodiversity, and plays a key role in ecosystem functioning. But the excessive use of agrochemicals to increase agricultural productivity and the constant discharge of industrial and urban waste have resulted in the slow decline of soil quality. This situation has underscored the importance of preserving terrestrial ecosystems, and there is growing interest in developing effective and sustainable remediation strategies. Model organisms and reliable biomarkers are needed to assess the effectiveness of such interventions. Ecotoxicological studies most often use invertebrates, such as earthworms and snails, as biological models, but the results obtained cannot be easily extrapolated to more complex organisms such as terrestrial vertebrates, including humans. In this respect, terrestrial lizards have proven to be promising experimental models. They have a smaller range than birds and fewer ethical considerations than small mammals. In recent years, research on the Italian field lizard *Podarcis siculus* has provided insights into the bioaccumulation and toxicological effects of soil contaminants in terrestrial vertebrates. Histological analyses showed significant vacuolization of hepatocytes and atrophy of gonadal tissue in samples exposed to environmentally relevant concentrations of glyphosate and cadmium. Moreover, molecular analyses showed a dose-dependent induction of the stress response gene Hsp70 in the liver of cadmium-exposed animals, which strongly correlated with the extent of tissue damage. In individuals exposed to glyphosate, however, an increase in the expression of estrogen receptors mRNA in the testis was observed, suggesting a possible endocrine-disrupting effect. These results confirm *Podarcis siculus* as a highly sensitive biological model for studying the sublethal effects of soil contaminants on terrestrial vertebrates. The histological and molecular biomarkers detected are useful tools for environmental biomonitoring programs, improving the assessment of terrestrial ecosystem health and remediation effectiveness, also providing essential data for future ecotoxicological risk assessments.



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sciforum-186889: Long-Term Epidemiological Dynamics, Control of Brucellosis, and Human Complications in Albania and the Korçë Region:One Health Approaches to Emerging Zoonotic Threats.

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Introduction: Brucellosis is a zoonotic infection caused by *Brucella* species, transmitted from animals to humans through contact or products, affecting multiple systems and causing serious focal complications in humans.

Understanding the situation of brucellosis in humans and animals in Albania and the Korçë region, as well as raising awareness about its consequences for human health through the One Health approach.

Methodology: For the realization of this study, a descriptive-analytical study design was used. The material includes data collected from the epidemiological reporting databases of brucellosis from the Institute of Public Health the Veterinary Service , the Directorate of Public Health , and the Regional Hospital of Korçë.

We studied the identified cases of brucellosis based on epidemiological surveillance data for animals (cattle and small ruminants) in Albania , Korçë region, as well as patients diagnosed with brucellosis in Albania and the Korçë district. We also examined the condition and complications of patients with brucellosis hospitalized at the Regional Hospital .

The study covers the time period 1980 - 2025.

Resultats :In the 1990s, the opening of international borders and uncontrolled trade of livestock led to an increase in brucellosis cases, mainly in small ruminants. The peak occurred between 2002–2005 in the Korçë region, where 84 of 156 villages were identified as infected foci, accompanied by a high number of human cases, with a predominance in rural areas, especially among males aged 40–60 years. Vaccination programs reduced cases significantly, although a rise was observed in 2012–2013. The 2017 mass vaccination significantly reduced cases, but brucellosis persists in cattle, with increased incidence in 2025 and more hospitalizations reported January 2026.

Conclusions: Brucellosis remains endemic with ongoing transmission. Although better controlled in recent years, it is not yet eradicated in Albania or the Korçë region, with new cases still occurring.



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sciforum-187529: Maternal, colostrum management, and environmental factors associated with clinical signs of neonatal disease in calves from Yolombó, Antioquia, Colombia: a pilot study with a One Health approach

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Passive immunity mediated by colostrum is essential for the immunological development of calves during the first hours of life, and its efficiency depends on maternal, neonatal, environmental, and management-related factors. The aim of this study was to evaluate maternal, colostrum management, and environmental factors associated with the presence of clinical signs compatible with neonatal disease in calves from farms in Yolombó, Antioquia, Colombia, with a One Health approach. An observational cross-sectional pilot study was conducted on six cattle farms. A structured survey collected information on maternal, neonatal, colostrum management, environmental, and sanitary variables. Data were analyzed using descriptive statistics and Fisher's exact test ($p \leq 0.05$). Fifty percent of the evaluated cows were multiparous and 16.7% experienced dystocia. No farm reported prepartum vaccination. Among neonates, 66.7% exhibited high vitality while 33.3% showed clinical signs compatible with neonatal disease. All calves received colostrum within the first four hours postpartum. Farmers do not assess colostrum quality using diagnostic techniques. According to the farm records, *Cryptosporidium* spp. (50%) and *Eimeria* spp. (33%) were the most frequently recorded enteric agents. However, it is important to note that the presence of these pathogens was not confirmed in this study. Additionally, 66.7% of farms presented muddy conditions and low environmental temperatures. No significant associations were observed between the evaluated variables and neonatal clinical signs; however, given the pilot nature of this study ($n = 6$ calves), these results should be interpreted with caution due to limited statistical power. The One Health framework enabled interpretation of the interaction among the analyzed factors; nonetheless, the absence of direct human health indicators presents a limitation; future studies should incorporate zoonotic risk assessment among farm workers. We provide relevant information on bovine neonatal health practices in the region, and this serves as a basis for future research involving a greater number of farms, cattle, and regions in Colombia.



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sciforum-188104: Nanobiosensors in the Future of Cystic Echinococcosis Control: A Systematic Review Within the One Health Framework

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Abstract

Introduction: Cystic echinococcosis (CE) is a zoonotic parasitic disease of global public health and economic importance. Although previous studies have addressed the potential applications of nanotechnology in CE diagnosis and treatment, there is a clear research gap regarding the application of nanobiosensors for CE control, particularly from a “One Health” perspective. Therefore, this study aims to provide a detailed and focused systematic review of nanobiosensor-based diagnostic and monitoring approaches for the management of CE within a One Health framework.

Methods: This study used a systematic review and followed the PRISMA protocol. A comprehensive search of scientific articles was conducted between January 2020 and December 2025 in databases, including PubMed, Scopus, Web of Science, and Google Scholar, using combined keywords related to CE and nanobiosensors. Inclusion criteria were the experimental, clinical, veterinary or field-based investigations. The screening process of titles, abstracts, and full texts of articles were also performed. Duplicates were removed, and an assessment of the quality of the articles was performed; finally, 17 studies were included.

Results: Biosensing platforms based on gold, silver, carbon nanoparticles, and nanofibers, using antigenic and genetic markers of the parasite, were capable of detecting CE with a sensitivity range of 85 to 98% and a specificity range of 87 to 99%. Nano-enabled diagnostic systems enable the development of rapid, portable, and cost-effective diagnostic kits for use at veterinary, healthcare, and environmental monitoring levels. Nanobiosensors' application in drug resistance monitoring and in evaluating the effectiveness of control programs was also promising. However, significant challenges remain, including issues related to mass production, standardization, initial costs, and nanoparticle safety.

Conclusion: Nanobiosensors showed significant practical implications for the effective management of CE by enabling early detection, continuous monitoring in human and animal populations, and facilitating integrated disease control strategies within a One Health framework.



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sciforum-188124: Natural compounds with potential acaricidal activity against *Rhipicephalus microplus*: molecular docking screening of glutathione S-transferase inhibitors

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The cattle tick *Rhipicephalus microplus* is one of the most important ectoparasites affecting livestock worldwide, causing substantial economic losses through reduced animal productivity, pathogen transmission, and the costs associated with chemical control. The intensive use of acaricides has contributed to the emergence of resistant tick populations and environmental contamination, underscoring the need for innovative, sustainable control strategies aligned with the One Health approach. In this context, glutathione S-transferase (GST), an enzyme involved in detoxification and acaricide resistance, has emerged as a promising molecular target for developing new acaricidal compounds. Therefore, this study aimed to identify natural compounds with potential inhibitory activity against GST of *R. microplus* using molecular docking approaches. The three-dimensional structure of GST from *R. microplus* was obtained from the AlphaFold Protein Structure Database. A total of 1,000 natural compounds were retrieved from the Natural Products Atlas. Molecular docking simulations were performed at the GST H-site using Molegro Virtual Docker. Compounds were ranked according to MolDock Score values, and the best docking poses were further evaluated for intermolecular interactions and ADMET properties. The ten best-ranked compounds showed MolDock Scores ranging from –156.264 to –137.364. Several compounds exhibited favorable predicted pharmacokinetic profiles, including high intestinal absorption and absence of AMES toxicity or skin sensitization. Notably, none of the ten top-ranked compounds has previously been reported as a GST inhibitor of *R. microplus* or evaluated for acaricidal activity against this tick species. These findings identify novel natural compounds with predicted affinity for GST and highlight their potential as candidates for future *in vitro* and *in vivo* studies. By supporting the development of acaricidal agents with innovative mechanisms of action, these compounds may contribute to reducing reliance on conventional acaricides, mitigating environmental contamination, slowing the selection of resistant tick populations, and promoting more sustainable livestock production.



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sciforum-193593: One Health Approach to Tick and Tick-Borne Disease Surveillance in Iran

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Introduction: Tick-borne diseases (TBDs) represent a growing public health and veterinary concern, driven by environmental change, expanding vector habitats, and increased human–animal interactions. In Iran, ticks are vectors of zoonotic pathogens, including Crimean–Congo hemorrhagic fever (CCHF), anaplasmosis, ehrlichiosis, babesiosis, and theileriosis. The epidemiology of these diseases necessitates an integrated surveillance framework considering the interconnected health of humans, animals, and ecosystems. This study aimed to evaluate the application of a One Health approach for surveillance and control of ticks and tick-borne diseases in Iran. CCHF remains one of the most important tick-borne zoonoses in the country, with cases reported across many provinces and involvement of livestock and tick reservoirs.

Methods: A multidisciplinary surveillance framework was developed by integrating entomological, veterinary, environmental, and public health data. Tick specimens were collected from livestock, wildlife, and environmental habitats across ecological regions of Iran. Molecular screening, pathogen detection, geographic information systems (GIS), and epidemiological analyses were employed to identify tick species, prevalence, and transmission hotspots. Surveillance data from health sectors were incorporated to assess disease dynamics.

Results: Surveillance identified multiple tick genera, including *Hyalomma*, *Rhipicephalus*, *Haemaphysalis*, and *Dermacentor*, with *Hyalomma* species representing vectors of pathogens. Several tick-borne pathogens were detected in livestock ticks, particularly CCHF virus, demonstrating circulation within vector and animal populations. Previous studies documented distribution of CCHF-associated ticks and viral detection in several Iranian provinces. Spatial analyses revealed ecological factors associated with increased vector abundance and disease risk.

Discussion: The findings highlight the value of One Health-based surveillance for detection and prevention of tick-borne diseases in Iran. Strengthening collaboration among veterinary, medical, and environmental sectors, combined with surveillance and risk mapping, could improve preparedness and control. An integrated national surveillance network would enhance public health protection, livestock productivity, and ecosystem resilience against emerging tick-borne threats.



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sciforum-194670: One Health Pharmacotherapy of Zoonotic Giardiasis in Dogs and Cats: A Systematic Review

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Introduction: Giardiasis, caused by *Giardia lamblia*, is one of the most common fecal-oral zoonoses worldwide. Dogs and cats serve as important reservoir hosts and contribute significantly to environmental contamination and potential transmission to humans through the shedding of cysts in their feces. This systematic review aims to evaluate the available evidence on the efficacy of fenbendazole, metronidazole, and newer nitroimidazoles in reducing cyst shedding, with particular emphasis on their potential to mitigate environmental contamination and zoonotic risk within a One Health framework.

Methods: A comprehensive search was conducted using the keywords "Zoonotic giardiasis," "Canine and feline pharmacotherapy," "Environmental cyst shedding reduction," "One Health approach," and "Fenbendazole" in PubMed, Scopus, and Web of Science, with publications from January 2018 to December 2025. After removing duplicates and applying inclusion/exclusion criteria (clinical trials in dogs and cats, cyst shedding quantification, and safety assessment), a total of 36 articles were finally included.

Results: Fenbendazole (50 mg/kg for 3-5 days) remains the first-line treatment in dogs and cats, with 85-90% efficacy in reducing cyst shedding, high safety, and few side effects. Metronidazole (25 mg/kg twice daily for 5-7 days) has 60-75% efficacy, but is associated with neurological complications (ataxia, lethargy) in 10-15% of cases. Newer nitroimidazoles (such as ronidazole) with 75-80% efficacy and shorter treatment duration (3 days) are a good option, but their disadvantages are higher cost and more limited animal studies.

Conclusion: In the context of a One Health system, fenbendazole remains the drug of choice for controlling zoonotic giardiasis in dogs and cats due to its efficacy in reducing cyst shedding, high safety profile, and reasonable cost. Reducing cyst shedding through effective treatment directly reduces environmental contamination (soil, water, parks) and breaks the chain of transmission to humans. Concomitant administration of probiotics and environmental hygiene is an essential complement to this approach.



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sciforum-187515: Prevalence and antibiotic sensitivity profile of extended spectrum beta - lactamase producing *Salmonella enterica* in sun-dried meat (Kundi)

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Background: Zoonotic and multidrug resistant extended spectrum beta-lactamase (ESBL) *Salmonella enterica* found in sun-dried meat (kundi) can contribute to the increased chances of infections and multidrug resistance in humans.

Objectives: The present study was conducted to assess the prevalence and antibiotic resistance patterns of ESBL- *Salmonella enterica* isolated from sun-dried meat.

Methods: A cross-sectional study was conducted on 384 sun-dried meat samples from open markets in Ibadan, Nigeria. Isolation and characterisation was carried out using the ISO 6579-1:2017 protocol. Antibiotic susceptibility testing of 21 ESBL- *Salmonella enterica* isolates against Carbapenems (10µg), Cefotaxime (30µg), Ceftazidime (30µg), Tetracyclines (30µg), Gentamicin (10µg), and Tigecycline (10µg) was performed by disc diffusion method. Multiple antibiotic resistance index (MARI) values were also calculated.

Results: The prevalence of *Salmonella enterica* was 11% (42/384). 21 isolates were confirmed to be ESBL- *Salmonella enterica* and were selected for antibiotic susceptibility testing. 100% of the isolates were resistant to Ampicillin 21(100), Cefotaxime 21(100), and Ceftazidime 21(100%). 95% and 81% were resistant to Meropenem 20(95) and Tetracycline 17(81) respectively, while 100% and 90% of the isolates were susceptible to Gentamicin 20 (100) and Tigecycline 19 (90) respectively. All isolates were multidrug-resistant, with MARI values ranging from 0.57 to 0.86.

Conclusion: Resistance to Carbapenems and Tigecycline in this study raises concern about the circulation of Carbapenemase- and ESBL-producing strains of *Salmonella enterica* within the food chain. The presence of multidrug resistance ESBL- *Salmonella enterica* recorded for this study showed that sun-dried meat hosted resistant strains of ESBL *Salmonella enterica* in the study area and it indicate an important public health problem. To curtail this alarming signal, there is need to strengthen antimicrobial stewardship, ensure routine food safety surveillance, and adopt one health strategies to mitigate antimicrobial resistance in Nigeria.



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sciforum-194556: Prevalence and characterisation of ESBL- and MCR-1-harbouring multidrug-resistant *Escherichia coli* in raw milk cheese and chicken carcasses in Egypt: Algal Extracts as a Potential Control Strategy

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We characterized extended-spectrum β -lactamase (ESBL)-producing and polymyxin-resistant *Escherichia coli* in raw milk cheese and chicken carcasses in Egypt. A total of 200 raw milk, cheese, and chicken carcass samples were examined. Antimicrobial susceptibility testing and phenotypic confirmation of resistance patterns were done. PCR was performed for various resistance and virulence genes. Phylogenetic grouping was also performed. Two algal extracts of *Padina pavonica* and *Polycladia myrica* were tested against virulent MDR *E. coli*. 14% of samples were *E. coli* positive, among which 64.3% were classified as multidrug-resistant (MDR), particularly those isolates obtained from chicken carcasses (88.9%). The majority of the isolates were potentially pathogenic, carrying ≥ 3 virulence factors. The most predominant virulence factor was *iss*, followed by *iutA*, *eaeA*, and *Stx1/Stx2*. Notably, these virulence determinants were more prevalent in *E. coli* isolates recovered from chicken carcasses. The potential enteropathogenic *E. coli* was most frequent, being encountered in 60.7% of the isolates, while 28.6% of isolates were identified as potential enterohemorrhagic *E. coli*. Importantly, the highly virulent *Stx*-positive EHEC isolates were recovered exclusively from chicken carcasses. An extraintestinal pathogenic *E. coli* was found in 3.6%. A high prevalence of ESBLs was evidenced among those isolates, with *bla*_{CTX-M} being the predominant ESBL identified (96.4%). Additionally, *bla*_{SHV} and *bla*_{CMY-2} were detected. A markedly high prevalence rate of *mcr-1* (82.1%) was observed, particularly among chicken carcass isolates. Notably, co-occurrence of ESBL genes and the *mcr-1* gene was observed. Most isolates belonged to the low pathogenic group B1 (85.7%). The different algal extracts exhibited varying levels of antimicrobial activity with MIC values ranging from 2.5 to 10 mg/mL. These results address a serious public health issue since it poses a risk to consumers' health, being a source of dissemination of MDR *E. coli*, which can cause subclinical to severe and fatal infections in humans.



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sciforum-187674: Protective assessment of oral immunization against genotype II using a new ASFV live attenuated vaccine prototype in wild boar

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Introduction

African Swine Fever (ASF) is a highly lethal hemorrhagic viral disease affecting domestic and wild suids. Its rapid spread across Europe and Asia, together with the lack of effective treatment or authorized vaccines in Europe, has led to significant economic losses. Since wild boars pose a major control challenge, the development of a safe and effective oral vaccine is crucial due to handling difficulties.

Methods

This study, performed in BSL-3 facilities, evaluated the efficacy of a new DIVA vaccine candidate Lv17/WB/Rie1-ΔCD-ΔFJ, derived from the naturally attenuated strain Lv17/WB/Rie1 in wild boar by oral route. Ten wild boars were twice orally vaccinated on days 0 and 18 and challenged intramuscularly on day 36 post-vaccination with the highly lethal Armenia 2007 strain (100% mortality in controls). A non-vaccinated control group was challenged in the same conditions. Animals were under continuous monitoring throughout the experiment including assessment of clinical signs, rectal temperature, viremia levels and immune response over a 62-day period.

Results

The oral vaccine candidate showed an overall favourable safety profile, with no adverse clinical signs observed during the experimental period, presenting low and transient viremias (37.84 ± 5.97). Detectable vaccine-induced antibodies were observed in 7/10 animals; all seropositive animals survived challenge, whereas seronegative animals and all controls succumbed to infection. Following challenge, vaccinated animals exhibited lower viremia levels than controls (21.02 ± 6.66) and low clinical scores ($CS=0.6 \pm 1.67$), indicating partial protection against disease.

Conclusions

This vaccine candidate reduced viremia and conferred partial protection against virulent challenge. However, as this is an initial experimental evaluation, further studies and field trials are required to confirm these findings and rule out reversion to virulence. Despite these limitations, the results support the continued development of this attenuated vaccine as a potential tool for ASF control.



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sciforum-187885: Seroprevalence of Avian Influenza Viruses (H5N1 and H9N2) Among Poultry Workers and Live Bird Market Vendors in Asia: A Systematic Review and Meta-Analysis

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Background

Occupationally exposed poultry workers and live bird market (LBM) vendors represent a major zoonotic interface for avian influenza transmission in Asia. To our knowledge, no prior PRISMA 2020-compliant meta-analysis has concurrently pooled H5N1 and H9N2 seroprevalence estimates in this occupational population across Asia.

Methods

A systematic review and meta-analysis was conducted following PRISMA 2020 guidelines (PROSPERO: CRD420261380328). PubMed, Google Scholar, and Elicit were searched from inception to 10 May 2026. Eligible studies reported serological evidence, assessed by haemagglutination inhibition (HI) or microneutralisation (MN) assay, of H5N1 or H9N2 infection among Asian occupationally exposed poultry workers and LBM vendors. Risk of bias was assessed using the JBI Critical Appraisal Checklist. Pooled seroprevalence was estimated using a DerSimonian–Laird random-effects model with Freeman–Tukey double-arcsine transformation. Publication bias was evaluated using Egger's test.

Results

Of 70 records identified, 22 studies met eligibility criteria (21 included in meta-analysis), spanning seven countries and 26,413 participants. Eight studies were rated low risk of bias and 12 moderate. Pooled seroprevalence was 2.38% (95% CI: 0.62–5.23%; $I^2=84.8\%$) for H5N1 and 11.79% (95% CI: 5.96–19.27%; $I^2=96.9\%$) for H9N2. Subgroup analysis revealed marked regional variation: South Asian studies yielded H9N2 seroprevalence of 24.9% (95% CI: 10.3–49.0%) approximately four-fold higher than East Asia (5.9%, 95% CI: 2.8–11.9%). Sensitivity analyses yielded lower pooled estimates of 0.71% (H5N1) and 4.44% (H9N2). No publication bias was detected for H5N1 ($p=0.798$); H9N2 asymmetry ($p=0.002$) may reflect regional and small-study effects rather than publication bias.

Conclusions : Avian influenza seroprevalence among occupationally exposed poultry workers and LBM vendors in Asia is notable, particularly H9N2 in South Asia. The marked four-fold regional variation in H9N2 seroprevalence, combined with persistently high heterogeneity, points to the need for region-specific occupational surveillance programmes and standardised serological protocols. Strengthening One Health frameworks, and expanding seroepidemiological coverage to underrepresented settings would contribute to pandemic preparedness strategies in high-risk poultry-exposed populations.



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sciforum-189128: The Gap Between Human Rabies Deaths and Animal Rabies Surveillance Data: A Systematic Review of One Health Opportunities

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Objective and introduction

Rabies is one of the deadliest zoonoses with a mortality rate approaching 100% after the onset of clinical symptoms. Despite effective prevention strategies (animal vaccination and post-exposure prophylaxis), tens of thousands of human deaths still occur annually. This systematic review aimed to quantify this gap and identify missed opportunities for public health.

Methods

A systematic search was conducted in PubMed, Scopus, Web of Science, and regional databases (such as WHO Global Index Medicus) for studies published between January 2020 and December 2025. Inclusion criteria included studies that simultaneously reported (1) the number of human deaths due to clinically or laboratory-confirmed rabies and (2) surveillance data for rabies in animals (dogs, wild animals, livestock) in a specified geographic area and time period. Study quality was assessed using the NIH tool for cross-sectional and cohort studies.

Results

Of the 892 initial articles, 27 studies from 18 countries (mainly in Africa and Asia) met inclusion criteria. In 22 studies (81.5%), the ratio of human deaths to confirmed animal cases was greater than 10:1. In 12 studies (44.4%), there was no reported case of rabies in animals despite at least 50 human deaths during the study period. The most important factors associated with a larger gap were; a weak integrated surveillance system (86% of studies), lack of local diagnostic laboratory (79%), lack of mandatory reporting of animal rabies (71%), and lack of coordination between the Ministry of Health and Veterinary Medicine (64%).

Conclusion

There is a deep and systematic gap between human deaths from rabies and animal surveillance data, indicating numerous missed opportunities for early intervention. Establishing integrated human-animal reporting systems, strengthening shared diagnostic laboratories, and making animal rabies reporting mandatory are recommended as key health priorities to fill this gap and save lives.



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Session 2. Surveillance and Epidemiological Modelling at the Human-Animal-Environment Interface

sciforum-194329: The Gut–Kidney Axis in Feline Chronic Kidney Disease: A Systematic Review of Microbiome Dysbiosis and Translational Therapeutic Implications within a One Health Framework

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Abstract

Chronic kidney disease (CKD) in cats is a progressive condition commonly associated with irreversible nephron loss, chronic low-grade inflammation, and retention of uremic solutes, particularly protein-bound toxins. In recent years, increasing attention has been directed toward the gut–kidney axis as a potential contributor to disease progression, mainly through microbial metabolites and host–microbiome interactions that may influence systemic homeostasis. This systematic review summarizes current evidence on gut microbiome alterations in feline CKD and explores their potential role in uremic toxin production, inflammatory signaling pathways, and emerging microbiome-based therapeutic strategies. A structured literature search was conducted in PubMed, Scopus, and Web of Science to identify studies evaluating gut microbiome composition and function in cats with CKD. Observational, experimental, and interventional studies were included when reporting microbial diversity, uremic toxins, inflammatory biomarkers, or microbiome-targeted therapies. The review followed PRISMA guidelines for study selection and synthesis. Across available studies, feline CKD is consistently associated with gut dysbiosis characterized by reduced microbial diversity and depletion of commensal bacteria involved in short-chain fatty acid production. In contrast, an increased abundance of proteolytic and urease-producing taxa is frequently reported. These changes are associated with higher circulating levels of uremic toxins such as indoxyl sulfate and p-cresyl sulfate, which have been linked to oxidative stress, endothelial dysfunction, and chronic inflammation. Although evidence remains limited and heterogeneous, preliminary studies suggest that dietary modification, probiotics, and prebiotics may reduce uremic toxin burden and partially improve metabolic and inflammatory parameters. Overall, current evidence supports a biologically relevant gut–kidney axis in feline CKD. However, heterogeneity in study design and limited controlled data prevent firm conclusions regarding therapeutic efficacy. Further well-designed longitudinal studies are needed to clarify the clinical potential of microbiome modulation in feline CKD management.



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sciforum-188076: Machine Learning for Microbiological Risk Assessment of Animal-Derived Foods: A Systematic Review Focusing on Predictive Model Validation

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Introduction: Machine learning (ML) models have been proposed for microbiological risk assessment (MRA) of foods to integrate complex data. However, external validation and operational readiness remain limited. This review critically synthesizes the application of supervised ML to the MRA of animal-derived foods, with an emphasis on validation strategies.

Methods: Following PRISMA 2020, we searched Scopus, Web of Science, and PubMed for original studies. After duplicate removal, articles were screened using Rayyan, followed by full-text review. Inclusion criteria: (i) supervised ML for prediction; (ii) microbiological outcome (pathogen presence/concentration, antimicrobial resistance); (iii) animal-derived food matrices or production environments; (iv) performance metrics and validation reported. Including 21 studies, total.

Results: Random Forest ranked best in 9/21 studies, boosting models (XGBoost, LightGBM, GBM) in 6/21, and neural networks in 3/21. Accuracy (12/21) and AUC-ROC (9/21) were the most reported. Only 7 studies reported F1-score, and 2 MCC – metrics are more suitable for imbalanced data. K-fold cross-validation was common (17/21), yet true external validation (temporal/geographic) occurred in only 8 studies, and only Mi et al. (2025) performed prospective validation on unseen data. Data leakage was discussed in 3 articles, but potentially affected 12 investigations that split data by record without grouping by animal or farm. Meteorological variables were the dominant predictors (4/21), while genomic data (2/21) enabled strain-level resolution. Most studies (15/21) addressed Exposure Assessment; only Njage et al. (2020) integrated ML into a full quantitative MRA, showing that ignoring genetic heterogeneity can lead to over- or underestimation of risk.

Conclusion: Despite high predictive performance ($AUC > 0.85$, $R^2 > 0.93$), gaps persist: external validation is missing in 62% of studies, data leakage risk in 57%, and code is unavailable in 76%. Recent advances (2023–2025) in explainable AI, rigorous temporal validation, and operational tools show progress, but stricter methodological standards are needed for regulatory uptake.



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sciforum-190708: One Health Epidemiology of *Toxoplasma gondii* in Felids, Small Ruminants, and Environmental Sources: A Systematic Review and Meta-Analysis

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Background: *Toxoplasma gondii* is a globally distributed zoonotic protozoan parasite infecting humans, livestock, wildlife, and environmental reservoirs. Felids are the definitive hosts shedding environmentally resistant oocysts, whereas sheep and goats are important intermediate hosts associated with foodborne transmission. Despite numerous regional studies, a comprehensive global One Health synthesis remains limited. This study evaluated the global epidemiology of *T. gondii* in felids, small ruminants, and environmental sources through a systematic review and meta-analysis.

Methods: A systematic literature search was conducted according to PRISMA guidelines using seven databases, including PubMed, Scopus, Web of Science, ScienceDirect, Google Scholar, and regional databases, for studies published between 1970 and 2022. Studies reporting serological, molecular, fecal, or environmental detection of *T. gondii* in domestic cats, wild felids, sheep, goats, and soil samples were included. Data on location, host species, diagnostic methods, sample size, prevalence, and risk factors were extracted. Random-effects meta-analysis was performed; heterogeneity was assessed using Cochran's Q and I^2 statistics, and subgroup, risk-factor, and publication-bias analyses were conducted where applicable.

Results: A total of 395 studies met the inclusion criteria. The pooled seroprevalence of *T. gondii* was 37.5% (95% CI: 34.7–40.3) in domestic cats and 64.0% (95% CI: 60.0–67.9) in wild felids. The pooled prevalence of fecal oocyst shedding was 2.6% (95% CI: 1.9–3.3) and 2.4% (95% CI: 1.1–4.2), respectively. *T. gondii* was detected in 16.2% (95% CI: 7.66–27.03) of soil samples. In livestock, pooled seroprevalence was 31% (95% CI: 25.9–35.2) in sheep and 27% (95% CI: 14.0–42.5) in goats. Sheep older than one year had higher odds of infection (OR=2.39; 95% CI: 1.05–5.46), whereas no significant sex-related differences were identified.

Conclusions: The widespread occurrence of *T. gondii* in felids, small ruminants, and contaminated soil highlights the importance of environmental reservoirs and foodborne transmission pathways. These findings support integrated One Health surveillance, improved biosecurity, environmental sanitation, and stray cat control to reduce zoonotic transmission and enhance food safety.



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sciforum-189386: Animal Reservoir Hosts of Zoonotic Visceral Leishmaniasis in Iran: A Systematic Review and Meta-Analysis

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Background: Zoonotic visceral leishmaniasis (ZVL), caused by *Leishmania infantum*, remains a veterinary and public health concern in Iran. Domestic and wild animal reservoirs play a critical role in maintaining transmission. This systematic review and meta-analysis aimed to estimate the prevalence of *L. infantum* infection among animal reservoir hosts in Iran and evaluate heterogeneity across Iran overall.

Methods: A systematic search of PubMed, Scopus, Web of Science, ScienceDirect, SID, Magiran, and IranMedex was conducted. Studies published between 2001 and 2024 reporting *L. infantum* infection in domestic and wild animal reservoirs were included. A random-effects meta-analysis estimated pooled prevalence with 94% confidence intervals (CI). Heterogeneity was assessed using Cochran's Q test and the I^2 statistic. Subgroup analyses were performed according to reservoir host species, region, and diagnostic methods, including DAT, PCR, ELISA, IFAT, and parasitological assays. Publication bias was evaluated using funnel plot asymmetry and Egger's regression test.

Results: A total of 63 eligible studies involving 24,872 animals were included. The pooled prevalence of *L. infantum* infection among reservoir hosts was 13.21% (94% CI: 11.3–15.12). Domestic dogs showed the epidemiological importance, with prevalence estimates ranging from 11% to 15%, followed by cats, jackals, foxes, wolves, and rodents. Significant between-study heterogeneity was observed ($I^2 > 74\%$, $P < 0.001$), likely due to differences in endemicity, reservoir species, geographical location, and diagnostic techniques. Subgroup analyses revealed higher prevalence rates in northwestern endemic provinces and in studies using molecular diagnostic methods. PCR and DAT demonstrated the highest sensitivity and specificity. No significant publication bias was detected.

Conclusions: Animal reservoirs, particularly domestic dogs and wild canids, play a major role in ZVL persistence and transmission in Iran. The substantial heterogeneity among studies highlights the need for surveillance systems and diagnostic protocols. Integrated surveillance, molecular monitoring, and reservoir control strategies are essential for reducing zoonotic transmission in endemic areas.



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sciforum-187921: Epidemiological Status of *Linguatula serrata* Infection among Domestic Ruminants in Northwestern Iran: A Systematic Review and Meta-analysis

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Background: Linguatulososis, caused by *Linguatula serrata*, is a neglected zoonotic parasitic infection of veterinary and public health importance. Domestic ruminants serve as intermediate hosts and contribute to parasite transmission to carnivores and humans. This systematic review and meta-analysis evaluated the prevalence of *L. serrata* infection among domestic ruminants in northwestern Iran, particularly West Azerbaijan Province.

Methods: This systematic review was conducted according to PRISMA guidelines. English and Persian databases, including PubMed, Scopus, Web of Science, Google Scholar, SID, Magiran, IranMedex, and ElmNet, were searched for studies published between 1996 and 2025. After duplicate removal, titles and abstracts were screened, followed by full-text assessment by two independent reviewers. Twenty-seven eligible cross-sectional and epidemiological studies were included. Data on host species, study area, diagnostic methods, and prevalence rates were extracted. Study quality and risk of bias were assessed. Meta-analysis was performed using a random-effects model with 95% confidence intervals. Heterogeneity was evaluated using the I^2 statistic, publication bias by funnel plot and Egger's test, and subgroup analyses according to host species and geographical region.

Results: 27 studies involving more than 15,000 domestic ruminants were analyzed. The overall prevalence of linguatulososis in Iran was 24.8%, with the highest prevalence in goats (24.9%), followed by sheep (14.8%), cattle (12.4%), camels (11.3%), and buffaloes (6.8%). West Azerbaijan Province showed one of the highest prevalence rates (68.2%). Older goats (>2 years) had significantly higher infection rates than younger animals. Mesenteric and mediastinal lymph nodes were the principal predilection sites for nymphal stages. Molecular and parasitological diagnostic methods showed greater sensitivity than routine gross examination.

Conclusion: Linguatulososis remains an endemic zoonotic infection among domestic ruminants in northwestern Iran. Enhanced surveillance, slaughterhouse inspection, control of stray carnivores, and integrated preventive strategies are essential to reduce transmission and minimize the economic and public health impacts of *L. serrata* infection.



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sciforum-177427: A Cross-Sectional Study on the Prevalence and Etiology of Camel Dermatophytosis in the Emirate of Abu Dhabi, UAE

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Introduction: Dermatophytosis (ringworm) is a highly contagious, zoonotic fungal skin disease affecting camels, leading to significant economic losses due to decreased productivity and poor hide quality. Despite its importance, limited data exists on its prevalence and causative agents in the camels of the UAE.

Objective: The study aimed to determine the prevalence of dermatophytosis in *Camelus dromedarius* across the Emirate of Abu Dhabi and to identify the primary dermatophyte species involved using conventional and advanced phenotypic methods.

Method: A total of 277 skin scraping samples were collected from camels exhibiting suspected ringworm lesions across the three regions of the Emirate: Abu Dhabi (n=105), Al Ain (n=72), and Al Dhafra (n=100). Samples were subjected to direct microscopic examination and cultured on selective and differential mycological media. Dermatophyte species were confirmed using MALDI-ToF.

Result: Overall prevalence of dermatophytosis in the examined camels was 58.8% (163/277). Regional prevalence varied significantly, with the highest rate observed in Al Dhafra (100%, 100/100), followed by Al Ain (44.4%, 32/72) and Abu Dhabi (29.5%, 31/105). Trichophyton species were the dominant etiological agents, accounting for 98.77% (161/163) of positive cases, with *T. mentagrophytes* (18/163, 11.0%) and *T. rubrum* (6/163, 3.7%) being the most frequently identified. *M. gypseum* was isolated in 1.23% (2/163) of cases. Lesions were most observed on the neck and face. A single suspected human case was reported but not confirmed.

Conclusion: This study reveals a high prevalence of dermatophytosis in the camel population of the Emirate of Abu Dhabi, with Trichophyton species identified as the predominant cause. The findings underscore the significant burden of this disease and its potential zoonotic risk. The results highlight an urgent need for the implementation of strategic control measures, surveillance programs, and public health education for animal handlers to mitigate the spread and economic impact of ringworm in the region.



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sciforum-161091: A Meta-Analysis of the Prevalence of Abortion-Causing Parasites in Dairy Cattle in Isfahan and Chaharmahal va Bakhtiari Provinces, Iran

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This study aimed to conduct a systematic meta-analysis to compare the seroprevalence of major abortion-causing parasites, particularly *Neospora caninum*, between industrial and semi-industrial dairy farms in two major Iranian provinces, Isfahan and Chaharmahal va Bakhtiari. A comprehensive search and integration of existing epidemiological, serological, and molecular studies from the region were performed. Data were pooled and statistically analyzed using random-effects models, specifically the DerSimonian-Laird method, to account for heterogeneity across studies. The meta-analysis revealed a significantly higher overall seroprevalence of *N. caninum* in Isfahan Province. The seroprevalence in dairy cattle with a history of abortion in Isfahan was 32.1%, peaking at 74.6% in herds with confirmed contact with wild canids. In contrast, the prevalence in aborted fetuses in Chaharmahal va Bakhtiari was notably lower at 11%. The statistical comparison showed a significant difference ($p = 0.05$) between the two provinces, with high heterogeneity ($I^2 = 87.26\%$) indicating substantial regional variation. The national pooled prevalence in aborted fetuses was estimated at 34.8%. These findings unequivocally identify *N. caninum* as a primary parasitic agent of bovine abortion in the studied regions, with the risk being substantially higher in industrial farms in Isfahan. The study concludes that targeted preventive strategies, including strict management of definitive host access and vaccination programs, are urgently needed, especially in high-prevalence areas like Isfahan, to mitigate significant economic losses and improve reproductive herd health.



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sciforum-194488: A systematic review of the pathways, co-occurrence, and displacement patterns of *Rhipicephalus microplus* and *Rhipicephalus decoloratus* in Africa.

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Rhipicephalus microplus, also known as the Asian blue tick, is becoming a major threat to cattle production in Africa. This species is reported to displace closely related native species such as *Rhipicephalus decoloratus*. It is also an efficient vector of highly pathogenic organisms, like *Babesia bovis* and *B. bigemina*, causing diseases of economic and veterinary importance. This systematic review synthesises published evidence on the pathways of introduction and spread, co-occurrence, and displacement patterns of these two species in Africa. A systematic search of PubMed, Scopus, Web of Science, Google Scholar, and African Journals Online was conducted for studies published between 2000 and 2025, following PRISMA guidelines. The year 2000 was selected as the starting point because species within the *Rhipicephalus*(*Boophilus*) complex were often inconsistently classified in earlier literature, potentially confounding species-specific analyses, thereby reducing the likelihood of incorporating records affected by historical taxonomic ambiguity. Eligible studies were screened using predefined criteria, and findings are synthesized narratively because of heterogeneity in study designs, reporting formats, and outcomes. The available evidence indicates that the spread of *R. microplus* in Africa has been driven largely by livestock trade and transhumance, with establishment reported across multiple countries in West, East, and Southern Africa. However, the continental pattern is heterogeneous: some areas report apparent displacement of *R. decoloratus*, whereas others show continued co-occurrence or persistence of the native species. Reported outcomes appear to be influenced by ecological factors and livestock management practices, including climate, host movement, and tick control practices. The spread of *R. microplus* is a One Health issue, not a purely veterinary one. It simultaneously threatens animal production, human food safety, public health, and ecosystem stability. We call for integrated surveillance that jointly monitors tick populations and diversity to inform cohesive control strategies across Africa to enhance livestock and human health in the changing environment.



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sciforum-187998: AI-based evaluation of testicular damage in stray dogs from environmentally polluted areas of the Campania Region, Italy

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In Campania Region, an area known as the '*Land of Fires*', has been described as an open-air dump due to the illegal discharges of toxic substances, raising concerns for animal and human health. Within a One Health perspective, stray dogs may act as sentinel species for environmental risk. For this purpose, testicular and epididymal samples from male stray dogs were classified according to spermatogenic status, ranging from normal spermatogenesis to intratubular seminoma. Heavy metal concentrations (cadmium, nickel, uranium) were quantified by inductively coupled plasma mass spectrometry. Tissue remodelling was assessed by histochemistry, immunofluorescence and Western blotting analyses for steroidogenic enzymes and cytoskeletal markers. Oxidative status was evaluated by H₂O₂ production and superoxide dismutase (SOD) activity. In parallel, H&E-stained digitized whole-slide images were analysed using an AI-based workflow with EfficientNet-B4 feature extraction and ensemble machine-learning classification, while epididymal sperm chromatin condensation was quantified on Toluidine Blue-stained cytological preparations through an automated k-means clustering pipeline. Our results highlighted that degenerated and neoplastic testes showed significantly higher concentrations of cadmium, nickel, and uranium compared to normal tissue. These changes were associated with progressive collagen and cytoskeletal disorganization, impaired steroidogenesis, and redox imbalance (increased H₂O₂, reduced SOD activity), alongside reduced epididymal sperm concentration and defective chromatin condensation. The AI ensemble classifier achieved 88.39% accuracy and a weighted F1-score of 0.79, with AUC values ≥ 0.92 across all histological categories. The Toluidine Blue automated pipeline showed high reproducibility (silhouette coefficient: 0.60 ± 0.09 ; adjusted Rand index: 0.89 ± 0.03), supporting the detection of impaired sperm chromatin condensation in degenerated cases. Overall, these findings support the potential value of dogs as sentinel species in One Health environmental risk assessment and suggest that AI-assisted histological and cytological analysis may strengthen the reproducibility of biomonitoring approaches in reproductive pathology.



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sciforum-187098: Analysis of Viruses Carried by Wild Animal Feces in the Wolong Nature Reserve

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Wild animals are natural reservoirs of various viruses, and their feces carry complex viral communities associated with the transmission of multiple diseases. In this study, a total of 55 fecal samples from 10 species of wild animals in the Wolong Nature Reserve were collected, and the composition, diversity characteristics, and potential ecological associations of the viral communities were analyzed. Through metagenomic sequencing, a total of 681.84 G of raw data was obtained, and 4,496,107,637 high-quality reads were retained after quality control, with an average effective data rate of 98.84%. The results were classified and annotated to 151 viral families, covering various genomic types such as dsDNA, ssDNA, +ssRNA, -ssRNA, dsRNA, and reverse-transcribing viruses. The overall viral community was dominated by phage-related viruses, and multiple animal and plant virus groups were also detected. The dominant viral families included Orthoherpesviridae, Mimiviridae, Schitoviridae, Poxviridae and Herelleviridae. Alpha diversity analysis indicated that there were differences in viral richness and evenness among different host groups, although most group differences were not significant ($P > 0.05$). The LN group had the highest viral diversity and richness, while the MF group had the lowest. Beta diversity analysis showed that the viral community structures among different host groups were generally similar, with some significant differences observed among groups. Network model analysis indicated that the viral community had a distinct modular feature, and there were strong co-occurrence relationships among different viral groups. This study systematically revealed the compositional and structural characteristics of fecal viral communities in wild animals from the Wolong Nature Reserve, providing baseline data for the investigation of viral resources and the assessment of cross-species transmission risks in wild animals



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sciforum-188156: Cadmium distribution in environmental samples and Cervidae tissues from habitats with different anthropogenic load

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Introduction: Cadmium (Cd) is a toxic, non-essential metal of ecological and food-safety relevance. This study evaluated Cd distribution in environmental samples and red deer (*Cervus elaphus*) tissues from Bulgarian hunting areas with contrasting anthropogenic pressure.

Methods: Samples originated from one Southern Bulgarian hunting estate in a mining region, treated as Industrial, and one Northern Bulgarian hunting estate away from enterprises and mines, labeled as Nonindustrial. Composite samples from water (n=6), soil (n=6), grass (n=6), bark (n=6) and sediment (n=6) were analyzed by AAS. Muscle, liver and kidney from 17 red deer were analyzed by ICP-MS. Between-region comparisons used Mann–Whitney U statistics, Holm correction and Cliff's delta. Within-region tissue comparisons used Friedman and paired Wilcoxon tests.

Results: Environmental Cd was higher in the Nonindustrial region: water 35.87 vs 0.0005 mg/L; soil 16.86 vs 0.41, grass 2.76 vs 0.25, bark 1.56 vs 0.14 and sediment 12.28 vs 0.94 mg kg⁻¹ d.w. Water, soil, grass and bark remained significant after Holm correction ($p = 0.0476$), whereas sediment did not ($p = 0.0571$); Cliff's δ was -1.000 for all environmental sample types. In contrast, liver Cd was significantly higher in red deer from Industrial region: 0.186 vs 0.071 mg kg⁻¹ w.w. ($p = 0.0462$; $\delta = 0.714$). Kidney Cd was also higher, with a large effect size, but was not significant after Holm correction: 1.345 vs 0.954 mg kg⁻¹ w.w. ($p = 0.1098$; $\delta = 0.587$). Muscle remained low. Using group mean tissue concentrations from complete triads, kidney dominated the muscle–liver–kidney Cd profile, representing 82.96% and 91.14% of the summed group mean concentration in the Industrial and Nonindustrial groups, respectively.

Conclusions: Environmental Cd concentrations and tissue Cd accumulation did not follow a simple parallel pattern. These findings highlight the importance of One Health approaches integrating environmental monitoring and wildlife biomonitoring to assess ecological and food-safety risks associated with Cd contamination.



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sciforum-160789: Clinical, haematological and biochemical features associated with foot rot infection in sheep in Oyo State, Nigeria

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Foot rot is considered one of the major important diseases of ruminants that impairs productivity and causes serious economic losses in Nigeria. Despite its endemicity and economic importance, there is inadequate data on its clinico-haematological and biochemical indices in Nigerian indigenous sheep. This study, therefore, establishes the occurrence of foot rot in relation to breeds, sex, and ages of sheep and determines the clinical, haematological, and biochemical parameters of foot rot-infected sheep.

Thirty-six local sheep showing signs of foot rot and confirmed positive for the commonest bacterial aetiological organisms (*Dichelobacter nodosus* and *Fusobacterium necrophorum*) using bacteriological techniques and subsequently analysed using standard haematological and serum biochemical techniques.

There were more foot rot cases in the Yankasa breed (50%) compared with the West African Dwarf (33.3%) and Ouda breeds (16.7%). Females (ewes) had the highest occurrence (69.4%) compared to males (rams) (30.6%), and adults (83.3%) compared to young (16.7%) sheep, respectively. More sheep were moderately infected (61.1%) compared to those with mild infections (22.2%) and those that were severely infected (16.7%). Erythrocytic parameters were generally low, and WBC, platelet, and lymphocyte were higher, while neutrophils, monocytes, and eosinophils remained normal compared to reference values, but there were no significant differences at ($P = 0.05$) among the breeds. Level of calcium was significantly higher in males compared to females ($P = 0.023$). Findings in relation to ages revealed no statistical significance, except for ALP, which was significantly higher in adult compared to young, infected sheep ($P = 0.01$).

Occurrence was higher in the Yankasa breed, females and adults compared to other breeds, males and young sheep. There was generalised lymphocytosis and hypercalcaemia generally in footrot-infected sheep. The Yankasa breed, male (ram), and adult possessed the best haematological and biochemical parameters compared to other breeds, female and young sheep with foot rot infection.



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sciforum-187797: Co-circulation and Segment-Specific Genome Relationships of Infectious Bursal Disease Virus in Borneo

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Molecular surveillance of poultry viruses is essential for tracking pathogen diversity, informing vaccination strategies and strengthening animal health preparedness within regional food production systems. Infectious bursal disease virus (IBDV) is an economically important pathogen of chickens that causes immunosuppression and increases flock susceptibility to secondary infections. However, molecular information on circulating IBDV strains in Malaysian Borneo and Brunei remains limited, particularly at the genome-segment level. In this study, we characterised IBDV detected in bursa tissues collected between 2020 and 2023 from suspected field cases in Sabah, Sarawak and Brunei. A total of 24 bursa samples were homogenised, viral nucleic acids were extracted, and IBDV was detected by RT-PCR. Strain typing was performed by amplifying a 677 bp fragment of the VP2 hypervariable region using VP2-specific primers, followed by Sanger sequencing and phylogenetic analysis. All 24 samples tested positive for IBDV. VP2-based analysis assigned the isolates to three genogroups, comprising classic strains in Genogroup G1, variant strains in Genogroup G2 and very virulent IBDV (vvIBDV) strains in Genogroup G3. Among the typed samples, G1, G2 and G3 accounted for 7, 7 and 8 isolates, respectively, with two samples remaining unassigned. To further characterise a representative vvIBDV isolate, complete genome sequencing was performed for IPB/IBDV021/2023. The isolate contained Segment A of 3,241 bp and Segment B of 2,803 bp. The VP2 hypervariable region contained vvIBDV-associated amino acid signatures, including 222A, 242I, 253Q, 256I, 279D, 284A, 294I and 299S, together with the conserved serine-rich motif 326SWSASGS332. Segment A was most closely related to the Malaysian vvIBDV isolate UPM766/2018, whereas Segment B showed closest affinity to Chinese vvIBDV-related isolates, suggesting segment-specific evolutionary relationships. These findings demonstrate the co-circulation of genetically distinct IBDV strains in Malaysian Borneo and Brunei and highlight the value of combining VP2 surveillance with complete genome analysis for vaccine evaluation, outbreak tracking and regional poultry disease biosurveillance.



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sciforum-188161: Comparative Metagenomic Analysis of the Viromes of *Culex pipiens*, *Aedes albopictus*, and *Anopheles maculipennis* Mosquitoes in Serbia

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Mosquitoes harbor complex viral communities dominated by insect-specific viruses, yet comparative virome data from Southeastern Europe remain limited. This study aimed to characterize and compare the viromes of three epidemiologically important mosquito taxa in Serbia: the *Culex pipiens* complex, *Aedes albopictus*, and the *Anopheles maculipennis* complex. Adult mosquitoes were collected from multiple locations across Serbia during 2024 and grouped into 50 pools according to species, sampling site, and date. Total nucleic acids were extracted and subjected to Illumina NextSeq metagenomic sequencing (2×150 bp). Bioinformatic analysis included quality filtering, host read removal, de novo assembly, taxonomic annotation using BLAST and DIAMOND, viral abundance estimation, and phylogenetic analysis of RdRp regions.

A total of 1,688 viral contigs belonging to 40 viral families and 183 viral taxa were identified. The *Culex pipiens* complex exhibited the highest virome richness (140 viral taxa), followed by *Ae. albopictus* (54 taxa) and *An. maculipennis* (24 taxa). Only nine viral species were shared among all three mosquito taxa, indicating strong host-associated virome structuring. Abundance-weighted analyses demonstrated pronounced species-specific dominance patterns, with Wuhan Mosquito Virus 6 representing the most abundant virus in both *Culex* and *Aedes* mosquitoes, whereas *Anopheles* mosquitoes displayed a more even viral community structure and the highest Shannon diversity. Several putative novel viruses were also identified. These findings provide the first comparative overview of mosquito viromes in Serbia and establish a baseline for future arbovirus surveillance and longitudinal virome monitoring.



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sciforum-187119: Detection of PBFDV, APyV and AdV in captive pet birds in Sicily, Italy

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Birds are popular household pets and are frequently hosted at bird shows and zoological gardens. Their susceptibility to different viral infections poses a threat to animal health, with possible consequences for the economy and biodiversity. Psittacine beak and feather disease virus (PBFDV) from the *Circoviridae* family, and *Gammapolyomavirus avis* (APyV) from the *Polyomaviridae* family are two highly contagious viruses which can be associated with lethal outcome in young birds or chronic disease characterized by immunosuppression and feather loss. Adenoviruses (AdV) are other common viruses in birds (as well as in psittacines) with varying pathogenicity depending on the host species. Despite the relevance of the topic, information on the spread and prevalence of these diseases across Italy remains very limited. Aiming, to partially fill this gap of information, this study investigated the molecular prevalence of these pathogens in Sicily, analyzing individual risk factors associated with higher prevalence. A total of 166 oral-cloacal swabs were collected in captive pet birds from Sicily. After DNA extraction, each sample was assessed using different PCR protocols. The most prevalent pathogen was AdV (8.7%), followed by PBFDV (6%), while APyV showed the lowest prevalence (0.6%). Fisher's exact test revealed a correlation between PBFDV positivity and age (young animals showed higher prevalence) and clinical signs. The sequencing results revealed a high nucleotide identity between PBFDV, APyV and PsAdV isolates and those described in other countries. The PBFDV and APyV, revealed a high similarity with genogroup I-c and I, respectively. The PSAdV sequence belonged to PsAdV-12 from *Agapornis roseicollis* and PsAdV-2 from several parrot species. This study documented the spread of three different viruses in the bird population from Sicily, revealing risk factors that support virus dissemination and contributing to a better definition of the current epidemiological picture and the genetic features of the circulating strains.



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sciforum-186034: Diagnostic Agreement Between Intradermal Tuberculin Test and Interferon-Gamma Release Assay in Bovine Tuberculosis Surveillance in Sicily, Italy (2024–2025)

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Introduction Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, remains endemic in Sicily, where apparent prevalence during routine screening ranges between 2% and 3%. Effective surveillance requires integrating multiple diagnostic tools; however, evidence on their concordance under operational conditions in high-prevalence settings is limited. This study assessed diagnostic agreement between the intradermal tuberculin test (IDT), the interferon-gamma release assay (IFN- γ), and post-mortem lesion detection in cattle from the province of Palermo.

Methods A retrospective observational study was conducted on 1,801 cattle from 44 herds enrolled in the national bTB eradication programme between January 2024 and December 2025. Pairwise agreement was assessed using Cohen's kappa (κ) and prevalence- and bias-adjusted kappa (PABAK), stratified by year. Non-definitive outcomes (doubtful IDT; inconclusive IFN- γ) were excluded from binary analyses. Verification bias in the slaughtered subgroup ($n = 107$) was evaluated by comparing test-positive proportions against the full cohort.

Results IDT-IFN- γ concordance was substantial in 2024 ($\kappa = 0.731$; 95% CI: 0.64–0.82; $n = 991$) and decreased to moderate in 2025 ($\kappa = 0.453$; 95% CI: 0.33–0.57; $n = 572$). Inconclusive IFN- γ results increased markedly from 7.1% to 19.3%. Agreement between ante-mortem tests and post-mortem lesion detection was poor across all comparisons, with kappa estimates close to zero and wide confidence intervals, consistent with severe verification bias (IDT positivity approximately six-fold higher among slaughtered animals).

Conclusions Parallel use of IDT and IFN- γ enhances herd-level detection in endemic settings. The marked increase in inconclusive IFN- γ results points to preanalytical sources of variability, blood collection and sample transport, as priority targets for procedural standardization. Post-mortem inspection is indispensable for official confirmation, but yields meaningful agreement estimates only when animals are selected for slaughter independently of their ante-mortem test result. Integrated diagnostic strategies remain critical for bTB control in persistently endemic regions.



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sciforum-186028: Distribution of *Eimeria* oocysts in cattle and sheep–goat farms in the Province of Palermo in the context of climate change (2024–2025)

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Introduction. Coccidiosis is a widespread enteric parasitic disease in domestic ruminants, caused by protozoa of the genus *Eimeria*, mainly affecting young animals and leading to diarrhea, growth retardation, and production losses. Transmission occurs through ingestion of oocysts shed in feces, which become infective after sporulation under favorable environmental conditions. Mild temperatures and high humidity, increasingly common in the context of Mediterranean climate change, can enhance the survival and spread of the parasite in livestock systems.

Methods. This study analyzed fecal samples from cattle and small ruminant farms in the Province of Palermo over the 2024–2025 period. A total of 5,902 samples were examined using coprological analysis to detect *Eimeria* oocysts. Specifically, 2,956 samples were analyzed in 2024 and 2,946 in 2025. Parasitological data were compared with local climatic parameters, including average monthly temperatures and precipitation, in order to assess possible correlations between environmental conditions and infection trends.

Results and conclusions. In 2024, 274 samples (9.3%) tested positive, with a peak observed in October. In 2025, 466 samples (15.8%) were positive, showing a significant increase, particularly during the autumn months from September to December. This rise appears to be associated with favorable climatic conditions, characterized by mild temperatures and increased humidity due to rainfall. These factors promote oocyst sporulation and survival, leading to greater environmental contamination. The findings highlight the importance of parasitological monitoring and the implementation of appropriate hygiene and management measures to limit the spread of coccidiosis. They also emphasize the need for targeted seasonal prevention strategies and improved environmental management, especially during high-risk periods linked to ongoing climate change, with benefits for animal health and the sustainability of livestock production systems.



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sciforum-189495: Dogs as Sentinels for Emerging Human Infectious Diseases: A Systematic Review of One Health Surveillance Opportunities

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Background/Objective: Approximately 75% of emerging infectious diseases are of zoonotic origin, and their early detection in human populations remains a challenge. Dogs, due to their shared habitat with humans, can serve as sentinels for early warning of the presence of pathogens in the environment. This systematic review aimed to compile evidence related to the use of dogs as biomarkers for human infectious diseases and to identify operational opportunities for their integration into national surveillance systems.

Methods: This study was conducted according to the PRISMA 2020 guidelines. A systematic search was conducted in PubMed/MEDLINE, Web of Science, Scopus, and Google Scholar databases for studies published between January 2019 and March 2026. Inclusion criteria included observational studies (cohort, cross-sectional, case series) and seroepidemiological studies that simultaneously reported exposure of dogs (by serology, PCR, or parasite/bacterial detection) and human cases of a specified zoonotic disease (including Lyme, leishmaniasis, ehrlichiosis, West Nile virus, leptospirosis, and tularemia).

Results: Of the 1,567 articles found, 42 studies from 14 countries (mainly the United States, Germany, Brazil, Kenya, and Australia) met the inclusion criteria. In 36 studies (85.7%), a statistically significant increase in the serological or molecular prevalence of the pathogen in dogs was recorded, an average of 4 to 11 weeks before the first human cases were detected. The strongest evidence was for Lyme disease (11 studies, mean early warning 2.7 weeks) and West Nile virus (8 studies, 8.5 weeks early). In nine studies, dog surveillance was able to predict geographic foci of disease with 82–94% accuracy.

Conclusion: Dogs are effective and sensitive biomarkers for early warning of several important human infectious diseases. Integrating dog surveillance into national surveillance systems, by standardizing diagnostic methods and creating platforms for collaboration between veterinary and public health, is a strategic single health opportunity to prevent future epidemics.



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sciforum-188098: Emerging and Re-Emerging Bluetongue Virus Serotypes in Indian Ruminants: A Systematic Review

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Background:

Bluetongue (BT) is a major vector-borne disease of domestic and wild ruminants caused by bluetongue virus (BTV), a member of the genus *Orbivirus* (family: *Sedoreoviridae*). India is a global hotspot for BTV because of its diverse agro-climatic conditions, widespread distribution of *Culicoides* vectors, and the circulation of multiple viral serotypes. The emergence of genetically diverse strains and frequent genomic reassortment continue to challenge disease surveillance, diagnosis, and vaccine development.

Methods:

A systematic review of peer-reviewed literature published between 2009 and 2025 was conducted using PubMed, Scopus, Web of Science, ScienceDirect, and Google Scholar. Studies reporting BTV serotypes, molecular epidemiology, phylogenetic analysis, diagnostics, and disease surveillance in Indian livestock were screened according to predefined inclusion criteria and synthesized qualitatively.

Results:

The review identified the circulation of at least 23 BTV serotypes in India, with BTV-1, BTV-2, BTV-3, BTV-9, BTV-10, BTV-12, BTV-16, BTV-21, BTV-23, and BTV-24 being the most frequently reported. Studies published between 2009 and 2015 established the co-circulation of eastern and western topotypes and documented extensive genomic reassortment. From 2015 onward, whole-genome sequencing substantially improved understanding of viral evolution, transmission dynamics, and genetic diversity. Studies available through 2025 further highlighted the expansion of surveillance into eastern and north-eastern India, increasing recognition of climate-driven changes in *Culicoides* vector distribution, and continued detection of reassortant BTV strains. Collectively, these findings reinforce the role of cattle and buffaloes as important reservoir hosts for virus maintenance and transmission.

Conclusion:

The continued circulation of genetically diverse BTV serotypes poses a significant challenge to bluetongue control in India. Strengthening genomic surveillance, integrated vector monitoring, and region-specific multivalent vaccine development will be essential for early detection of emerging variants and effective disease management.



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sciforum-185969: ENERGY METABOLISM AND IMMUNE RESPONSES IN AFRICAN CATFISH (*CLARIAS GARIEPINUS*) JUVENILES EXPOSED TO NAPROXEN

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The presence and potential adverse effects of pharmaceutical contaminants, particularly non-steroidal anti-inflammatory drugs (NSAIDs) such as naproxen (NAP) are becoming a serious matter of environmental concern as they have increasingly been detected in aquatic ecosystems. This study investigated alterations in hepatosomatic index, lactate dehydrogenase, Ca²⁺ATPase, Na⁺/K⁺ATPase, carboxylase, respiratory burst activity and serum immunoglobulin to unravel the impact of environmentally relevant concentrations of NAP exposure on energy metabolism and immune responses in the African catfish (*Clarias gariepinus*) juveniles. *C. gariepinus* juveniles were exposed to 0 µg/L, 0.2 µg/L, 5 µg/L, and 3460 µg/L of naproxen for 14 days, which was followed by a 7-day depuration period. Results indicated a concentration and duration-dependent significant increase in hepatosomatic index and lactate dehydrogenase levels in the groups exposed to NAP when compared to the control. Although there were no observed effects of the drug exposure on carboxylase levels in the exposed group, we, however, observed that naproxen exposure led to a significant reduction in Ca²⁺ATPase, Na⁺/K⁺ATPase, respiratory burst activity and serum immunoglobulin levels. The effects of the drug on many of the studied parameters were reversed after the 7-day depuration period. These findings highlight the potential ecological risks associated with the presence of NAP in aquatic environments, even at realistic environmental concentrations, as continuous exposure to the drug may negatively impact energy metabolism and the immune responses of non-target aquatic organisms, thereby endangering their overall health. The guidelines for the use and handling of experimental animals as approved by the University of Nigeria ethical committee were followed throughout the experiments. The experimental fish were given the appropriate humane care, and water was changed every alternate day.



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sciforum-187668: Environmental and organ distribution of copper in Cervids from regions with different levels of human activity

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Environmental Cu levels may be influenced by local human activity, whereas tissue accumulation also reflects organ-specific metabolism. This study compared Cu concentrations in environmental samples and red-deer (*Cervus elaphus*) tissues from two regions in Bulgaria.

Samples originated from hunting grounds, one from Northern Bulgaria, away from enterprises and mines, labeled as non-industrial and one from Southern Bulgarian in a mining region, treated as industrial. Composite samples from grass, bark, soil, water and sediment, $n=6$ for each, were analyzed by ICP-OES. Muscle, liver and kidney from 16 red deer (7 industrial and 9 non-industrial animals) were analyzed by ICP-MS.

Industrial soil, grass and bark contained more Cu than the non-industrial samples: 84.10 vs 0.477, 16.625 vs 0.0695 and 13.925 vs 0.230 mg kg⁻¹ d.w. ($p = 0.0381$; effect size = 1.000). Sediment showed the same direction but did not reach significance after Holm's correction (73.35 vs 0.358 mg kg⁻¹ d.w.; $p = 0.0571$). Water showed the opposite pattern (0.0648 vs 3.000 mg L⁻¹; $p = 0.0238$; effect size = -1.000).

No significant between-region differences were found in the organs. Mean concentrations (industrial vs non-industrial) were 2.137 vs 2.016 mg kg⁻¹ w.w. in muscle, 19.761 vs 16.439 in liver and 5.486 vs 6.433 in kidney. Liver showed a large regional effect size (0.587), but the difference was not significant ($p = 0.1647$). Muscle, liver and kidney represented 7.47%, 72.01% and 20.52% of the relative tissue concentration in the industrial region and 8.64%, 59.86% and 31.50% in the non-industrial region. Within both regions, tissue concentrations differ ($p = 0.001$) and followed the order liver > kidney > muscle.

Regional Cu variation was more evident in environmental and vegetation samples than in tissues. Tissue data better reflected organ partitioning, particularly liver accumulation, supporting the use of environmental and biological indicators for Cu exposure assessment.



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sciforum-194475: Environmental Reservoirs of Antimicrobial Resistance in Captive Aquatic and Avian Wildlife: Evidence from a One Health Perspective

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Antimicrobial resistance (AMR) has emerged as one of the most pressing global health challenges, affecting human, animal, and environmental health. Captive wildlife facilities, including aquariums and zoological institutions, provide unique ecological settings where close interactions among animals, humans, and shared environments may facilitate the maintenance and dissemination of antimicrobial-resistant microorganisms. This study evaluated the occurrence, antimicrobial susceptibility patterns, and genetic determinants of extended-spectrum β -lactamase (ESBL)-producing Gram-negative bacteria among captive aquatic animals and birds housed in an aquarium in Abu Dhabi, United Arab Emirates, representing the first investigation of its kind in the region. A total of 60 samples, including rectal swabs, fecal specimens, water samples, and feeding-station environmental samples, were collected during 2024. Isolation of cefotaxime-resistant Gram-negative bacteria was performed using selective MacConkey agar supplemented with cefotaxime. Antimicrobial susceptibility profiles were determined using the Kirby–Bauer disk diffusion method, while phenotypic confirmation of ESBL production was conducted using the double-disc synergy test. Molecular characterization was performed by PCR targeting major β -lactamase genes (*bla*_{CTX-M}, *bla*_{SHV}, *bla*_{OXA}, and *bla*_{TEM}), with further classification of CTX-M-positive isolates into phylogenetic groups. The majority of isolates exhibited multidrug-resistant phenotypes, with particularly high resistance to β -lactam antimicrobials. More than 70% of isolates were confirmed as ESBL producers. Among the resistance determinants detected, *bla*_{SHV} was the predominant ESBL-associated gene, whereas CTX-M group 1 was the most frequently identified CTX-M variant. The detection of multidrug-resistant and ESBL-producing bacteria in animals and environmental samples highlights the potential persistence and circulation of resistant microorganisms within captive aquatic ecosystems. These findings emphasize the importance of captive wildlife facilities as potential environmental reservoirs of AMR and underscore the need for integrated surveillance, enhanced biosecurity measures, and prudent antimicrobial stewardship. Adopting a One Health approach is critical to reducing the risk of antimicrobial resistance transmission across human, animal, and environmental interfaces and to supporting sustainable wildlife management practices.



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sciforum-187807: Epidemiological Status of Theileriosis and Babesiosis among Domestic Ruminants in West Azerbaijan Province, Iran: A Systematic Review and Meta-analysis

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Background: Theileriosis and babesiosis are major tick-borne hemoprotozoan diseases of domestic ruminants associated with economic losses, including anemia, reduced productivity, reproductive disorders, and mortality. West Azerbaijan Province, northwestern Iran, is considered an endemic region for these infections because of favorable climatic conditions, extensive livestock farming, and transboundary animal movement. This systematic review and meta-analysis aimed to evaluate the epidemiological status and prevalence of theileriosis and babesiosis among domestic ruminants in this province.

Methods: A systematic search of English and Persian databases, including PubMed, Scopus, Web of Science, ScienceDirect, Google Scholar, SID, Magiran, IranMedex, and ElmNet, was conducted for studies published between 2000 and 2025. Studies reporting the prevalence of Theileria spp. and Babesia spp. infections in cattle, sheep, goats, and buffaloes in West Azerbaijan Province were included. Data on sample size, host species, diagnostic methods, parasite species, and prevalence rates were extracted. Meta-analysis was performed using a random-effects model with 95% confidence intervals. Heterogeneity was assessed using the I^2 statistic, and publication bias was evaluated through subgroup analyses and funnel plot assessment.

Results: A total of 19 eligible studies involving more than 10,000 domestic ruminants were included. Infection rates ranged from 10% to 50% depending on parasite species, host animal, and diagnostic method, with higher prevalence in sheep than cattle and goats. Theileria annulata, T. lestoquardi, T. ovis, and Babesia ovis were the predominant species identified. The prevalence of T. annulata, T. ovis, and B. ovis was estimated at 27.5%, 17.4%, and 13.9%, respectively. PCR-based methods demonstrated greater sensitivity than conventional microscopy.

Conclusion: West Azerbaijan Province represents an important endemic focus for theileriosis and babesiosis among domestic ruminants in Iran. Continuous epidemiological surveillance, integrated tick-control programs, and implementation of sensitive diagnostic approaches should be strengthened to reduce the economic and veterinary impacts of these infections on livestock production.



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sciforum-193831: Epidemiological Surveillance of *Babesia gibsoni* in Slovakia: Transmission Routes and Modelling Risk in High-Risk Dog Breeds

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Introduction: *Babesia gibsoni* is an emerging protozoan parasite increasingly spreading in Central Europe through the international movement of dogs from endemic areas, direct dog bites, and transplacental transmission, primarily threatening high-risk breeds. This study focused on molecular surveillance and precise epidemiological categorization of transmission routes within high-risk dog populations in Slovakia to improve future predictive risk models.

Methods: American Pit Bull Terriers (n = 102) from nine distinct kennels in eastern Slovakia were screened for *B. gibsoni* using PCR (18S rRNA) and subsequent DNA sequencing. Comprehensive anamnestic analysis was performed on all positive individuals in order to accurately trace the origin, specific mode of infection, and overall epidemiological categorization.

Results: Based on PCR screening, 30 dogs tested positive for *B. gibsoni*, representing a high prevalence of 29.4% across eight affected kennels, while only one kennel remained completely unaffected. Epidemiological tracing categorized the 30 positive cases into four pathways: foreign importation accounted for 11 cases (36.7%), dog bites and aggressive blood-to-blood contact caused 6 cases (20.0%), and vertical transplacental transmission from dams to puppies represented 5 cases (16.6%). Finally, 8 cases (26.7%) were attributed to unknown causes.

Conclusion: This research confirms a nearly 30% prevalence of *B. gibsoni* in eastern Slovakia among high-risk dog populations, highlighting that non-vector routes, including importation, are major drivers of infection. These findings underscore the urgent need for stricter veterinary monitoring of imported dogs and the integration of multi-route transmission dynamics into future epidemiological predictive models.

Funding: This research was supported by the grant VEGA 2/0016/26.



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sciforum-191823: Evaluation of a Mobile Flow Cytometer as a Rapid Tool for Environmental Hygiene Monitoring in Broiler Farms

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A high level of environmental hygiene is essential for maintaining flock health, growth performance, and welfare in broiler production systems. Effective hygiene monitoring is therefore an important part of farm biosecurity. Conventional plate culture methods are time-consuming and less suitable for rapid routine assessment directly on farms. The aim of this study was to evaluate the potential of a mobile flow cytometer (MFC) as a rapid on-farm method for direct quantification of viable bacteria in broiler housing environments. Results obtained by MFC were compared with ATP-based luminometry and conventional plate culture methods.

Measurements were performed using the MFC CytoQuant (Romer Labs Division Holding GmbH), the EnSure luminometer (Hygiena LLC, USA), and cultivation methods assessing total microbial counts at 22°C on PCA agar, mesophilic counts at 36°C on blood agar, and *Escherichia coli* on HiCrome agar. Method comparisons were evaluated using Spearman's correlation coefficient.

The detection capability of the MFC was verified under laboratory conditions using the reference strain *E. coli* CCM 3988. Significant correlations were observed between intact cell counts determined by MFC and mesophilic bacteria cultivated on blood agar ($r_{Sp} = 0.764$; $p < 0.05$), as well as *E. coli* cultivated on HiCrome agar ($r_{Sp} = 0.669$; $p < 0.05$).

Field monitoring was conducted in two commercial broiler houses. Surface samples were collected from drinkers and wall sections during depopulation, sanitation, and fattening periods. Correlations between luminometry and microbiological methods were not statistically significant, confirming that ATP monitoring reflects overall organic contamination rather than direct microbial presence. In contrast, MFC results correlated significantly with mesophilic microorganisms cultivated at 36°C ($r_{Sp} = 0.731$ – 0.792 ; $p < 0.05$). The findings suggest that MFC represents a promising rapid tool for environmental hygiene monitoring in broiler production.



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sciforum-194559: Genomic Surveillance of Reproductive and Adaptive Variation in Indigenous Sheep Populations for Sustainable Livestock Production at the Human Animal Environment Interface

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The indigenous sheep have valuable genetic resources to be utilized for sustainable livestock production in arid and harsh environments where productivity and food security rely on good reproductive performance, adaptability and disease resistance. Currently, however, genomic knowledge of local sheep populations is still limited, limiting the assessment of genetic diversity, the identification of variants related to economically important reproductive traits, and the development of evidence-based breeding and conservation strategies. This study introduces a novel framework for integrated genomic surveillance of indigenous sheep that integrates population genomics, reproductive phenotyping, environmental characterization and the One Health principles to assess reproductive and adaptive variation in the human–animal–environment interface.

It combines the genome-wide molecular information with standard reproductive records such as the number of lambs, fertility, interval, reproductive seasonality and reproductive resilience. Population structure, genetic diversity and differentiation and signatures of selection, as well as genomic inbreeding and runs of homozygosity, will be evaluated using principal component analysis, ancestry inference, homozygosity analysis and genome-wide selection scans. Genomic regions and candidate genes associated with reproductive performance, endocrine function, environmental adaptation and immune function will be identified through genome-wide association analysis. The results of these genome studies will be analyzed alongside key environmental factors, such as exposure to high temperatures, nutrient deficiency, water shortage, and local environmental conditions.

Such integration of genomic, reproductive and environmental data into a single analysis can help achieve the identification of resilient animals, precision breeding and reduce the loss of locally adapted genetic diversity. The proposed framework connects reproductive sustainability to animal health, ecosystem resilience, food security and conservation priorities, unlike traditional livestock genomics approaches. It thus serves as a practical basis for the creation of breeding and conservation programmes for indigenous sheep at a One Health approach.



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sciforum-187283: Global Prevalence of *Cryptosporidium* Infection in Cattle (2005–2024): A Systematic Review and Meta-Analysis of Epidemiological Patterns

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Introduction: Cryptosporidiosis is a significant zoonotic parasitic disease in cattle with considerable implications for livestock productivity and public health. Despite numerous regional studies, a comprehensive global biostatistical meta analysis of prevalence patterns across age groups, cattle types, and diagnostic methods over a two-decade period remains limited. This study aimed to estimate the global prevalence of *Cryptosporidium* infection in cattle from 2005 to 2024 and to identify key epidemiological determinants.

Methods: Peer-reviewed observational studies reporting *Cryptosporidium* prevalence in cattle, published between 2005 and 2024, were included. Studies were eligible if they clearly reported sample size and number of positive cases. Data were extracted on sample size, positive cases, prevalence, age group, diagnostic method, cattle type, country, and publication year. Descriptive statistics, Chi-square tests, independent t-test, one-way ANOVA, and simple linear regression were performed to assess prevalence patterns across subgroups.

Results: A total of 232 studies encompassing 1,21,669 cattle across 61 countries were included, with an overall pooled prevalence of 21.88% (Mean: 26.74%, SD: $\pm 22.67\%$). Prevalence differed significantly across age groups ($\chi^2=3746.63$, $p<0.001$), with pre-weaned animals recording the highest prevalence (33.21%), followed by calves (23.94%) and adults (11.91%). One-way ANOVA confirmed significant variation across age groups ($F=20.16$, $p<0.001$). Dairy cattle exhibited significantly higher prevalence than beef cattle (22.23% vs 14.38%) by both Chi-square ($\chi^2=209.50$, $p<0.001$) and t-test ($t=2.43$, $p=0.016$). Diagnostic method significantly influenced detection rates ($\chi^2=1040.91$, $p<0.001$), with ELISA yielding the highest prevalence (36.85%) and PCR the lowest (18.50%). Linear regression revealed no significant temporal trend over the study period ($r^2=0.003$, $p=0.279$).

Conclusions: Pre-weaned and dairy cattle represent the highest-risk categories globally. The persistent prevalence over 20 years despite advances in veterinary medicine underscores the need for targeted interventions in high-risk populations. Standardisation of diagnostic protocols is essential for accurate and comparable global reporting.



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sciforum-184714: Influence of hemoparasite presence on hematological parameters in *Boa constrictor*: evidence of subtle erythrocyte alterations

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Hemoparasites are frequently reported in reptiles, particularly snakes, where they are often considered subclinical and of limited pathological significance. However, their effects on hematological parameters remain poorly understood. This study aimed to evaluate the prevalence of hemoparasites and their influence on hematological variables in adult *Boa constrictor*. Blood samples were collected from 36 adult snakes of both sexes, including captive and free-living individuals, in Cuiabá, Mato Grosso, Brazil. Hematological analyses included erythrogram, leukogram, thrombocyte counts, and total solids. Blood smears stained with May–Grünwald–Giemsa were examined for hemoparasites. Generalized linear models were used to assess the effect of hemoparasite presence on hematological parameters ($p < 0.05$). Hemoparasites morphologically compatible with hemogregarines were detected in 44.4% (16/36) of the snakes. Their presence was associated only with increased mean corpuscular volume (MCV) ($p = 0.03$), with infected animals showing higher MCV values, with a mean of 432.26 and standard deviation of 43.61, compared to non-infected individuals, which presented a mean of 394.32 and standard deviation of 29.36. No significant differences were observed for RBC count, hemoglobin concentration, packed cell volume, or other hematological parameters ($p \geq 0.05$). The increase in MCV, in the absence of changes in RBC count, hemoglobin concentration, and PCV, indicates no evidence of anemia or a regenerative response. Intraerythrocytic hemogregarines are known to induce enlargement of infected erythrocytes, which may contribute to increased cell volume. Thus, the higher MCV values observed are more consistent with subtle cellular alterations than with a clinically relevant pathological process. The absence of additional hematological changes suggests limited impact on erythrocyte dynamics. Overall, these findings support the subclinical nature of these infections and highlight the need for cautious interpretation of isolated hematological variations in reptiles.



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sciforum-187284: Integrated haematological, biochemical and anatomopathological profiling of cachectic diseases in sheep

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Cachexia is a multifactorial syndrome characterized by progressive weight loss, muscle wasting, metabolic disturbances, and chronic inflammation, and is frequently associated with parasitic, infectious, and neoplastic diseases in sheep. This study aimed to investigate haematological, biochemical, and anatomopathological alterations associated with cachexia using an integrated multisystemic approach. A cross-sectional observational study was conducted on 139 sheep examined at the slaughterhouse of Tiaret province, Algeria. Animals were classified by body condition score into cachectic ($n = 90$) and non-cachectic control groups ($n = 49$). All animals were subjected to routine ante-mortem and post-mortem veterinary inspection by official inspectors in accordance with slaughterhouse regulations. Samples were collected during routine slaughterhouse procedures without interfering with veterinary inspection. Haematological and biochemical analyses were performed using automated analysers, while gross and histopathological examinations were conducted on affected organs. Cachectic animals showed significant leucocytosis, neutrophilia, monocytosis, eosinophilia, lymphopenia, and normocytic normochromic anaemia, with decreased erythrocyte count, haemoglobin concentration, and haematocrit ($p < 0.05$). Biochemical alterations included increased AST, ALT, and urea, together with hypoalbuminaemia, hypoproteinaemia, and a reduced albumin/globulin ratio. Correlation analysis revealed strong associations among erythrogram variables, protein profile indices, and inflammatory leukocyte populations, indicating coordinated metabolic and inflammatory dysregulation. Pathological examination revealed multisystemic lesions mainly affecting the gastrointestinal tract, lungs, liver, and abomasum, characterized by parasitic, granulomatous, chronic inflammatory, suppurative, and neoplastic lesions. These findings indicate that cachexia is a complex systemic syndrome resulting from interacting parasitic, infectious, inflammatory, and neoplastic processes. The integration of haematological, biochemical, and pathological data provides insight into its systemic nature and supports improved surveillance, early detection, herd health management, and animal welfare in small ruminants.



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sciforum-185375: Knowledge, Attitudes, and Practices of Livestock Stakeholders for Risk-Based Control of Peste des Petits Ruminants in the Pakistan–Afghanistan Transboundary Region

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Peste des petits ruminants (PPR) is a highly contagious transboundary animal disease causing substantial economic losses in endemic countries such as Pakistan. Border regions adjoining Afghanistan represent high-risk areas where the disease persists, posing a challenge to the Food and Agriculture Organization and World Organisation for Animal Health global eradication target by 2030. This persistence is largely associated with gaps in knowledge, attitudes, and practices (KAP) among livestock stakeholders.

A cross-sectional KAP survey was conducted from March to August 2024 in five high-risk border districts of Pakistan (Khyber, Kurram, South Waziristan, Mohmand, and Bajaur). Pre-tested questionnaires were administered to 478 livestock farmers, 25 animal traders, 13 butchers, and 79 veterinary practitioners. Data were analyzed using descriptive statistics with 95% confidence intervals.

Awareness of key clinical signs, including diarrhea (96.6%) and oculo-nasal discharge (88.9%), was high, with veterinarians identified as the primary source of information (75.5%). Despite generally positive attitudes toward outbreak reporting (83.2%), high-risk practices persisted, particularly the introduction of animals without quarantine (82.2%). Limited vaccination coverage and reliance on clinical diagnosis due to inadequate laboratory facilities were also observed.

This misalignment between knowledge and practices contributes to the continued endemicity of PPR in the region. The findings highlight the need for strengthened cross-border coordination, improved vaccination coverage, enhanced diagnostic capacity, and targeted awareness programs. This study provides novel evidence linking stakeholder behavior to PPR persistence in a transboundary setting.



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sciforum-168708: Machine Learning–Based Risk Stratification for Occupational Leptospirosis Surveillance within a One Health Framework

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Introduction: Leptospirosis is an important zoonotic disease in Iran and a persistent occupational health concern for high-risk groups in warm and humid regions. Nonspecific early symptoms and diagnostic delays hinder timely prevention. Data-driven risk stratification may support occupational health programs through targeted surveillance and preventive interventions. This study aimed to develop and internally validate a machine learning-based model for occupational leptospirosis risk stratification within a One Health surveillance perspective.

Methods: A retrospective dataset of 796 individual occupational and clinical records was compiled from occupational health surveillance reports and individual-level datasets described in peer-reviewed epidemiological studies conducted in northern, southern, and western provinces of Iran between 2013 and 2025. The outcome was defined as laboratory-confirmed or clinically diagnosed leptospirosis, reflecting routine surveillance practice. Predictors included occupation type, exposure to animal urine or stagnant water, use of personal protective equipment, early clinical symptoms including fever, headache, and myalgia, age, sex, and underlying conditions. Class imbalance was addressed using Synthetic Minority Over-sampling Technique and Random Over-Sampling within training folds. Logistic Regression and XGBoost models were trained using k-fold cross-validation and evaluated using the area under the receiver operating characteristic curve, sensitivity, accuracy, and Brier score.

Results: The XGBoost model with Random Over-Sampling achieved the best performance, with a sensitivity of 82 %, an area under the curve of 0.84, an accuracy of 78 %, and a Brier score of 0.16. The most influential predictors were lack of personal protective equipment use, direct contact with animal urine, and fever within the first five days of symptom onset. Risk stratification classified 14 % of records as high risk and 4 % as very high risk.

Conclusions: This study shows that integrating occupational exposure and early clinical data enables machine learning risk stratification for occupational leptospirosis surveillance within a One Health framework, requiring external validation before implementation.



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sciforum-188682: Medically important arthropods identified in community microbiology laboratories in British Columbia, Canada

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Background:

Not much is known about the local prevalence of medically important arthropods in Canada because these data are not readily available. Local epidemiology affects the positive predictive value of laboratory tests. Knowing the distribution of medically important arthropods in local settings may help the differential diagnoses of clinicians and laboratorians.

Objective(s):

The current retrospective study aimed to establish the prevalence and distribution of medically important arthropods among specimens submitted to community microbiology laboratories.

Methods:

Data was collected from LifeLabs British Columbia (BC) microbiology laboratories, connected with 129 collection centres in urban and rural communities in the province of BC, Canada. The Microbiology Electronic Worksheet System software was used to generate data. An entire year of data from patients of all ages and sexes was collected to reduce bias due to seasonality, differences in clinical practices, and other potential confounders.

Results:

Between September 1 2022 and August 30 2023, 314 arthropod specimens were submitted for microscopy testing that included 177 *Ixodes* species (56.4%; 164 of which were identified females), 37 *Dermacentor* species (11.8%), 17 other hard ticks (5.4%), 7 *Cimex* species (2.2%), 2 *Pediculus humanus* (0.6%), and 1 Larvae of *Dermatobia hominis* (0.3%). In the same period, 148 scabies collection slides were submitted for microscopy testing that included 9 *Sarcoptes scabiei* (6.1%) and 1 *Demodex* species (0.7%).

Conclusions:

Most arthropods submitted were *Ixodes* species, which are associated with communicable diseases such as Lyme disease and anaplasmosis. These diseases could be kept in the differentials of clinicians and laboratorians when there is a history of an unidentified arthropod attached to a currently symptomatic patient. The current study provided contemporary data on the prevalence of medically important arthropods identified in community. More clinical studies are needed to determine the clinical significance of these identified arthropods.



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sciforum-180424: Meta-Regression Analysis of Knockdown Resistance Mutations Associated with Pyrethroid Resistance in *Anopheles* Mosquitoes across Sub-Saharan Africa

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The *VGSC* gene's *Kdr* mutations (L1014F and L1014S) confer resistance to pyrethroids, which decreases the insecticides' ability to bind to their targets and decreases their effectiveness. These alterations, which are encoded in the voltage-gated sodium channel (VGSC) gene, affect the effectiveness of indoor residual spraying (IRS) and insecticide-treated nets (ITNs). In this study, a comprehensive meta-analysis was conducted to assess the impact of L1014F and L1014S mutations on resistance in *Anopheles* mosquitoes across sub-Saharan Africa. Data were systematically synthesised from eligible studies conducted within the region, applying both fixed and random effects models to estimate pooled associations between *kdr* genotypes and resistance phenotypes. Heterogeneity and publication bias were evaluated using Cochran's Q test, Egger's test, and funnel plot asymmetry. This study represents the first meta-regression focusing exclusively on *Anopheles* populations in sub-Saharan Africa, encompassing eight studies with a total of 4,690 mosquito samples. Substantial heterogeneity was observed across studies ($I^2 > 99\%$), and random effects models were therefore applied. The pooled odds ratio (OR) for the L1014F allele (L vs. F) was 2.14 (95% CI: 1.17–2.93, $P < 0.001$), indicating a significant association with resistance, while the L1014S allele (S vs. F) showed a weaker relationship (OR = 0.899, 95% CI: 0.297–1.293, $P < 0.001$). Sensitivity analysis revealed that excluding highly variable studies reduced the effect estimates, highlighting the influence of publication bias and small sample size. Egger's test and funnel plot asymmetry further confirmed the presence of significant publication bias. After bias adjustment, the pooled effects remained statistically significant but reduced in magnitude, refining the true genetic contribution of these mutations. The analysis also demonstrated mutation-specific resistance gradients, with L1014F conferring stronger resistance than L1014S. This study offers new insights into the molecular epidemiology of pyrethroid resistance in African malaria vectors, establishing a baseline for continent-wide genomic surveillance and vector management strategies.



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sciforum-182646: Mite Eggs in Equine Faeces: An Incidental Finding with First Molecular Evidence of *Chorioptes bovis* and *Psoroptes ovis* in Nigerian Horses

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Mange mites are obligate ectoparasites of horses and are responsible for significant skin disease, yet their detection in equine faecal samples remains largely unreported. During a routine coprological survey of horses attending a polo tournament in Ibadan, Nigeria, oval structures inconsistent with known equine helminth eggs were unexpectedly observed in a proportion of faecal samples. This study aimed to determine the prevalence of mite eggs in faecal samples from horses originating from six states in Nigeria, evaluate associations with host-related factors, and perform molecular characterisation of selected positive samples for species-level identification. Faecal samples from 167 horses were examined using the zinc sulphate flotation concentration method. Mite egg-positive samples were identified morphologically, and two randomly selected positive samples were subjected to PCR amplification of the 18S ribosomal RNA gene and Sanger sequencing for molecular identification. Mite eggs were detected in 39 horses (23.35%). State of origin was the only factor significantly associated with prevalence ($p = 0.041$), with Lagos (30.00%) and Ibadan (26.15%) recording the highest rates. No significant associations were found with breed, sex, or age group. Molecular analysis identified *Chorioptes bovis* and *Psoroptes ovis*, representing the first molecular confirmation of these species in Nigerian equines. These findings highlight the importance of training laboratory personnel to recognise mite eggs as incidental but diagnostically significant findings during routine faecal parasitological examinations, given their morphological similarity to certain helminth eggs. Concurrent skin examination and expanded molecular surveillance are recommended in future studies.



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sciforum-194703: Mobile Genetic Elements Driving the Cross-Sector Dissemination of ESBL-Producing Enterobacteriaceae Across Human, Animal and Environmental Interfaces: A One Health Systematic Review

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Introduction: The global dissemination of ESBL-producing Enterobacteriaceae is a critical One Health threat. While phenotypic spread is well documented, the underlying role of mobile genetic elements (MGEs) in driving cross-sector transmission remains incompletely characterized across interconnected One Health sectors. This systematic review critically evaluates the molecular epidemiology of MGEs plasmids, integrons, transposons, and ICEs as primary drivers of ESBL gene transfer across human, animal, and environmental interfaces.

Methods: Following PRISMA 2020 principles, peer-reviewed literature (2020–present) was systematically searched. Molecular and genomic data detailing associations between ESBL determinants and MGEs were extracted to map horizontal gene transfer (HGT) networks.

Results: MGEs function as dynamic evolutionary hubs. IncF multireplicon plasmids dominate human settings (mobilizing *bla*CTX-M-15), while IncI1/IncN plasmids are endemic in livestock (driving *bla*CTX-M-1). Insertion sequences ISEcp1 and IS26 are critical for ESBL capture and mobilization. Wastewater and agricultural soils act as mixing vessels for inter-species recombination. Co-selection via heavy metals and non-beta-lactams stabilizes MGEs even without direct antibiotic pressure.

Conclusions: ESBL dissemination is an MGE-governed ecological phenomenon transcending sectoral boundaries. Mitigation requires a shift to mobilome-centric surveillance. The WHO Tricycle protocol, integrated with predictive machine learning and long-read plasmidomics, may substantially improve the identification, prediction, and interruption of ESBL transmission pathways across the One Health continuum.



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sciforum-194683: Molecular analysis of nasal exudates from cattle in Chihuahua to detect *Mannheimia haemolytica* by endpoint PCR

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Extensive cattle farming is one of the main economic activities in the state of Chihuahua, Mexico; however, its productivity can be affected by infectious agents involved in the Bovine Respiratory Disease Complex (BRDC). Therefore, the aim of this study was to detect *Mannheimia haemolytica* associated with BRDC in nasal exudates from extensively raised cattle in Chihuahua by endpoint PCR.

For this purpose, a total of 39 nasal exudates were collected from adult female cattle, with or without clinical signs compatible with BRDC, from Ejido Huizopa (Municipality of Madera, Chihuahua), with informed consent from the owner, in December 2025. DNA extraction was carried out using the FavorPrep™ Viral DNA/RNA Kit, followed by endpoint PCR amplification with Taq DNA Polymerase Master Mix RED. The PCR protocol included an initial denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 57 °C for 30 s, and extension at 72 °C for 30 s, with a final extension at 72 °C for 1 min. Primers F3MH (TAC CAT CGC CTT TAC GG) and B3MH (GCC TTT AAC GGT GGT GAT) targeted an expected amplicon size of 190 bp. PCR products were visualized on 1.8% agarose gels.

As a result, no bands corresponding to the expected product size appeared in any of the analyzed samples.

In conclusion, *M. haemolytica* DNA was not detected in the analyzed nasal exudates during the sampling period. However, these results require cautious interpretation due to the limited sample size and the restriction of sampling to a single location and time point. Further molecular surveillance that includes additional pathogens associated with BRDC is recommended to support early detection of potential outbreaks and to enable the implementation of preventive measures that improve cattle health and productivity in the region.



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sciforum-186406: Molecular Characterization of Canine Distemper Virus (CDV) in Suspected Dogs Referred to Civil Veterinary Hospital, Peshawar, Khyber Pakhtunkhwa, Pakistan

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Canine distemper (CD) is a highly contagious viral disease caused by Canine Distemper Virus (CDV) and remains a major health concern in dogs worldwide. This study investigated the molecular prevalence and associated risk factors of CDV infection in clinically suspected dogs presented to the Civil Veterinary Hospital, Peshawar, Khyber Pakhtunkhwa, Pakistan. Clinically suspected dogs were identified based on signs including anorexia, pyrexia, vomiting, diarrhea, coughing, and respiratory distress. Blood samples were collected from owned dogs presented for clinical examination during the study period. Because sampling was restricted to a single veterinary hospital and only clinically suspected animals were included, the findings may be influenced by selection bias and should not be generalized to the broader dog population. A total of 392 blood samples were analyzed by RT-PCR targeting the nucleocapsid (N) gene of CDV, with appropriate positive and negative controls included in each reaction. Overall, 47.95% of samples tested positive. Among positive dogs, anorexia was the most common clinical sign (67%), while vomiting showed the strongest statistical association with CDV positivity ($p = 0.000$). Statistical analysis revealed significant associations between CDV infection and breed, season, and vaccination status ($p < 0.05$), whereas age and sex were not significantly associated. Certain breeds, including Dachshunds, local “Enty,” “Kochani,” and Pointer dogs, showed 100% positivity; however, these findings should be interpreted cautiously given the limited breed-specific sample sizes. Summer had the highest seasonal prevalence (70.40%). Vaccinated dogs also tested positive (61.9%), although this should not be interpreted as vaccine failure, as detailed vaccination histories were unavailable. Phylogenetic analysis of partial N gene sequences showed close clustering with the America-1 vaccine strain, with nucleotide identities ranging from 94.36% to 98.43%, highlighting the need for continued molecular surveillance and vaccine efficacy studies.



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sciforum-194678: Molecular Detection of *Trypanosoma evansi* and *Trypanosoma vivax* in Household Dogs from Semnan Province, Iran: Implications for One Health Surveillance at the Wildlife–Livestock–Human Interface

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Background: Salivarian trypanosomes, particularly *Trypanosoma evansi* and *Trypanosoma vivax*, are important hemoflagellate parasites causing veterinary and public health concerns worldwide. These pathogens infect diverse domestic and wild animals and have recognized zoonotic potential. Semnan Province, central Iran, includes protected ecosystems, including Kavir and Touran National Parks, where interactions among wildlife, domestic animals, vectors, and humans may facilitate pathogen transmission. This study investigated the occurrence and distribution of salivarian trypanosomes in household dogs from Semnan Province using molecular diagnostic techniques.

Methods: Blood samples were collected from 140 healthy household dogs (93 from Semnan and 47 from Shahroud). Thin blood smears were examined microscopically after Giemsa staining. Genomic DNA was extracted and analyzed by polymerase chain reaction targeting the internal transcribed spacer 1 region for detection of *Trypanosoma* spp. Samples positive for *T. vivax* were confirmed using species specific TVW primers.

Results: No trypanosomes were detected by microscopy. However, PCR identified 17 infected dogs (12.14%). *Trypanosoma evansi* was detected in 10 dogs (7.14%), whereas *T. vivax* was identified in seven dogs (5.00%). Coinfection with both species occurred in two animals. Estimated prevalences of *T. evansi* and *T. vivax* were higher in Semnan (11.45% and 8.50%, respectively) than in Shahroud (2.82% and 1.47%, respectively). No significant association was found between infection status and sex or geographic location ($P > 0.05$). PCR showed markedly greater sensitivity than smear examination.

Conclusions: Molecular detection of *T. evansi* and *T. vivax* in apparently healthy dogs highlights the potential role of canines as reservoirs or sentinels of infection in sensitive areas. The presence of zoonotic trypanosomes near protected wildlife habitats raises concerns regarding pathogen circulation at the human animal environment interface. These findings emphasize the need for molecular surveillance, vector monitoring, and One Health based control strategies to reduce transmission risks to domestic animals, wildlife, and human populations.



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sciforum-188091: Molecular profile and B-cell epitope mapping of trypsin inhibitor-like proteins of *Hyalomma anatolicum* and *Rhipicephalus linnaei* as potential anti-tick vaccine candidates

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Ticks are important ectoparasites of livestock that cause major economic losses and transmit a wide range of pathogens. Trypsin inhibitor-like (TIL) proteins are involved in blood feeding and modulation of the host immune responses, making them promising targets for anti-tick vaccine development. However, studies on TIL proteins in *Hyalomma anatolicum* and *Rhipicephalus linnaei* remain limited. This study provides the first molecular characterization and B-cell epitope mapping of TIL proteins from these tick species as potential anti-tick vaccine candidates. *Hyalomma* ticks were collected from cattle in Pakistan, while the *R. linnaei* specimens were obtained from a laboratory colony in Brazil. *Hyalomma* species identification was confirmed using fragment of mitochondrial *cytochrome c oxidase subunit 1 (cox1)* sequencing. TIL coding sequences were retrieved from corresponding species genomes, primers were designed, and target genes were amplified from synthesized cDNA. Bioinformatics analyses were performed to determine sequence similarity, conserved domains, phylogenetic relationships, antigenicity, allergenicity, secretory properties, and linear B-cell epitopes. *Hyalomma* ticks were morphologically identified as *H. anatolicum* and confirmed by *cox1* sequences that showed 100% identity with previously reported sequences. The amino acid sequences of HaTIL905 from *H. anatolicum* showed 100% identity, whereas RsTIL401 amino acid sequence from *R. linnaei* exhibited 96.3% identity with similar amino acid sequences derived from the same species. HaTIL905 and RsTIL401 contained one and three conserved cysteine-rich TIL domains, respectively. Phylogenetic analysis showed that both sequences clustered within the clades of similar proteins from their respective species. Both TIL amino acid sequences were predicted to be antigenic, non-allergenic, and secretory. Four and fifteen potential linear B-cell epitopes were identified in HaTIL905 and RsTIL401, respectively. These findings highlight the potential of TIL proteins as candidates for future anti-tick vaccine development and provide a foundation for further functional and immunological studies to control tick infestations.



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sciforum-193940: Molecular Survey of Zoonotic *Rickettsia* spp. in Wildlife, Companion Animals and Arthropod Vectors in Sicily: A One Health Approach

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Rickettsia spp. are arthropod-borne intracellular bacteria of growing concern for animal and human health. Sicily (southern Italy), owing to its climate, biodiversity, and strategic location in the Mediterranean basin, provides favorable conditions for vector circulation and pathogen maintenance. This study investigated the occurrence and diversity of *Rickettsia* spp. across multiple hosts and vectors.

Between 2024 and 2025, a molecular survey was conducted across Sicily. A total of 3,203 samples were collected throughout all seasons and included blood from companion animals, ticks from companion animals, wildlife and vegetation, fleas from dogs, cats and foxes, and hematophagous dipterans. Following nucleic acid extraction, samples were screened for *Rickettsia* spp. by PCR targeting the *gltA*, *ompA* and *ompB* genes. Selected amplicons were further characterized by sequencing for species identification.

Overall, 279/3,203 samples (8.7%) tested positive for *Rickettsia* spp. The highest positivity rates were observed in fleas from dogs and cats (39.6%, 38/96) and dog-associated ticks (33%, 177/536), followed by free-living ticks (19%, 26/137), ticks from cats (18.2%, 2/11), and fallow deer ticks (5.2%, 13/248); one positive sample was detected among ticks collected from wild boars. Lower prevalences were found in feline blood (3.6%), hematophagous dipterans (2%), and canine blood (0.4%), whereas equine blood, horse ticks and fox fleas tested negative. Molecular characterization identified *R. conorii*, *R. africae*, *R. felis*, *R. asemboensis*, *R. massiliae*, *R. slovaca*, *R. aeschlimannii*, *R. monacensis*, *R. helvetica*, *Candidatus R. barbariae*, *Candidatus R. yungkouensis* and *Candidatus R. shennongii*. Pathogenic species were detected in vectors associated with both domestic animals and wildlife, suggesting complex transmission networks and potential zoonotic exposure.

The remarkable diversity of *Rickettsia* spp. circulating in Sicily highlights the complexity of transmission cycles linking wildlife, vectors and peri-domestic environments. Continuous multi-host and multi-vector surveillance within a One Health framework is essential to improve risk assessment and strengthen preparedness against emerging tick-borne zoonoses in the Mediterranean region.

Funding: Italian Ministry of Health – Projects IZSSI03/23RC and GR-2021-12373930



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sciforum-165280: Preliminary survey of in-feed mycotoxin contamination and *Eimeria* infection co-occurrence in Nigerian chicken farms: implications for disease control and food safety

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Mycotoxins in poultry feed may act synergistically with *Eimeria* infections, leading to increased severity of coccidiosis and mycotoxicosis, thereby compromising effective disease control and food safety. Field-based data on the dynamics of their co-occurrence however remain limited. This study provides baseline data on the prevalence and associated risk factors of *Eimeria* parasites and in-feed mycotoxigenic fungi co-occurrence on commercial poultry farms in Lagos, Nigeria. Pooled faeces/litter and composite feed samples were collected from 126 chicken farms located in four poultry settlements. *Eimeria* oocysts were detected using the salt floatation method and classified into three size categories corresponding to the ten recognized *Eimeria* species of chickens. Feed samples were cultured on Potato Dextrose Agar, and pure isolates were obtained and characterized based on macroscopic and microscopic features. Farm management, biosecurity, and feeding practices were assessed using semi-structured questionnaires. *Eimeria* parasites and mycotoxigenic fungi occurred concurrently in 23/126 (18.3%) farms and did not vary across settlements ($P > 0.05$). Farms positive for small-sized oocysts showed a strong association with mycotoxigenic fungi contamination ($P = 0.001$). Most farms with *Fusarium*-contaminated feed were also positive for *Eimeria* oocysts ($P = 0.01$). High-Performance Liquid Chromatography revealed four Aflatoxin classes (AFB1, AFB2, AFG1, AFG2) in at least 60% of the *Aspergillus*-contaminated feed samples. Co-occurrence was significantly higher in broiler farms (5/10, 50%) compared with layer farms (18/116, 15.5%) ($P = 0.01$) but did not differ between farms using manufactured versus self-compounded feed ($P > 0.05$). Wet feeding troughs (OR: 80.1, $P = 0.05$) and the presence of flies or insects (OR: 9.1, $P = 0.05$) were significant predictors of co-occurrence. Further research is needed to characterize the risks of coccidiosis and mycotoxicosis co-occurrence to poultry, public, and environmental health from a One Health perspective.



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sciforum-187465: Prevalence of *Neospora caninum* Antibodies and Associated Risk Factors in Dairy Herds in Bangladesh

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Introduction: *Neospora caninum* is a major cause of bovine abortion and reproductive failure worldwide, but epidemiological evidence from Bangladesh dairy systems remains limited. This study estimated *N. caninum* antibody prevalence and associated herd- and cow-level risk factors.

Methods: A cross-sectional study was conducted in 14 districts of Bangladesh from January 2023 to December 2024. Bulk milk samples from 113 dairy herds and individual cow milk samples (n = 873) were tested using the ID Screen® *Neospora caninum* Indirect ELISA (Innovative Diagnostics, Grabels, France). Herd-level risk factors were assessed using univariable logistic regression followed by multivariable and stepwise logistic regression. Cow-level risk factors were assessed using univariable and multivariable mixed-effects logistic regression, with farm included as a random intercept.

Results: Herd-level and cow-level antibody prevalences were 8.8% (95% CI: 4.6–16.1%) and 6.5% (95% CI: 5.0–8.4%), respectively. At the herd level, univariable analysis identified herd size greater than 120 animals (OR: 9.33; 95% CI: 1.07–81.77), more than four calves (OR: 5.16; 95% CI: 1.04–25.48), and more than three repeat breeding cases (OR: 4.16; 95% CI: 1.02–17.07) as significantly associated factors. In the final stepwise herd-level model, only herds with more than four calves were retained (OR: 5.16; 95% CI: 1.04–25.48; P = 0.044). At the cow level, mastitis was the only significant factor in univariable analysis (OR: 0.316; 95% CI: 0.100–0.997; P = 0.049); no factor reached significance in the final multivariable model.

Conclusions: These findings demonstrate *N. caninum* exposure in Bangladesh dairy herds. The association with calf number may reflect herd structure and possible vertical transmission dynamics. Routine surveillance, improved reproductive health monitoring, and strengthened biosecurity practices are recommended.



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sciforum-192054: Retrospective Analysis of Serological Positivity Patterns for Bovine Viral Diarrhea, Infectious Bovine Rhinotracheitis, and Leptospirosis in Brazilian Cattle Herds: Insights from a 16-Year National Dataset

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Bovine viral diarrhea (BVD), infectious bovine rhinotracheitis (IBR), and leptospirosis are among the most important infectious diseases affecting cattle health, reproductive performance, and productivity worldwide. Understanding their spatial and temporal distribution is essential for supporting disease surveillance and control programs. This study aimed to characterize the distribution of serological positivity for these diseases in Brazilian cattle using a large retrospective dataset collected between 2005 and 2021. A total of 24,445 serum samples originating from 3,892 cattle farms distributed across 22 Brazilian states were evaluated. Serological testing for BVD, IBR, and leptospirosis was performed using established diagnostic methods, including enzyme-linked immunosorbent assay (ELISA), viral neutralization, and the microscopic agglutination test (MAT). Data were analyzed descriptively according to year, state, and geographic region. Among the analyzed samples, positivity frequencies of 64.34%, 58.64%, and 33.44% were observed for BVD, IBR, and leptospirosis, respectively. Higher frequencies of positive results for BVD and IBR were identified between 2008 and 2013. Spatial analysis revealed marked heterogeneity in the distribution of positive samples across the country. The South, Southeast, and Midwest regions accounted for the largest number of tested animals, reflecting greater diagnostic coverage. Nevertheless, elevated positivity frequencies were also observed in several states of the North and Northeast regions, suggesting active pathogen circulation in areas with comparatively lower testing intensity. Although the dataset does not represent a population-based prevalence survey, its extensive temporal and geographic coverage provides valuable insights into disease occurrence patterns in Brazilian cattle herds. The findings reinforce the importance of expanding diagnostic surveillance, particularly in historically underrepresented regions, and support the development of region-specific prevention and control strategies for economically relevant cattle diseases.



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sciforum-187240: Spatial-Temporal Risk Mapping and Epidemiological Modeling of Bovine Fascioliasis in Uganda: A One Health Surveillance Framework at the Livestock, Snail, and Water Interface (*IOCVS 2026*)

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Background: Fascioliasis is a neglected zoonotic infection that causes significant burdens at the livestock, human, and environmental interface in sub-Saharan Africa. In Uganda, despite notable economic losses in veterinary fields, the spatiotemporal patterns, environmental factors, and epidemiological clustering of bovine fascioliasis have not been fully characterized using integrated surveillance and predictive modeling.

Methods: Passive disease surveillance records from Uganda's national livestock disease database for 2023 to 2024 were georeferenced across three major lake basins. These records were combined with high-resolution bioclimatic (WorldClim 2.1), hydrological, topographic, soil (ISRIC SoilGrids), and vegetation (MODIS) datasets at a 1 km² resolution. We used multivariable logistic regression, checked for variance inflation factor, and performed receiver operating characteristic analysis to determine key environmental predictors. Spatial and space-time clustering were identified using SaTScan v9.4.4 with Bernoulli and Poisson models, evaluating significance through 999 Monte Carlo permutations.

Results: Fascioliasis showed significant spatial variation across Uganda's lake basins. The Lake Victoria basin (Jinja-Mayuge) stood out as the main high-prevalence area, with a prevalence of 18.0% and a relative risk of 4.9 (p 0.001). This was linked to wetland ecosystems, high annual rainfall, and frequent human and livestock contact through fishing, irrigated farming, and abattoir operations. Moderate-risk clusters were found in the Albert Nile basin (Hoima: 2.1%) and temporary clusters in the Kyoga basin (Lira: 4.4%). Important environmental predictors included temperature variability, changes in precipitation, soil organic carbon levels, and the enhanced vegetation index. Projections from 1970 to 2030 showed expanding ecological suitability and transmission hotspots focused in southwestern and peri-urban areas.

Conclusions: This first combined spatiotemporal surveillance and modeling shows fascioliasis as a varied, environmentally driven zoonotic threat with specific geographic

transmission areas in Uganda. Targeted interventions, including managing snail habitats, strategic livestock deworming, and community health education within a one health framework that provides a replicable and scalable model for regional disease control.



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sciforum-192354: Splenic and Systemic Lymphoma in an FIV-Positive Cat: A Case Report Highlighting Diagnostic Discordance in Cytology Interpretation

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Feline immunodeficiency virus (FIV) causes chronic immune dysregulation that provokes lymphoid hyperplasia, often complicating the cytologic diagnosis of neoplasia. We present a 3-year-old female domestic shorthair cat from Iran evaluated for chronic pyrexia, approximately 12% weight loss, and generalized lymphadenopathy. Ultrasonography revealed marked splenomegaly with a “Swiss-cheese” or mottled parenchymal pattern, hepatomegaly, and bilateral renal medullary rim signs. Hematological analysis demonstrated persistent hyperglobulinemia, hypoalbuminemia, and a markedly decreased albumin-to-globulin (A/G) ratio (~0.24), indicative of sustained antigenic stimulation. Virologic testing confirmed persistent FIV infection via PCR. Notably, a single initial FeLV ELISA was positive, but subsequent PCRs were negative, suggesting transient antigenemia or false-positive detection. Cytologic evaluations of different lymph nodes yielded highly discordant results: mandibular aspirates indicated reactive lymphoid hyperplasia, whereas mesenteric aspirates 16 days later revealed high-grade lymphoblastic lymphoma. This striking disparity illustrates profound lesion heterogeneity and spatial sampling bias under retroviral immunosuppression. Despite partial initial responsiveness to a vincristine-prednisolone-based chemotherapy protocol and supportive care, the patient’s condition deteriorated, culminating in death 15 months post-diagnosis. This case emphasizes the diagnostic challenges of differentiating FIV-induced reactivity from lymphoma. It highlights the necessity of serial, multisite cytologic sampling integrated with advanced imaging and precise virologic testing for the accurate diagnosis of feline hematopoietic malignancies.



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sciforum-187580: Surveillance of *Varroa destructor* in Honey Bees: A One Health Approach and Epidemiological Modelling

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Introduction

Varroa destructor is one of the major drivers of honey bee colony decline worldwide. Beyond its direct parasitic effects, this mite facilitates the transmission of viral pathogens, particularly Deformed Wing Virus, resulting in increased colony mortality and reduced productivity. Within a One Health framework, honey bee health is closely linked to biodiversity conservation, crop pollination, and food security.

Methods

A descriptive observational study was conducted on 120 honey bee colonies distributed across three ecological zones: intensive agricultural areas (n=45), peri-urban areas (n=35), and semi-natural areas (n=40). Infestation levels of *Varroa destructor* were assessed from March to September 2025 using natural mite fall counts and alcohol wash methods on standardized samples of 300 bees per colony. Environmental variables including temperature, relative humidity, vegetation cover, apiary density, and proximity to pesticide-treated crops were recorded. Multivariate statistical analysis was performed to identify risk factors associated with high infestation rates.

Results

The overall mean infestation rate was $5.6 \pm 1.9\%$. Colonies located in intensive agricultural areas showed significantly higher infestation levels (7.1%) compared with peri-urban (5.3%) and semi-natural areas (3.8%). Clinical signs suggestive of viral infection were observed in 42% of heavily infested colonies. Colonies exceeding an infestation threshold of 6% demonstrated an average 28% reduction in adult bee population and increased risk of autumn weakening. Moderate temperatures (22–28°C) and high brood density were significantly associated with accelerated parasite population growth.

Conclusions

Integrating parasitological and environmental data improves early surveillance of *Varroa destructor* and facilitates identification of high-risk colonies. This integrated approach provides a strategic tool for sustainable pollinator protection within a One Health perspective.



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sciforum-194350: The One Health role of interplay between canine parvovirus and Gram-negative bacterial translocation in sepsis and multi-organ failure in dogs

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Abstract

Introduction: Canine parvovirus (CPV-2) is one of the most lethal gastrointestinal viruses in dogs, characterized by hemorrhagic gastroenteritis, severe intestinal mucosal destruction, and depletion of crypt stem cells. Mortality in CPV infection is often not directly caused by the virus, but rather as a result of sepsis and multiorgan failure (MODS) following enteric Gram-negative bacterial translocation. This systematic review aimed to evaluate the role of One Health in the association between parvovirus, bacterial translocation, and sepsis in dogs.

Methods: A systematic search was conducted in PubMed, Google Scholar, and ScienceDirect for studies published between January 2018 and December 2024 following the PRISMA guidelines. Inclusion criteria were clinical and experimental studies that simultaneously examined CPV infection, endotoxin (lipopolysaccharide, LPS) in the blood, organ failure, and outcomes related to antimicrobial resistance. Of the 956 studies found, 34 studies met the inclusion criteria.

Results: Among CPV-infected dogs with sepsis, Gram-negative bacterial translocation (*E. coli*, *Salmonella*, *Klebsiella*) was reported in 82% of cases (descriptive summary). Intestinal barrier disruption elevated serum LPS, triggering TLR4/MYD88-mediated cytokine storm (IL-1 β , IL-6, TNF- α), which was associated with ARDS, renal tubular necrosis, and myocarditis. Antimicrobial resistance to first-line antibiotics (cephalexin, enrofloxacin) was observed in 43% of isolates. However, due to heterogeneity among observational studies, these pooled percentages should be interpreted cautiously and are presented as aggregated summaries rather than definitive estimates.

Conclusion: From a One Health perspective, three levels of intervention were defined. First, animal health with widespread CPV vaccination and the use of probiotics to maintain the integrity of the intestinal barrier. Second, human health by reducing the selective pressure of antibiotics through targeted therapy based on an antibiogram. Third, environmental health is achieved by properly managing contaminated waste and feces from infected puppies, which can serve as reservoirs of antimicrobial resistance genes.



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sciforum-189074: The peregrine falcon (*Falco peregrinus*) as a sentinel species for environmental contamination at the human–animal–environment interface

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Introduction

Within the One Health framework, sensitive non-invasive indicators are needed for surveillance at the human–animal–environment interface. This study evaluates the peregrine falcon (*Falco peregrinus*) as a sentinel species for trace element exposure across an environmental gradient in Italy, using feathers (long-term accumulation) and faeces (recent dietary intake).

Methods

We compared individuals from high (HEI) and low (LEI) environmental impact areas. Trace elements including mercury (Hg) and lead (Pb) were quantified in both matrices. Feathers provided integrated bioaccumulation data, while faeces reflected short-term exposure patterns. Crucially, this multi-matrix approach is rapid and painless for the raptors, involving only non-invasive collection of naturally moulted feathers and fresh faeces, with no impact on animal welfare or health. Sampling requires minimal handling and can be repeated over time without disturbing the birds or their breeding activity.

Results

Feathers from HEI falcons showed significantly higher concentrations of most trace elements, particularly Hg (p 0.01) and Pb (p 0.05), indicating enhanced trophic transfer in impacted environments. Faecal analyses complemented these findings, revealing elevated levels of several elements in HEI individuals, though some elements showed no differences due to rapid excretion. The combined matrix approach captured both persistent bioaccumulation and recent dietary fluctuations, offering a more complete exposure profile. Notably, faecal variability also reflected short-term changes in prey contamination, providing real-time dietary snapshots.

Conclusions

These findings support the peregrine falcon as a sensitive, non-invasive bioindicator for surveillance at the human–animal–environment interface. The feather–faecal matrix model provides a standardized, rapid, and animal-friendly framework for long-term monitoring of terrestrial ecosystem contamination, with direct applications in exposure modelling and early warning systems for emerging environmental risks to wildlife, domestic animals, and human health. This approach enables ethically sound biomonitoring programs aligned with animal welfare principles and One Health surveillance strategies.



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sciforum-188147: Tipping the Balance: A One Health Analysis of Climate-Driven Mosquito Expansion and Emerging Vulnerabilities (Case Study: Iceland)

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Introduction:

Anthropogenic climate change is reshaping ecosystems and altering vector and pathogen distributions. The unprecedented discovery of *Culiseta annulata* in Iceland in 2025—previously one of the world’s only mosquito-free nations—signals a major ecological shift. This paper applies a One Health systemic review framework to explore the interconnections between climate warming, mosquito ecology, and emerging health vulnerabilities.

Methods:

This study systematically synthesized climatological, ecological, and epidemiological data from published literature, official databases (IPCC, ECDC, WHO, NASA Earth Observatory, Icelandic Meteorological Office), and verified news sources. Data were analyzed through a One Health lens to evaluate environmental, animal, and human health risks. A tripartite vulnerability assessment was conducted to identify potential cross-sectoral impacts.

Results:

Iceland’s 2025 record-breaking heatwave, with sustained temperatures above 20 °C for ten consecutive days, disrupted its historic freeze–thaw defense, allowing the successful breeding of *C. annulata*. The species’ cold-tolerant biology and overwintering strategy enabled permanent establishment. Findings indicate new ecological pressures, potential introduction of avian and livestock pathogens, and emerging human health risks in a previously naïve population.

Conclusions:

The colonization of mosquitoes in Iceland represents a climate-driven tipping point in sub-Arctic ecosystems. It demonstrates the tangible interdependence of environmental, animal, and human health within the One Health paradigm. Proactive integrated surveillance, research capacity building, and public awareness strategies are urgently needed to safeguard high-latitude regions against future vector-borne disease emergence.



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sciforum-194884: Veterinary Abortion Surveillance as an Epidemiological Tool: A Seven-Year Study in South Bačka and Srem, Serbia (2019–2026)

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Abortions represent one of the most important reproductive disorders in livestock production, causing substantial economic losses and providing valuable epidemiological information on circulating infectious diseases. This study analyzed reported abortion cases in domestic animals from the South Bačka and Srem districts of Serbia during the period 2019–2026.

A total of 1,262 abortion cases were investigated, including 255 in cattle, 972 in pigs, 33 in sheep, and 2 in mares. Maternal sera were examined serologically for major viral, bacterial and parasitic abortifacient pathogens, while aborted fetuses were tested using PCR/RT-PCR, qPCR/RT-qPCR and bacterial culture when appropriate (*Listeria* sp.).

In cattle abortion cases, *C. burnetii* and *Leptospira* spp. were the most prevalent pathogens detected (7.06%), followed by *Listeria* spp. (3.92%), *N. caninum* (3.53%) and BVDV (3.14%). *T. gondii* (1.18%), and *B. abortus*, *C. abortus* and BHV1 (0.39%) were less prevalent. Highest seroprevalence was detected for BVDV (66.27%), BHV1 (28.63%) and *C. burnetii* (18.82%) followed by *N. caninum* (12.16%).

In pigs, *Leptospira* spp. was the most commonly detected pathogen (6.53%), followed by *T. gondii* (2.61%), PRRSV (2.65%) and PCV2 (2.26%). *B. suis* was found in 0.93% cases. Interestingly, PPV was detected very rarely (0.73%), although the seroprevalence was the highest (97.84%; 951/972). Seroprevalence was also high for PRRSV (62.65%) and PrV (36.73%), while it remained below 5% for all other tested pathogens.

Among sheep abortions, *C. burnetii* was the most prevalent pathogen (9.09%), followed by *N. caninum* and *T. gondii* (6.06% each). No abortion cases were recorded in goats during the study period. Of the two equine abortion cases, one was positive for EHV1 and the other for EAV.

The obtained results could be used, as already implemented in Serbia, to develop more detailed herd- or region-based surveillance programs and to design targeted, small-scale (hotspot-based) pathogen prevention and control strategies.



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sciforum-188132: WILD UNGULATES AS SENTINELS OF CRIMEAN-CONGO HEMORRHAGIC FEVER VIRUS CIRCULATION IN SPAIN

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Introduction:

Crimean-Congo hemorrhagic fever virus (CCHFV) is an emerging tick-borne pathogen in southwestern Europe, maintained in enzootic cycles involving *Hyalomma* spp. ticks and vertebrate hosts. In Spain, evidence of viral circulation highlights the need for effective surveillance systems. Wild ungulates, particularly red deer, may serve as useful sentinels for monitoring CCHFV transmission and assessing zoonotic risk. This study aimed to determine the seroprevalence against CCHFV in wild ungulates and to evaluate their role as reservoirs of the virus in natural ecosystems.

Methods:

Between 2024 and 2026, a total of 184 wild ungulates from central and southern Spain were sampled during hunting activities. The study included red deer (*Cervus elaphus*), wild boar (*Sus scrofa*), and fallow deer (*Dama dama*). Serum samples were analyzed for antibodies against CCHFV using a commercial double-antigen ELISA (ID Screen CCHF Multispecies, IDvet), following the manufacturer's instructions.

Results:

Antibodies against CCHFV were detected in 107 of 184 animals (58.15%). By species, 87 (70.16%, 95% CI 62.1%–78.2%) of the 124 red deer, 12 (24.49%, 95% CI 12.4%–36.5%) of the 49 wild boar, and 8 (72.73%, 95% CI 46.4%–99.1%) of the 11 fallow deer analyzed were seropositive. Evidence of CCHFV exposure was found across all sampling sites.

Conclusions:

The high seroprevalence observed supports widespread exposure to CCHFV among wild ungulates in Spain. These findings are consistent with previous findings that support the important role of cervids in the epidemiological cycle maintenance, while wild boar may have a more limited contribution. Additionally, as ungulates are major hosts for *Hyalomma* spp. ticks, the main vectors of CCHFV in the Iberian Peninsula, they may contribute to viral persistence in natural ecosystems and highlight their value as useful sentinels for CCHFV surveillance, reinforcing the importance of active monitoring programs in high-risk areas within a One Health framework.



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sciforum-193946: Zoonotic pathogens in fallow deer (*Dama dama*) from Sicily (Southern Italy): implications for wildlife–livestock–human interface

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Increasing interactions among wildlife, livestock, and humans have enhanced opportunities for pathogen transmission, raising concerns for both animal and public health. In Sicily, the expansion of fallow deer (*Dama dama*) populations and the widespread presence of extensive farming systems may facilitate the circulation of zoonotic and vector-borne pathogens. This study investigated the occurrence of *Toxoplasma gondii*, *Leptospira* spp., *Coxiella burnetii*, and selected tick-borne pathogens (*Babesia* spp., *Theileria* spp., *Anaplasma* spp., *Rickettsia* spp., and *Borrelia burgdorferi* sensu lato) in 56 fallow deer carcasses collected through population control programs in Sicily between 2023 and 2025. Multiple tissue samples, including spleen, liver, heart, kidney, and lymph nodes, were collected from each animal for DNA extraction and molecular analyses. Pathogen DNA was detected by real-time PCR targeting the 529-bp repeat element (*T. gondii*), 16S rRNA and *lipL32* (*Leptospira* spp.), IS1111 (*C. burnetii*), and *ospA* (*B. burgdorferi* s.l.). Conventional PCR followed by Sanger sequencing targeted 18S rRNA (*Babesia* spp. and *Theileria* spp.), 16S rDNA (*Anaplasma* spp.), and *rOmpB* (*Rickettsia* spp.).

Toxoplasma gondii DNA was detected in 4/56 animals (7.1%), while *Leptospira interrogans* was identified in 1/56 (1.8%). No samples tested positive for *C. burnetii* or *B. burgdorferi* s.l. Piroplasm DNA was detected in 8/56 deer (14.3%), *Anaplasma* spp. DNA in 43/56 (76.8%), and *Rickettsia* spp. DNA in 2/56 (3.6%). Sequence analysis identified *Theileria cervi*, *Theileria ovis*, *Theileria capreoli*, *Anaplasma phagocytophilum*, and *Rickettsia slovaca*. These findings demonstrate that free-ranging fallow deer may serve as reservoirs of several zoonotic and vector-borne pathogens, highlighting the importance of integrated wildlife surveillance within a One Health framework to support the prevention of interspecies pathogen transmission.

This study was funded by the Italian Ministry of Health (Grant No. GR-2021-12373930).



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Session 3. Antimicrobial Resistance and Food Safety: A One Health Perspective

sciforum-187920: Evaluation of the Effect of Doxycycline Administration on Growth Performance and Tissue Residue Accumulation Kinetics in Hubbard Broiler Chickens

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Antibiotic administration in poultry production remains an important One Health concern, particularly because inappropriate use may contribute to antimicrobial resistance and the persistence of antimicrobial residues in food products. This study aimed to evaluate the association between oral doxycycline administration and growth performance in Hubbard broiler chickens, as well as to assess the kinetics of residual antimicrobial activity in selected tissues.

A total of 200 one-day-old Hubbard broiler chicks were divided into two groups of 100 birds each: a control group receiving a standard diet without doxycycline treatment and a treated group receiving doxycycline at 20 mg/kg body weight through drinking water from day 22 to day 42 of rearing. Growth performance was assessed by monitoring body weight, feed intake, and average daily gain. In parallel, tissue samples, including liver, kidneys, muscle, and adipose tissue, were collected to evaluate residue accumulation using a microbiological inhibition assay based on the detection of residual antimicrobial activity.

The doxycycline-treated group showed higher body weight and greater weight gain compared with the control group. Statistical analysis confirmed a significant association between doxycycline administration and improved growth-related parameters ($p < 0.001$). Residual antimicrobial activity was detected in all analysed tissues, with greater accumulation observed in the liver and kidneys.

These findings indicate that, under the conditions of this study, doxycycline administration was associated with improved growth performance in Hubbard broiler chickens. However, the persistence of residual antimicrobial activity in edible tissues raises important food safety concerns. Therefore, doxycycline use in poultry production should be strictly controlled to ensure food safety and compliance with One Health principles.



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sciforum-194676: *In vitro* evaluation of synergistic antimicrobial effect of lactoferrin and nisin along with penicillin and gentamicin, and potential application in mastitis treatment

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Mastitis is a leading challenge to the production and welfare of dairy animals, caused by a variety of pathogens. Existing antimicrobial strategies have failed to treat mastitis while contributing to the development and dissemination of antimicrobial resistance. This situation demands investigation of the antimicrobial properties of new candidates. Lactoferrin and nisin have been reported to have strong antimicrobial effects in previous studies. This study aimed to assess the synergistic antimicrobial activities of lactoferrin, nisin, and antibiotics (penicillin, gentamicin) alone and in combination against major pathogens, including *Escherichia coli*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, and *Streptococcus uberis*. 100 dairy cows were selected for milk sampling from different herds in the district of Bahawalnagar, Pakistan. The California mastitis test was performed to screen for cases of mastitis. Bovine lactoferrin was purchased, the MIC of the mentioned bacteria was determined, and the effect of lactoferrin concentrations on the growth of these bacteria was assessed. After isolating the bacteria through colony culture, different combinations were applied to these bacterial colonies. The minimum inhibitory concentration of lactoferrin for *L. monocytogenes*, *S. uberis*, and *E. coli* was recorded 0.1%, 0.5%, and 1%, respectively. The application of nisin for the treatment of subclinical mastitis is advantageous 93% of the time. Sensitivity analysis reveals that treatment with nisin is beneficial for 73% of primiparous cows. Significant synergistic effects against resistant microbes were observed with different combinations, especially the combination of lactoferrin and nisin with penicillin. This *in vitro* study may be useful in establishing formulations to combat antimicrobial resistance issues at the commercial level. These findings can also help design further effective research plans to set the dose rate of these animal-origin compounds in combination with existing antibiotics to mitigate mastitis at the herd level.



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sciforum-188649: Detection of Antibiotic Residues in Raw Bovine Milk and Environmental Risks Associated with Improper Disposal: A One Health Approach

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Bovine milk is a physiological secretion produced by the mammary gland of healthy cows during lactation under adequate hygienic-sanitary conditions. However, mastitis, commonly associated with infectious agents, frequently requires the use of antibiotics in dairy cattle farming, which may result in antibiotic residues in milk and pose risks to public health and the environment. This study aimed to evaluate antibiotic residues in bovine milk over a three-month period and discuss their environmental implications from a One Health perspective. A retrospective and descriptive study was conducted based on routine analyses performed in a bovine milk processing unit. During 90 days, 675 milk samples from different rural properties were analyzed using a rapid immunochromatographic test for the detection of antibiotic residues. Among the analyzed samples, 93 (13.8%) tested positive, with 39 (5.8%) positive for tetracyclines, 30 (4.4%) for β -lactams, and 24 (3.6%) showing simultaneous presence of both classes, demonstrating the occurrence of multiple antibiotic residues in bovine milk. Physicochemical parameters also showed significant alterations, especially titratable acidity values above the limits established by current legislation, suggesting failures in hygienic-sanitary management, refrigeration, or milk quality control. The presence of these residues represents a significant public health concern, since continuous exposure to antimicrobials may contribute to the selection of resistant microorganisms, making therapeutic treatments more difficult and increasing antimicrobial resistance challenges, particularly in hospital environments. Furthermore, although contaminated milk was disposed of in a specific area, no environmental monitoring of the disposal site was carried out, making it impossible to ensure the absence of soil or water contamination. Therefore, the findings highlight impacts that extend beyond the dairy production chain, involving environmental and collective health issues, reinforcing the importance of rational antibiotic use and One Health strategies.



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sciforum-192613: Cracking the Shell: Genomic Insights into Antimicrobial-Resistant *Escherichia coli* on Retail Eggs in the United Arab Emirates

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Background:

Antimicrobial-resistant bacteria associated with foods of animal origin are an increasing food safety concern. However, data on generic *Escherichia coli* from retail eggs in the Middle East remain scarce.

Objective:

This study provides baseline evidence on the occurrence, antimicrobial resistance, virulence determinants, and genomic diversity of generic *Escherichia coli* recovered from retail table eggs in the United Arab Emirates.

Methods:

A total of 200 retail egg packs, representing 2,400 individual eggs, were collected from supermarkets in three major United Arab Emirates cities between October 2024 and June 2025. Eggshells and egg contents from each pack were analyzed separately. Phenotypic antimicrobial susceptibility testing was performed on 50 isolates, and whole-genome sequencing was conducted on 20 selected isolates to characterize resistance genes, virulence determinants, phylogroups, sequence types, and genomic backgrounds.

Results:

Escherichia coli was recovered from 50 of 200 eggshell pools, corresponding to 25.0% prevalence with a 95% confidence interval of 19.2–31.6%. No isolates were detected in egg contents, indicating contamination restricted to the external shell surface. Recovery was significantly higher from cage-laid eggs than cage-free eggs. Phenotypic testing revealed frequent non-wild-type profiles to ciprofloxacin, nalidixic acid, tetracycline, ampicillin, and chloramphenicol. Multi-class resistance was detected in 52.0% of isolates, while all remained wild type to colistin, meropenem, and tigecycline. Genome analysis revealed a diverse resistome dominated by quinolone-associated determinants, including *gyrA* mutations and *qnrS1*, alongside *tet(A)*, *blaTEM-1*, *cmiA1*, *floR*, and one *blaCTX-M-55*-positive isolate. Isolates belonged to 12 sequence types, mainly phylogroups B1 and A, indicating heterogeneous genomic backgrounds. Virulence-associated genes related to adhesion, iron acquisition, serum survival, toxins, and stress adaptation were widely detected.

Conclusion:

These findings establish the first integrated phenotypic and genomic baseline for eggshell-associated generic *Escherichia coli* in United Arab Emirates retail eggs and support targeted surveillance, improved eggshell hygiene, and consumer practices that reduce cross-contamination.



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sciforum-181451: Diversity and Characterization of Lytic Bacteriophage Plaque Morphotypes Targeting *Escherichia coli* from Anthropized Aquatic Environments in Curitiba, Brazil: Implications for Phage Therapy

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The global antimicrobial resistance crisis urgently demands innovative therapeutic alternatives, with lytic bacteriophages emerging as highly specific biocontrol agents against pathogenic *Escherichia coli* strains in both human and veterinary medicine. This study aimed to characterize the macromorphological diversity of bacteriophage plaque phenotypes isolated from highly anthropized aquatic environments (Belém River Sites I and II, Vila Formosa River, and Barigui River) in Curitiba, Paraná, Brazil, using the reference strain *E. coli* ATCC 25922 as the propagation host. Environmental samples underwent standardized enrichment protocols involving Luria-Bertani/TSB broth co-cultivation, chloroform treatment, and plaque assay quantification on TSB agar, enabling morphotype discrimination. Macroscopic analysis identified six distinct plaque morphotypes: (1) large clear plaques with halos; (2) large clear plaques without halos; (3) large plaques with central clearing; (4) diffuse large plaques exhibiting central clearing with turbid edges; (5) confluent microplaques resembling rainfall patterns; and (6) discrete small pinhead plaques. Site-specific distribution patterns suggested environmental phage heterogeneity, with Types 1 and 2 predominating in heavily sewage-contaminated Belém Site I, Types 3 and 4 in Belém Site II, and Types 5 and 6 in the comparatively less contaminated Vila Formosa and Barigui river systems. These findings demonstrate that plaque morphology can serve as a rapid and cost-effective preliminary indicator of environmental bacteriophage diversity. However, the exclusive use of the reference strain *E. coli* ATCC 25922 may not capture the full spectrum of phages capable of infecting clinically relevant or antimicrobial-resistant *E. coli* strains. Therefore, the observed morphotypic richness should be interpreted as an initial biodiversity screening. Future studies incorporating host-range analysis, electron microscopy, and genomic characterization are needed to evaluate the therapeutic potential of these phages. Nevertheless, the results highlight urban aquatic environments as promising reservoirs of bacteriophages and support their future application within a One Health framework linking environmental contamination, animal health, and public health.



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sciforum-187944: Genotypic and Phenotypic Characterization of *Listeria Monocytogenes* Reveals Challenges to Sanitization Efficacy in Brazilian Food Industries

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Introduction: *Listeria monocytogenes* is a critical hygiene indicator in food processing environments (FPEs) and a lethal pathogen. Industrial sanitation eliminates most microbiota; however, suboptimal efficacy exerts strong selective pressure in clean niches, threatening food safety. Persistent, biofilm-forming, stress-tolerant strains predominate, frequently combining enhanced virulence and environmental adaptability. This study characterized the genotypic (serogroup, virulence, biofilm-associated genes) and phenotypic (biofilm formation ability and antimicrobial resistance profile) profiles of *L. monocytogenes* isolated from food contact surfaces after standard industrial sanitation.

Methods: Seventeen isolates came from industrial polystyrene and stainless-steel surfaces across three facilities (one poultry, one pork, and one dairy plant) after the pre-operational hygiene stage, following ISO 11290. Phenotypic characterization assessed susceptibility to 12 antimicrobials from 10 classes and adhesion on polystyrene microplates (CLSI, 2021; Stepanović, 2000). Genotypic analysis included multiplex PCR serogrouping (I, III, IV) and detection of virulence genes (*inA*, *inB*, *inC*, *hlyA*, *actA*) alongside genes for biofilm formation, regulation, and stress adaptation (*prfA*, *flaA*, *agrABCD*, *luxS*).

Results: Isolates belonged to serogroups I (1/2a), III (1/2b), and IV (4b), with I predominating in poultry and IV in pork, comprising 10 pork, 6 poultry, and 1 dairy isolates. All were resistant to clindamycin, and 64.7% to penicillin, yielding two profiles, with combined clindamycin-penicillin resistance dominating. All carried the full virulence gene set (*hlyA*, *inA*, *inB*, *inC*, *prfA*) plus the *agrABCD* system and *luxS*, while *actA* was restricted to pork isolates. Despite this biofilm-associated genotype, all strains exhibited weak polystyrene adhesion.

Conclusions: The repeated isolation of *L. monocytogenes* serogroups 4b and 1/2a with multivirulence characteristics and adhesion capacity demonstrates the selection and survival of high-risk strains after industrial cleaning. Widespread clindamycin resistance and dominant penicillin co-resistance amplify this public health alert. Revising sanitation validation protocols to include sessile-cell assays is imperative to eliminate these persistent pathogens, mitigating cross-contamination and food safety risks under a One Health perspective.



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sciforum-194353: Antimicrobial-Resistant Foodborne Bacteria in Algeria: A Systematic Review at the Animal–Food–Human Interface

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Introduction:

Antimicrobial resistance (AMR) in food-producing animals and animal-derived foods is a major One Health concern, particularly in settings where surveillance data remain fragmented across animal, food, human, and environmental sectors. Algeria represents an under-synthesized North African context in which several microbiological studies have reported resistant bacteria in livestock, poultry, meat, milk, dairy products, and ready-to-eat foods, but the evidence has not been comprehensively integrated. This systematic review aimed to summarize published evidence on antimicrobial-resistant foodborne bacteria in Algeria and to identify gaps limiting One Health interpretation.

Methods:

A PRISMA 2020-compliant systematic review was conducted using PubMed, Scopus, Web of Science, Google Scholar, and African Journals Online. Eligible studies reported phenotypic antimicrobial susceptibility testing and/or molecular detection of resistance genes in bacteria isolated from food-producing animals, slaughterhouse samples, retail meat, milk, dairy products, eggs, ready-to-eat foods, or related food-chain environments in Algeria. Human-only clinical studies, environmental-only studies without food-chain relevance, narrative reviews, and non-AMR contamination studies were excluded.

Results:

The available literature mainly addressed poultry, cattle, raw milk and dairy products, meat, slaughterhouse samples, and ready-to-eat foods. Frequently investigated bacteria included *Escherichia coli*, *Klebsiella pneumoniae*, *Salmonella* spp., *Campylobacter* spp., *Staphylococcus aureus*, including methicillin-resistant *S. aureus*, and *Enterococcus* spp. Recurrent findings included multidrug-resistant phenotypes, extended-spectrum beta-lactamase-producing Enterobacterales, AmpC-associated resistance, colistin resistance markers, and resistance to antimicrobial classes relevant to veterinary and public health. However, studies differed substantially in sampling design, geographic coverage, laboratory methods, antimicrobial panels, molecular confirmation, and reporting standards.

Conclusions:

Published Algerian evidence indicates that AMR in animal-derived food chains is a relevant but incompletely integrated One Health issue. Standardized surveillance combining farm, slaughterhouse, retail-food, environmental, and public-health data would strengthen risk assessment and support AMR control strategies in Algeria and comparable North African contexts.



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sciforum-164926: Integrating AI, Machine Learning, and Geospatial Technologies for One Health Management of Emerging Zoonoses: Distributed Surveillance and Communication Solutions for Antimicrobial Resistance and Food Safety

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The increasing prevalence of emerging zoonotic diseases, antimicrobial resistance (AMR), and food safety threats requires integrated approaches aligned with the One Health framework. This study evaluates the application of Artificial Intelligence (AI), Machine Learning (ML), and Geospatial Technologies to strengthen distributed surveillance and predictive health management across human, animal, and environmental domains. Multi-source datasets collected between 2021 and 2025 from veterinary health records, environmental monitoring systems, agricultural reports, antimicrobial usage databases, and public health surveillance platforms in selected East African regions were analyzed.

A hybrid analytical framework combining machine learning algorithms, geospatial hotspot analysis, and distributed communication-enabled surveillance systems was developed to detect zoonotic disease patterns, identify AMR risk clusters, and monitor food contamination pathways. Random Forest, Support Vector Machine (SVM), and Long Short-Term Memory (LSTM) models were applied for predictive risk assessment, while Geographic Information Systems (GIS) techniques supported outbreak mapping and spatial correlation analysis. Distributed surveillance networks integrated heterogeneous clinical, environmental, and agricultural data streams for near real-time situational awareness.

Results indicate that the proposed framework significantly improved zoonotic outbreak prediction and AMR hotspot identification. The Random Forest model achieved 91.3% classification accuracy in outbreak detection, while geospatial analysis successfully identified high-risk regions associated with intensive livestock and agricultural activities. The integrated system also enhanced inter-agency communication, food safety traceability, and antimicrobial stewardship through data-driven monitoring and anomaly detection.

The study demonstrates that integrating AI, ML, geospatial intelligence, and distributed communication systems within a One Health framework provides a scalable and adaptive solution for managing emerging zoonoses, mitigating AMR risks, and improving food safety governance in resource-constrained environments.



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sciforum-189035: Molecular Detection, Antimicrobial Resistance Profiling, and Genetic Diversity of *Campylobacter jejuni* and *Campylobacter coli* Isolated from Urban Backyard Poultry, Companion Animals, and Environmental Samples: A One Health Approach in Peri-Urban Regions

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Background: Campylobacteriosis caused by *Campylobacter jejuni* and *Campylobacter coli* is among the leading bacterial zoonotic gastroenteritis diseases worldwide. The increasing practice of backyard poultry keeping in urban and peri-urban areas may facilitate the circulation of antimicrobial-resistant *Campylobacter* strains at the human–animal–environment interface. However, integrated One Health investigations in these settings remain limited.

Objectives: This study aimed to determine the prevalence, antimicrobial resistance patterns, and genetic diversity of *C. jejuni* and *C. coli* isolated from backyard poultry, companion animals, and environmental sources in peri-urban areas.

Methods: A cross-sectional study was conducted from April to September 2025. A total of 420 samples, including cloacal swabs from backyard poultry ($n = 180$), fecal samples from dogs and cats ($n = 120$), and environmental samples ($n = 120$), were collected using systematic random sampling. Following enrichment and culture on mCCDA under microaerophilic conditions, isolates were confirmed by species-specific PCR targeting the *hipO* and *asp* genes. Antimicrobial susceptibility testing was performed using disk diffusion and broth microdilution methods according to CLSI and EUCAST guidelines. Genetic diversity was evaluated by Multi-Locus Sequence Typing (MLST) and sequencing of resistance-associated genes.

Results: Overall, 34.8% (146/420) of samples were positive for *Campylobacter* spp., including 64.4% *C. jejuni* and 35.6% *C. coli*. The highest prevalence was detected in backyard poultry (46.7%), followed by environmental samples (29.2%) and companion animals (22.5%) ($p < 0.01$). High resistance rates were observed against ciprofloxacin (74.7%), tetracycline (65.8%), and erythromycin (41.8%), while 61.6% of isolates showed multidrug resistance. MLST identified 19 sequence types, several closely related to human clinical isolates.

Conclusions: The widespread occurrence of antimicrobial-resistant *Campylobacter* in peri-urban settings highlights the importance of integrated One Health surveillance, antimicrobial stewardship, and public education regarding backyard poultry management.



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sciforum-194893: A Bacteriophage Holin-Derived Antimicrobial Peptide with Membrane-Disruptive Activity and Therapeutic Efficacy Against MDR *Pseudomonas aeruginosa* Burn Wound Infections

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Introduction: Multidrug-resistant (MDR) *Pseudomonas aeruginosa* is a major cause of burn wound infections and represents a significant antimicrobial resistance challenge. Antimicrobial peptides (AMPs) derived from bacteriophage proteins offer a promising alternative to conventional antibiotics. This study aimed to identify and evaluate a novel bacteriophage holin-derived AMP against MDR *P. aeruginosa*.

Methods: An artificial intelligence-guided approach was employed to identify AMP, a 12-amino-acid cationic peptide derived from a *Pseudomonas* bacteriophage holin protein. Antibacterial, antibiofilm, membrane-disruption, stability, hemocompatibility, and cytotoxicity assays were performed. Therapeutic efficacy was further evaluated using a carbomer hydrogel formulation in a murine burn wound infection model caused by MDR *P. aeruginosa*.

Results: AMP exhibited potent antibacterial and antibiofilm activity against *P. aeruginosa*, achieving complete bacterial killing within 90 min. Mechanistic studies demonstrated concentration- and time-dependent membrane permeabilization and disruption. The peptide showed minimal cytotoxicity, high hemocompatibility, and retained activity under physiologically relevant salt, serum, and temperature conditions. *In vivo*, topical administration of AMP-hydrogel significantly reduced bacterial burden, accelerated wound closure, enhanced collagen deposition, and favorably modulated inflammatory cytokine responses compared with untreated controls.

Conclusions: The findings highlight bacteriophage holins as an underexplored source of antimicrobial peptides and demonstrate the potential of a novel AI-designed holin-derived peptide as a stable, biocompatible, and effective therapeutic candidate for managing MDR *P. aeruginosa* wound infections within a One Health framework addressing antimicrobial resistance.



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sciforum-193100: A Canine Commensal *Escherichia coli* Exhibits Anti-Proliferative Effects on Mammary Tumor Cells While Displaying a Multidrug-Resistant Phenotype: Implications for One Health

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Introduction: Antimicrobial resistance (AMR) is a major One Health challenge, and companion animals may act as reservoirs of resistant bacteria. Concurrently, growing evidence suggests that gut microbiota can influence cancer biology. However, the relationship between AMR phenotypes and anti-tumor activity in canine commensal bacteria remains poorly understood. This study investigated whether a canine commensal *Escherichia coli* isolate exhibits both anti-proliferative activity against canine mammary tumor (CMT) cells and clinically relevant AMR traits.

Methods: An *E. coli* isolate obtained from a clinically healthy dog (no reported antibiotic treatment within the previous four weeks) was co-cultured with primary CMT cells at 0, 1×10^5 , and 1×10^6 CFU/mL for 72 hours. Cell proliferation was assessed using the MTT assay, while reactive oxygen species (ROS), caspase-3/7 activity, and expression of *BAX*, *BCL-2*, *TLR4*, and *TNF- α* were evaluated. Antimicrobial susceptibility was determined using Kirby-Bauer disc diffusion according to CLSI guidelines against eight commonly used veterinary antimicrobials.

Results: The *E. coli* isolate reduced CMT cell proliferation in a dose-dependent manner, with a 17 percent decrease observed at 1×10^6 CFU/mL ($p = 0.032$; $R^2 = 0.84$). Exposure to the isolate was associated with increased ROS production (1.68-fold, $p = 0.006$), elevated caspase-3/7 activity (1.56-fold, $p = 0.011$), and upregulation of *BAX* (2.1-fold), *TLR4* (1.7-fold), and *TNF- α* (1.5-fold), suggesting activation of apoptosis-related pathways. Antimicrobial susceptibility testing demonstrated resistance to enrofloxacin, amoxicillin clavulanate, tetracycline, and cefalexin, intermediate susceptibility to gentamicin, and susceptibility to trimethoprim sulfamethoxazole, marbofloxacin, and chloramphenicol, consistent with a multidrug-resistant phenotype.

Conclusions: This preliminary study demonstrates that a canine commensal *E. coli* isolate can exhibit anti-proliferative effects on CMT cells while simultaneously carrying multidrug-resistant traits of One Health concern. The coexistence of potentially beneficial biological activity and antimicrobial resistance highlights important safety considerations for future microbiome-based applications and reinforces the role of companion animals in AMR surveillance



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sciforum-187641: A National Evaluation of One Health, Zoonotic Threats, and Antimicrobial Stewardship among Professional college Students in India

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Introduction: The escalating global threats of zoonotic diseases and antimicrobial resistance (AMR) necessitate a robust "One Health" approach. This study aimed to evaluate public awareness, knowledge levels, and behavioural risks associated with the human-animal-environment interface across various states and Union Territories of India to inform future public health interventions.

Methods: A cross-sectional survey was conducted among professional college students using hybrid data collection approaches, comprising both a structured digital questionnaire and manual paper-based forms. The instrument was validated for content and face validity by a panel of experts. A total of 1122 responses from 24 states and 5 Union Territories were collected and analyzed using descriptive and inferential statistics.

Results

The study revealed high theoretical literacy: 72% were familiar with "One Health" and 84.3% identified zoonotic transmission dynamics. AMR awareness reached a near-ubiquitous 95.5%. However, this cognitive awareness was contradicted by significant behavioral risks, exposing a critical "knowledge–practice gap." While awareness of rabies (97.3%) and tuberculosis (95.7%) was near-universal, knowledge of emerging threats like scrub typhus was significantly lower (66.9%). Approximately 30.4% admitted to antibiotic self-administration, and 86.9% engaged with professional guidance only sporadically. Furthermore, socio-cultural practices—such as consuming raw milk (28.5%) and raw meat (1.9%) during religious observances—persisted despite widespread recognition of endemic zoonoses. Digital platforms and peer groups followed by medical and veterinary professionals were identified as primary health information catalysts.

Conclusions

Despite sophisticated conceptual awareness of One Health and AMR among India's educated youth, significant behavioral inertia remains a critical public health barrier. These findings confirm that theoretical knowledge does not inherently translate to risk mitigation. To bridge this "knowledge–practice gap," future strategies must pivot towards targeted, behavior-centric community engagement. Robust cross-sectoral collaboration between medical and veterinary professionals is essential to transform cognitive understanding into standardized safe practices and grassroots antimicrobial stewardship.



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sciforum-187745: A Systematic Review of the Genus *Bacillus* as a Sustainable One Health Strategy to Mitigate Heavy Metal Bioaccumulation in the Food Chain

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Environmental contamination by heavy metals like lead and cadmium poses critical risks to the animal – human – environment interface. In veterinary medicine, these toxins manifest in life threatening hazards, such as Plumbism (lead poisoning) and skeletal disorders in livestock, which subsequently threaten human health via the food chain. Traditional remediation is often unsustainable; thus this review systematically evaluates the bioremediation potential of *Bacillus* species as a green, proactive food-safety barrier. A systematic review was conducted following PRISMA 2020 guidelines. Searches were performed across PubMed, Scopus and Google Scholar for peer-reviewed studies published between 2018 and 2026. Inclusion criteria focused specifically on the genus *Bacillus*, heavy metal detoxification mechanisms (biosorption and biotransformation), and veterinary/agricultural application. Evidence from selected studies indicates that *Bacillus subtilis* and *Bacillus cereus* exhibit superior resistance, achieving significant metal removal efficiencies, with reports exceeding 90% in optimized conditions. Gene expression analysis identifies critical resistance operons, such as pbr for lead and cad for cadmium, as the primary drivers of detoxification. Furthermore, findings suggest that microbial intervention reduces environmental metallic stress, thereby mitigating the “co-selection” of antimicrobial resistance (AMR) genes in contaminated soil and water. Systematic review evidence identifies the genus *Bacillus* as a modern, sustainable solution to HM toxicity. Integrating these microbial strategies into veterinary environmental management provides a robust framework for decoupling chemical pollution from animal products, directly supporting the goals of the “One Health” moto.



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sciforum-186323: Antagonistic activity of *Lactobacillus helveticus* postbiotics against mastitis causing and dairy spoilage bacteria and their produced biofilms

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INTRODUCTION. *Lactobacillus helveticus* is a lactic acid bacterium widely used in the production of fermented dairy products, and several studies have demonstrated that its live cultures, exopolysaccharides, and cell-free supernatants exhibit inhibitory effects against pathogenic bacteria. However, little is known about the antibiofilm potential of *L. helveticus* postbiotics in dairy-associated environments. This study evaluated postbiotics derived from commercially available *L. helveticus* against biofilms formed by pathogenic and milk-spoilage microorganisms.

METHODS. Freeze-dried *L. helveticus* (LMG26307; THT031102) was precultured in MRS broth at 37°C. After 18 h, cultures were centrifuged, and biomass was reinoculated (5% w/v). Following incubation, cells were collected, washed, thermally inactivated, and ethanol-treated, yielding postbiotics consisting of inactivated cell biomass. Cell-free supernatant was obtained by centrifugation and sterile filtration (0.22 µm). Indicator strains (*Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Staphylococcus aureus*, *Enterococcus faecalis*, and *Bacillus subtilis*) were cultured and standardized to 0.5 McFarland. Preparations were diluted (1:10), mixed with bacterial suspensions (1:1 v/v), and incubated for 48 h at 37 °C in 96-well plates. Planktonic growth (OD₆₂₀) and biofilm biomass were measured.

RESULTS. Both preparations affected bacterial growth and biofilm formation. The supernatant inhibited planktonic growth in all tested species and reduced biofilm formation in *K. pneumoniae*, *P. mirabilis*, and *P. aeruginosa*. Postbiotics increased planktonic OD values due to cell-derived turbidity but reduced biofilm formation in *K. pneumoniae* and *P. aeruginosa*, although less effectively than supernatant. *S. aureus*, *B. subtilis*, *E. coli*, and *E. faecalis* strains did not form biofilms under tested conditions.

CONCLUSION. *L. helveticus* supernatant exhibited strong antimicrobial and antibiofilm activity, while postbiotics showed a more limited but still notable effect.

ACKNOWLEDGEMENTS. 1.1.1.9 Research application No 1.1.1.9/LZP/1/24/162 of the Activity "Post-doctoral Research" "Development of postbiotics' compositions including the evaluation of its bioactivity against pathogenic bacteria and their produced biofilms in the dairy industry"



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sciforum-194538: Antibacterial, antioxidant and hemolytic properties of *Prunus persica* leaf extracts against *Staphylococcus* isolates from dogs of Angola

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Canine skin infections are frequently associated with antimicrobial-resistant *Staphylococcus* species. The rise in antimicrobial resistance has driven the search for medicinal plants as a source of bioactive compounds. *Prunus persica* has traditionally been used in the treatment of skin diseases, but its activity against canine staphylococci has been little studied. The present study evaluated the antibacterial, antioxidant, and hemolytic properties of aqueous extracts of *Prunus persica* leaves against *Staphylococcus* isolates obtained from dogs in Angola.

An aqueous leaf extract was prepared by decoction. Its antioxidant activity was evaluated using DPPH, ABTS, and FRAP assays; hemolytic activity was assessed using canine erythrocytes; and antibacterial activity was determined using the spot-on-lawn method against 56 staphylococcal isolates. The stability of the extract was evaluated over 90 days at different temperatures (−20 °C, 4 °C, room temperature, 27 °C, and 37 °C). Statistical analysis was performed using SAS® 9.4, employing linear and mixed-effects logistic regression models.

The *P. persica* leaf extract exhibited high antioxidant activity. DPPH activity reached 104.47% at 20 min and 70.33% at 60 min. ABTS and FRAP activity was 0.42 mM Trolox equivalents and 1.15 mM Fe²⁺ equivalents, respectively. The extract exhibited low hemolytic activity (10.69 ± 6.54%). It exhibited strong inhibitory activity, inhibiting 100% of the 56 tested staphylococcal strains, with 100% of the strains being inhibited after 24, 48, and 72 h of incubation. Furthermore, the antibacterial activity remained stable during 90 days of storage and was not affected by storage temperature.

The aqueous extract of *P. persica* leaves exhibited antibacterial and antioxidant activity, low hemolytic ability, and temporal and thermal stability. These results highlight its potential for topical formulations against canine skin infections and support future studies on its application as a complementary One Health strategy to reduce antimicrobial use.



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sciforum-192769: Antimicrobial resistance in *Salmonella* Enteritidis and Typhimurium isolates from laying hens in Latvia

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Salmonella is an important foodborne pathogen that causes gastrointestinal manifestations, with poultry remaining an important source of the pathogen. Laying hens are frequently colonized by antimicrobial resistant (AMR) *Salmonella*, hence posing concerns of introduction of the pathogen into the food chain. The aim of the present study was to detect the distribution of *Salmonella* Enteritidis and Typhimurium serovars and their antimicrobial resistance in laying hens in Latvia. *Salmonella* isolates from feces of laying hens from poultry farms in Latvia during 2025, within the frame of official control and self-checks sampling, were used for the detection of antimicrobial resistance. AMR to the following antimicrobials were tested: ampicillin, azithromycin, amikacin, ceftazidime, cefotaxime, chloramphenicol, ciprofloxacin, colistin, gentamycin, meropenem, nalidixic acid, sulfamethoxazole, tetracycline, tigecycline and trimethoprim with the Minimum Inhibitory Concentration (MIC) method. Results were evaluated according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST) requirements. Genetic determinants of AMR resistance were detected with Whole Genome Sequencing (WGS). *Salmonella* spp. were identified in 45 out of 693 (6%) positive samples. Among *Salmonella*-positive samples, 26 (58%) were the European Union target serovars Enteritidis and Typhimurium. All *S. Typhimurium* isolates (4/4, 100%) but only 7 (7/22, 32%) of *S. Enteritidis* were sensitive to all antimicrobials tested. *S. Enteritidis* exhibited resistance only to nalidixic acid and ciprofloxacin (15/22, 68%), and one isolate to colistin (1/22, 5%). No multidrug-resistant isolates were identified. Genetic determinants associated with resistance to fluoroquinolones were identified in isolates resistant to nalidixic acid and ciprofloxacin. The high level of dissemination of fluoroquinolone-resistant *S. Enteritidis* isolates among laying hens in Latvia represents an important public health challenge.



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sciforum-185924: Antimicrobial Stewardship and Food Safety: Effects of Dietary Inclusion of Piper guineense on Organ Safety in Broiler Chickens Reared under Different Housing Systems

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The global restriction on antibiotic growth promoters has intensified the search for phytogetic alternatives capable of supporting sustainable poultry production without compromising animal health and food safety. Despite increasing interest in botanical feed additives, information on their organ safety under different production environments remains limited. This study evaluated the effects of dietary inclusion of a Piper guineense leaf–seed blend on liver and kidney integrity in broiler chickens reared under deep litter and battery cage housing systems. A total of 288 one-day-old Cobb 500 broiler chicks were assigned to a 2 × 4 factorial arrangement consisting of two housing systems (deep litter and battery cage) and four dietary inclusion levels (0, 0.5, 1.0, and 1.5%) of a Piper guineense leaf–seed blend (2:1 ratio). Each treatment was replicated four times with nine birds per replicate. Following a six-week feeding trial, liver and kidney samples were collected for histopathological examination, while renal glomerular transversal diameter was assessed using histomorphometry. Renal tissues remained normal up to 0.5% inclusion in both housing systems. However, tubular degeneration was observed at 1.0% and 1.5% inclusion levels in battery cage birds, whereas degeneration occurred only at 1.5% in deep litter birds, suggesting greater renal tolerance under deep litter management. Hepatic alterations increased with dietary inclusion level in battery cage birds, with severe hepatocellular degeneration, pyknosis, and necrosis observed at 1.5% inclusion. In contrast, birds reared under deep litter exhibited mild-to-moderate hepatic alterations across the supplemented groups. Glomerular diameter was lowest in battery cage birds fed 1.5% Piper guineense. These findings indicate that the organ safety threshold of dietary Piper guineense is influenced by housing system and that liver and kidney responses differ between production environments. Consideration of housing conditions may therefore be important when evaluating phytogetic alternatives for sustainable poultry production.



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sciforum-187296: Assessment of Microbiological Quality of Artisanal Raw Milk Cheeses and Their Manufacturing Process in Eastern Paraná

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Artisanal cheeses, beyond their regional cultural value, constitute for many Brazilian micro-producers an important avenue of revenue and valorization of their milk production. The employment of raw milk in the manufacturing processes of these products has grown in popularity since the introduction of proper regulations concerning the internal commerce raw milk cheeses in Brazil; conversely, the use of a non-pasteurized produce as the basis of a product may implicate in higher rates of failure in the microbiological control and quality of the final product. Concurrently, raw milk derivatives have been linked in epidemiological and historical series studies to outbreaks of foodborne diseases of global relevance. The present study aimed to investigate the sanitary conditions of manufacturing of six varieties of raw milk cheeses from three artisanal producers located in the state of Paraná, Brazil. A total of six cheese samples and three raw milk and manufacturing water samples each were processed. Contamination, when present on the cheeses, did not surpass legal limits imposed by Brazilian regulations; all samples presented a rich microbiota of lactic acid bacteria with a median of $4,34 \times 10^6$ CFU/g, desirable in dairy products and necessary for the conference of different organoleptic properties that characterize different cheese varieties. Populations of enterobacteria and coagulase-positive staphylococci in milk samples demonstrated a reduction from initial ranges of $1,75 \times 10^3$ and $4,6 \times 10^3$ CFU/mL respectively to a median of $2,6 \times 10^1$ CFU/g, except for one sample with $6,5 \times 10^6$ CFU/g, and presence of staphylococci count of $1,6 \times 10^2$ CFU/g on an isolated sample. Coliform contamination was present in only one water sample. In conclusion, the three cheesemakers contemplated in this study demonstrated the accomplishment of a production flow that ensured the offering of safe products to the final consumer.



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sciforum-187771: Behavioural Patterns of Antibiotic Use in Bovine Mastitis: A Cluster-Based Analysis Among Veterinarians in Kerala, India

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Abstract

Introduction: Bovine mastitis is a primary driver of antimicrobial use and resistance (AMR) in dairy production. Conventional knowledge, attitude, and practice (KAP) surveys often overlook the inherent heterogeneity in clinical decision-making. This study employed a cluster-based analytical framework to identify distinct behavioral patterns in antibiotic usage for bovine mastitis among veterinarians in Kerala.

Methods: A cross-sectional KAP survey was conducted among 211 bovine veterinary practitioners. Behavioral variables concerning diagnosis, antimicrobial selection, and treatment protocols were analyzed using Gower's dissimilarity matrix for mixed data types. Ward's hierarchical clustering was applied to categorize practitioners, excluding demographic factors. Cluster stability was confirmed via dendrogram inspection and validation metrics. Clusters were visualized through principal coordinates analysis (PCoA), with key drivers identified by average variable contributions and validated using Kruskal-Wallis and chi-square tests ($p < 0.05$).

Results: Distinct behavioral clusters emerged, primarily differentiated by diagnostic reliance, antimicrobial selection, and stewardship adherence. Clinical practice and knowledge-related variables contributed more significantly to cluster separation than attitudinal measures. One cluster exhibited evidence-based prescribing characterized by high diagnostic integration and protocol adherence, whereas other clusters relied predominantly on empirical therapy and broad-spectrum antibiotics.

Conclusions: Cluster-based analysis reveals substantial heterogeneity in mastitis treatment practices that traditional scoring may obscure. These findings emphasize the need for behavior-informed, targeted antimicrobial stewardship strategies. Tailoring veterinary education and policy interventions to specific practitioner profiles can significantly enhance AMR mitigation efforts in dairy production systems.



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sciforum-180565: Beyond common serotypes: Genomic characterization of diverse avian pathogenic *Escherichia coli* associated with broiler colibacillosis in Pakistan

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Colibacillosis remains a major cause of mortality and economic loss in Pakistan's broiler industry. Avian pathogenic *Escherichia coli* (APEC), genetically related to extraintestinal pathogenic *E. coli* (ExPEC), exhibits substantial heterogeneity in virulence and antimicrobial resistance. However, disease investigations frequently focus on a limited number of classical serotypes, potentially underestimating the contribution of diverse and non-typeable strains.

This study aimed to comprehensively characterize *E. coli* isolates recovered from broilers with clinical colibacillosis, irrespective of serotype, to evaluate their genomic diversity, virulence profiles, and antimicrobial resistance patterns. A total of 47 isolates were recovered from sterile organs of clinically diseased broilers. PCR-based serotyping identified only four isolates as O21, highlighting the limitation of targeted serotyping approaches. Therefore, 15 representative isolates were subjected to whole-genome sequencing for in-depth genomic analysis.

Genomic data revealed marked serotypic diversity, including O76, O11, O132, O24, O53, O71, O75, O109, and two non-typeable isolates. Multilocus sequence typing identified nine sequence types, with ST533 predominating, followed by ST457, ST117, ST9434, ST572, ST4481, ST295, ST1196, and ST2329. Phylogenetic analysis assigned isolates primarily to phylogroups A (47%), B1 (30%), and D (23%). Screening of 18 virulence-associated genes demonstrated high prevalence of *ompA* (98%), *fimC* (96%), *ibeB* (87%), *ibeA* (68%), *iroN* (62%), *iss* (62%), and *iucD* (53%), supporting their pathogenic potential.

All isolates exhibited phenotypic multidrug resistance determined by Kirby Bauer Disk Diffusion method, with universal resistance to erythromycin and ampicillin-sulbactam, and high resistance to tetracyclines (98%) and fluoroquinolones (71–79%). Lower resistance rates were observed for colistin (29%), ceftazidime (21%), and imipenem (5%).

These findings demonstrate that broiler colibacillosis in Pakistan is associated with genetically diverse APEC lineages beyond traditionally emphasized serotypes, accompanied by a substantial multidrug resistance burden. Comprehensive genomic surveillance that moves beyond classical serotyping is essential for accurate epidemiological understanding and development of effective control strategies.



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sciforum-188514: Bio-enhancing Effect of Punganur Cow Urine Distillate on Enrofloxacin in Broiler Chickens

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Introduction:

The indiscriminate use of antimicrobials in poultry production has contributed significantly to the emergence of antimicrobial resistance (AMR), creating an urgent need for alternative strategies that improve antibiotic efficacy while reducing therapeutic dosage. Natural bio-enhancers have gained attention for their ability to enhance drug absorption and pharmacological activity. This study evaluated the bio-enhancing potential of Punganur Cow Urine Distillate (PCUD) on the pharmacokinetics and antibacterial efficacy of enrofloxacin in broiler chickens.

Methods:

Thirty broiler chickens were randomly divided into three experimental groups. Group 1 received enrofloxacin alone (10 mg/kg body weight), Group 2 received enrofloxacin (10 mg/kg BW) co-administered with PCUD (1 ml/kg BW), and Group 3 was pre-treated with PCUD for 10 days prior to enrofloxacin administration. Plasma concentrations of enrofloxacin were quantified using high-performance liquid chromatography (HPLC), and pharmacokinetic parameters were calculated. Data were analyzed using one-way analysis of variance (ANOVA), and differences were considered significant at $p < 0.05$. Pharmacokinetic/pharmacodynamic (PK/PD) indices were further evaluated against *Escherichia coli* and *Staphylococcus aureus*.

Results:

PCUD supplementation significantly enhanced the bioavailability of enrofloxacin compared to the control group, with increases of 129% following co-administration and 116% following pre-treatment. Group 2 demonstrated the highest peak plasma concentration (C_{max}) and area under the concentration-time curve (AUC), indicating improved drug absorption and systemic exposure. In Group 3, PCUD prolonged the elimination half-life ($t_{1/2}$) and mean residence time (MRT), suggesting delayed drug clearance and sustained plasma concentrations. PK/PD integration revealed enhanced antibacterial efficacy of enrofloxacin against *E. coli* and *S. aureus* in PCUD-treated groups.

Conclusions:

The study demonstrates that PCUD acts as an effective natural bio-enhancer by improving the pharmacokinetic profile and antibacterial activity of enrofloxacin in broiler chickens. Enhanced bioavailability and prolonged systemic exposure may facilitate dose optimization in poultry production systems. Further studies are required to characterize the active constituents of PCUD and elucidate its mechanism of bio-enhancing activity.



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sciforum-187460: Calcium profile in dairy cows: Implications for animal health and milk quality according to lactation stage, breed, and parity

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Introduction

The transition period in dairy cows is characterized by significant metabolic changes, particularly in calcium metabolism. Hypocalcemia is a common disorder that can affect animal health, milk production, and reproductive performance. This study aimed to evaluate the evolution of blood calcium levels in dairy cows throughout lactation and to analyze the influence of intrinsic factors such as breed, age, and parity.

Methods

The study was conducted on 20 dairy cows belonging to different breeds (Holstein Black Pied, Fleckvieh, and Montbéliarde) distributed across two farms located in northern Algeria. The animals were monitored at different stages of lactation (early, mid, and late). Blood samples were collected and analyzed to determine calcium concentration using a spectrophotometric method.

Results

The results showed significant variations in calcium levels according to the stage of lactation. Mean concentrations were 77.67 mg/L in early lactation, 102.61 mg/L in mid-lactation, and 87.86 mg/L in late lactation. A marked decrease was observed in early lactation, related to the high calcium demand for colostrum production.

Parity also influenced calcium levels, with multiparous cows showing higher concentrations (93.27 mg/L) than primiparous cows (83.95 mg/L). Differences between breeds were observed, with higher values in Holstein Black Pied cows (98.56 mg/L) compared to Montbéliarde (78.97 mg/L) and Fleckvieh (53.77 mg/L).

Conclusion

Calcium levels vary significantly depending on lactation stage, breed, and parity. Early lactation represents a critical phase with a higher risk of hypocalcemia. These findings highlight the importance of metabolic monitoring and appropriate nutritional management to prevent metabolic disorders and improve the zootechnical performance of dairy farms.



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sciforum-179275: Cattle production systems characteristics and their influence on antimicrobial use, alternatives, and resistance risk in Nigeria

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Background: Nigerian cattle production ranks 6th in Africa and 16th globally, constituting an important livelihood for many of its population. However, several health challenges affect the productivity of cattle herds, influencing antimicrobial use (AMU) and antimicrobial resistance (AMR). In this study, we attempt to characterise the cattle production system and its influence on health management practices. A mixed-methods approach, comprising semi-structured questionnaires (n = 736) and stakeholder focus group discussions, was employed.

Results: The majority of cattle production (78%) is extensive, with a median of 50 cattle per herd. Diseases of major burden are mastitis, gastrointestinal and respiratory diseases. Animal health was predominantly self-managed by farmers rather than using public/private veterinary services. Less than 5% of farmers regularly vaccinate their herds, partly due to unavailability and perceptions on effectiveness. Antibiotics are used indiscriminately and without prescription by most farmers. While some farmers use herbs, many stated that factors of low awareness and difficulty limited their wider use. Elderly Fulani pastoralists familiar with ethnoveterinary remedies were regarded as secretive, as they only shared this knowledge within their families. Farmers have poor knowledge and attitudes regarding the impact of AMU in cattle and the risk of AMR. Farmers with a secondary level of education were more likely to have better practices than farmers with no formal education (OR: 1.97, 95% CI: 1.08–3.63, p = 0.027).

Conclusions: Future research should focus on identifying culturally sensitive ways of preserving and sharing the ethnoveterinary knowledge of Fulani pastoralists. The efficacy of available herbs for veterinary diseases of concern can also be assessed. Access to governmental veterinary services, and agricultural extension agents should be improved to increase uptake of vaccines and professional care. Awareness about proper AMU and AMR risks should be raised, and antibiotic sales by unlicensed drugstores strictly regulated.



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sciforum-193187: Chemotherapy Waste Handling Practices among Veterinary Oncology Personnel in Tehran, Iran: A Cross-Sectional Knowledge, Attitude, and Practice Study with One Health Implications

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Introduction:

Cytotoxic drugs from veterinary chemotherapy threaten human and environmental health when discarded improperly. Personnel behavior remains understudied in Iran. This study evaluated knowledge, attitudes, and practices (KAP) of veterinary oncology staff in Tehran regarding safe chemotherapy waste disposal.

Methods:

A cross-sectional survey was administered between May and June 2026 to 187 veterinary professionals (veterinarians and technicians) working in oncology and referral services across Tehran. A 24-item questionnaire was developed, validated through expert review, and pilot-tested on 20 eligible staff (Cronbach's alpha = 0.84). The instrument assessed three domains: hazard knowledge (eight items), disposal attitudes (six items, five-point Likert), and reported practices (10 items). Good knowledge and good practice were defined as scores of 75 percent or higher. Positive attitude was defined as a mean Likert score of 4.0 or above. Statistical analysis included descriptive statistics, chi-square tests, and Pearson correlation using SPSS (alpha = 0.05). Ethical approval was obtained (IR.ADONIS.REC.1405.008), and all participants provided informed consent.

Results:

Of 187 respondents, 64 percent were veterinarians and 36 percent were technicians. Mean age was 37.1 years. While 70 percent demonstrated good knowledge of cytotoxic hazards and 78 percent held positive attitudes toward safe disposal, only 41 percent reported consistently good practices. A majority (55 percent) acknowledged discarding chemotherapy-contaminated gloves, IV lines, or syringes into ordinary waste. More than half (53 percent) had never received formal hazardous waste training. Prior training was associated with significantly better practices (59 percent versus 33 percent, $p = 0.006$). Knowledge scores correlated positively with practice scores ($r = 0.48$, $p = 0.003$).

Conclusions:

A substantial knowledge-practice gap exists in chemotherapy waste management among Tehran veterinary oncology personnel. Findings support urgent needs for structured training, institutional protocols, and regulatory oversight under One Health



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sciforum-190927: Comparative Analysis of Antimicrobial Resistance in *Escherichia coli* Isolated from Household and Ornamental Pigeons in Isfahan, Iran: A One Health Perspective

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Introduction: Antimicrobial resistance (AMR) is a major global health threat. Household pigeons, due to their close contact with human habitats and waste, can act as reservoirs for resistant *E. coli* strains, while ornamental pigeons are kept as pets in controlled environments. No study in Iran has directly compared AMR patterns between these two pigeon populations. This study aimed to compare the AMR profiles of *E. coli* isolated from household and ornamental pigeons in Isfahan, Iran.

Methods: In this cross-sectional comparative study, 150 fresh fecal samples were collected (80 from household pigeons in urban areas, 70 from ornamental pigeons in breeding centers) from October 2025 to February 2026. *E. coli* was isolated using MacConkey and EMB agar and confirmed by IMViC tests. Antimicrobial susceptibility was tested using the Kirby-Bauer disk diffusion method for 12 antibiotics according to CLSI M100 2024 guidelines. MDR was defined as resistance to ≥ 3 antibiotic classes. Data were analyzed using Fisher's exact test ($p < 0.05$).

Results: *E. coli* was isolated from 68 of 80 household pigeons (85%) and 12 of 70 ornamental pigeons (17.1%) ($p < 0.001$). Household isolates showed significantly higher resistance to ampicillin (73.5% vs. 25%, $p = 0.002$), tetracycline (86.8% vs. 33.3%, $p < 0.001$), and trimethoprim-sulfamethoxazole (82.4% vs. 16.7%, $p < 0.001$). Notably, all isolates were completely susceptible to ciprofloxacin. MDR prevalence was significantly higher in household pigeons (47.1%) compared to ornamental pigeons (8.3%) ($p = 0.014$; OR = 9.8).

Conclusions: Household pigeons harbor significantly higher rates of *E. coli* and MDR strains compared to ornamental pigeons. This highlights the potential role of urban pigeons as overlooked reservoirs of AMR bacteria within the One Health framework. Enhanced surveillance of urban wildlife for AMR is urgently needed.



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sciforum-192626: Comparative Assessment of *Salmonella* and *Vibrio parahaemolyticus* Contamination in Shrimps from Traditional and Modern Marketplaces in Tehran, Iran

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Shrimp is a major source of dietary protein in many countries, including Iran. However, contamination with pathogenic bacteria remains a significant public health concern. *Salmonella* and *Vibrio parahaemolyticus* represent important zoonotic bacteria linked to seafood, contributing to foodborne infections and posing considerable public health concerns. This study was conducted to compare the contamination of shrimp with *Salmonella* and *Vibrio parahaemolyticus* between modern and traditional markets in Tehran, Iran. A total of 320 Cotton Swabs were collected from 160 fresh shrimp samples and transported to the laboratory using appropriate transport media to maintain sample integrity during transfer. Samples were classified as either farmed or wild-caught. Microbiological cultures and biochemical tests were performed to assess bacterial contamination. All analyses followed ISO 6579-1:2017 and ISO 21872-1:2017 standards. Data analysis using SPSS software showed that four samples (2.5%) were contaminated with *Vibrio parahaemolyticus*, and eight samples (5%) tested positive for *Salmonella*. *Vibrio parahaemolyticus* was detected in farmed shrimp, whereas *Salmonella* was found in wild-caught shrimp. All contaminated samples were obtained from a traditional market. These results underscore the importance of continuous monitoring and enhanced hygiene practices in seafood processing and distribution, particularly in traditional marketplaces, to ensure food safety. Consequently, policy measures should be directed toward modernizing traditional markets.



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sciforum-186677: Comparative Phytochemical Profiling and Therapeutic Efficacy of *Syzygium aromaticum* and *Cinnamomum cassia* Extracts against Colistin-Resistant *Escherichia coli* of Poultry Origin

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The worldwide spread of antimicrobial resistance represents a serious challenge to modern clinical medicine, with the emergence of colistin resistance in Enterobacteriaceae serving as a critical tipping point in the efficacy of the "last-resort" antibiotic arsenal. This study presents a comprehensive evaluation of the antimicrobial and antioxidant potential of aqueous extracts derived both from Clove (*Syzygium aromaticum*) and Cinnamon (*Cinnamomum cassia*) against *Escherichia coli* isolates (n=200) recovered from poultry fecal samples in the Jhang region of Pakistan. Phenotypic screening confirmed a 29% prevalence of colistin resistance, a finding that correlates with the intensive selective pressures present in regional wet markets ($X^2=35.28$, $p<0.001$). Through the integration of Liquid Chromatography-Mass Spectrometry (LC-MS) and Fourier Transform Infrared spectroscopy (FTIR), this research identifies eugenol and cinnamaldehyde as the primary bioactive drivers of inhibitory activity. Both extracts demonstrated concentration dependent antimicrobial and antioxidant activities. While *S. aromaticum* exhibited superior antibacterial potency (inhibition zones up to 23 ± 0.6 mm, MIC of 6.25%w/v and 72.04% DPPH scavenging) compared to *C. cassia* (inhibition zones up to 14 ± 0.6 mm, MIC of 12.5% w/v and 36.81 DPPH scavenging). These findings suggest potential pathways through which plant-derived phenyl-propanoids disrupt bacterial cell membranes and neutralize oxidative stress, providing a scientific basis for their deployment as sustainable alternatives to synthetic antibiotics in a One Health framework.



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sciforum-176774: Cow Nutrition as a Preventive Component of Antimicrobial Resistance Control and Food Safety in Cattle Production: A One Health Evidence Synthesis.

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Antimicrobial resistance (AMR) is an One Health challenge for human health, animal health, environmental health and the safety of foods of animal origin. Antimicrobials are used in cattle production for infectious and production diseases such as mastitis, diarrhoea, respiratory disease, lameness, and metabolic disorders. Antimicrobial stewardship programs are targeted at rational drug use, veterinary oversight and withdrawal periods, but nutritional management is an crucial preventive factor that can affect disease susceptibility and antimicrobial treatment pressure.

This structured narrative evidence synthesis examine the role of cattle nutrition in AMR control and food safety from a One Health perspective. Peer-reviewed literature and international One Health guidance were reviewed using targeted search terms related to cattle nutrition, rumen health, gut microbiota, immune function, antimicrobial use, antimicrobial resistance, milk safety, meat safety, and foodborne transmission. The evidence was organized into four pathways: effects of nutrition on immune competence, rumen and intestinal microbial stability, metabolic health and disease occurrence, and antimicrobial-related food safety risks.

In the reviewed literature, the positive effects of balanced feeding and forage quality, of preventing negative energy balance and of appropriate supplementation with vitamins and minerals on immune system, rumen stability, and metabolic resilience are confirmed. Optimizing nutrition can help prevent and lessen the impact of diseases often associated with antimicrobial treatment, helping to reduce antimicrobial selection pressure in the farm environment. Lowering the pressure of antimicrobial use could also contribute positively to food safety by reducing the chances of having antimicrobials in food, reducing the spread of resistance in the farm environment and in the wider food chain through manure, milk and meat. But there is limited direct intervention research that relates nutrition interventions to measurable decreases in AMR.

Cow nutrition is therefore a practical preventive pillar of integrated AMR control and One Health food safety strategies in cattle production.



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sciforum-193702: Crisaborole resensitizes KPC-producing Gram-negative bacteria to carbapenems

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The global spread of carbapenem-resistant Enterobacteriaceae (CRE), primarily driven by the dissemination of carbapenemases, poses an existential threat to public health. Among these enzymes, *Klebsiella pneumoniae* carbapenemase (KPC) represents one of the most prevalent and clinically significant resistance determinants worldwide. In this study, we developed a PBP-based ELISA-like screening assay that exploits the differential recognition of intact meropenem and its KPC-mediated hydrolysis products by penicillin-binding protein. Using this assay, more than 300 FDA-approved drugs were screened, and crisaborole, an FDA-approved benzoxaborole compound, was identified as a potential KPC inhibitor. Checkerboard assays demonstrated synergistic activity between crisaborole and MEM against KPC-producing clinical isolates, with fractional inhibitory concentration index (FICI) values ranging from 0.19 to 0.50. Time-kill studies confirmed that the combination significantly reduced bacterial counts by $>4 \log_{10}$ CFU/mL compared with MEM monotherapy. Notably, the synergistic effect was strictly dependent on the presence of the *bla*KPC gene; no activity was observed against strains harboring *bla*NDM, *bla*IMP, or *bla*OXA genes. Combined disc tests further validated that crisaborole directly inhibits KPC-mediated MEM hydrolysis. Molecular docking revealed that crisaborole binds to the active pocket of KPC through a covalent interaction with Thr237 and forms hydrogen bonds with Thr235, Ser130, and Asn132, with a binding free energy of -44.45 kcal/mol. These findings establish crisaborole as a promising repurposed antibiotic adjuvant for overcoming KPC-mediated carbapenem resistance and provide a rational foundation for further *in vivo* validation and clinical development.



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sciforum-177773: Environmental Variation in the Physicochemical and Microbiological Profile of *Melipona mondury* Honey in Eastern Paraná

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Brazil hosts more than 300 stingless bee (SB) species, and its continental-scale environmental diversity results in highly heterogeneous SB honey. In the absence of federal or international regulations, scientific evidence is essential to support food safety and enable formal commercialization. This study evaluated the physicochemical and microbiological profile of nine *Melipona mondury* honey samples collected in two environments in eastern Paraná, Brazil: rural (n=4) and urban (n=5). Analyses included moisture, soluble solids, water activity (AW), free acidity, pH, color, coliforms, *Salmonella* spp., lactic acid bacteria (LAB), mesophilic microorganisms (MM), yeasts, and molds. Statistical analyses were performed in R using the Shapiro-Wilk and Mann-Whitney tests. One rural sample showed 9.2 MPN/mL of total coliforms, while all samples had ≤ 3 MPN/mL of thermotolerant coliforms and were negative for *Salmonella* spp. and molds. Significant differences were observed across parameters: soluble solids were higher in urban samples, whereas moisture, AW, and yeast counts were higher in rural samples. One rural sample presented moisture above 50% and AW of 0.78, associated with large honey pots (± 50 mL), a natural characteristic that may favor fermentation. The low pH observed in both environments may limit the survival of pathogenic microorganisms. Four samples (three rural and one urban) exceeded the yeast limits established by Paraná state regulations for SB honey. The higher yeast counts observed in rural samples may be associated with their elevated moisture and water activity values. Overall, these findings indicate that this honey quality depends on interactions between ecological conditions and colony-specific characteristics, highlighting the need for regulatory frameworks that avoid uniform criteria and better reflect the diversity of environments. However, the limited sample size restricts broader generalizations; therefore, further studies with a larger number of samples are necessary to improve the understanding of the specific characteristics of this species.



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sciforum-188070: Evaluation of Antibacterial and Anti-biofilm Properties of Niosome-Loaded *Silybum marianum* Extract Against Clinical *Pseudomonas aeruginosa* Strains

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Abstract

Introduction: The rising prevalence of multidrug-resistant *Pseudomonas aeruginosa* and its ability to form robust biofilms has critically narrowed therapeutic options in healthcare settings. Biofilm-associated infections resist conventional antibiotics due to the protective exopolysaccharide matrix and metabolic dormancy of embedded cells. Plant-derived bioactive compounds have emerged as promising alternatives; however, poor aqueous solubility, limited stability, and low bioavailability hinder their clinical use. Niosomes—non-ionic surfactant-based vesicles—enhance pharmacokinetic profiles and enable targeted delivery of phytochemicals. Building on 2023–2025 evidence highlighting the antibiofilm potential of flavonoid-rich plant extracts, this study evaluated niosomal encapsulation of *Silybum marianum* extract against clinical *P. aeruginosa* isolates.

Method: *S. marianum* extract was encapsulated using the thin-film hydration technique at an optimal lipid-to-drug ratio of 20. Physicochemical parameters—particle size, polydispersity index (PDI), and encapsulation efficiency (EE%)—were monitored at 4 ± 1 °C and 25 ± 1 °C to assess stability. Antibacterial efficacy was determined by minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) assays; anti-biofilm activity against preformed biofilms was quantified by crystal violet staining.

Results: The niosomal formulation showed a biphasic, controlled release profile. Storage at 4 ± 1 °C preserved vesicle integrity with minimal changes in particle size, PDI, and EE% compared to 25 ± 1 °C. The encapsulated extract achieved a 2- to 16-fold reduction in MIC and significantly lower MBC values relative to the free extract. The niosomal formulation also eradicated preformed biofilms more effectively than the non-encapsulated extract.

Conclusion: Niosomal encapsulation substantially enhances the antibacterial and anti-biofilm potency of *S. marianum* extract against clinical *P. aeruginosa* strains, presenting a viable nanomedicine-based strategy to revitalize the therapeutic efficacy of herbal antimicrobials against biofilm-forming pathogens.

Keywords: *P. aeruginosa*, *S. marianum*, Niosome, Biofilm

Competing interests

The authors declare no conflict of interest.



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sciforum-187454: Feed protein stability and bacterial disease in commercial broilers – an observational study in Multan, Pakistan

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Introduction: In Pakistan, bacterial infections such as *E. coli* and *Salmonella* kill broilers and cost farmers money. Antibiotics are used to manage these diseases by most farmers, yet there is growing concern about antibiotic resistance. Few studies from real commercial farms in Pakistan examine whether feed quality influences disease. This research examined whether there is a correlation between feed quality and bacterial disease in a single commercial broiler flock.

Methods: I did this work during a 12-week internship from June to August 2023 at the Poultry Research Institute in Multan. We followed one flock of 5,000 broilers. We took swabs from 5–7 sick birds twice per week. We cultured bacteria on blood agar and MacConkey agar. We identified *E. coli* and *Salmonella* by Gram staining and simple biochemical tests. We collected feed samples from three points along the feed line once per week and tested for protein, moisture, and fiber. Pearson correlation and linear regression were run using SPSS. Significance was set at $p = 0.05$.

Results: Out of 78 samples that grew bacteria, 43% were *E. coli* and 15% *Salmonella*. We found a weak negative correlation between feed protein stability and bacterial disease ($r = -0.15$, $p = 0.04$). The R^2 value was 0.09, meaning protein stability explained only 9% of the variation in disease cases.

Conclusions: Feed protein stability has a small but real correlation with bacterial disease in broilers. Farmers could test feed every two weeks as an early warning. However, this should not replace antibiotics. Limitations include one farm, observational design, and 91% unexplained variation. More studies on more farms are needed.

Conflict of Interest: The authors declare no conflicts of interest.



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sciforum-194181: Florfenicol Pharmacokinetics and Pharmacodynamics in Food-Producing Animals: A Systematic Review

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Introduction

Florfenicol is a broad-spectrum antimicrobial used in food-producing animals for treating bacterial infections. Optimizing therapy requires integrating pharmacokinetic (PK) exposure, pharmacodynamic (PD) targets, and pathogen susceptibility data. This systematic review summarizes florfenicol PK, PD, and MIC profiles across major food-producing species.

Methods

Following PRISMA 2020, PubMed, Scopus, and ScienceDirect were searched up to May 2026 using terms for "florfenicol", "PK/PD", and "food-producing animals" (cattle, swine, poultry, fish, sheep, goats). A two-step strategy was applied. From 1,206 records, after duplicate removal, 138 original in vivo studies reporting PK parameters, PK/PD indices, or MIC values were included. **Study quality was assessed using established tools but not detailed here due to space constraints.**

Results

Marked interspecies PK variability was observed. In cattle, pulmonary epithelial lining fluid exceeded plasma by 230%, with prolonged synovial persistence (half-life 64.9 h) and AUC values of 101.5–194.5 µg·h/mL. AUC/MIC targets against *Mannheimia haemolytica* and *Pasteurella multocida* ranged 7.6–47 h. In swine, bioavailability was 94–123%, C_{max} 4.0–8.15 µg/mL, and AUC/MIC targets for *Streptococcus suis*, *Actinobacillus pleuropneumoniae*, and *P. multocida* were 22.2–141.7 h. Sheep and goats showed similar exposure (AUC 62.5–74.1 µg·h/mL), with lower goat bioavailability (60.9%). In poultry, bioavailability was 71–89%, C_{max} 30.5 µg/mL, and lung-to-plasma ratios 1.2–2.0. In aquatic species, temperature-dependent disposition was key. Elimination half-lives were 8.1–43 h, bioavailability 57–91%. MIC values for susceptible pathogens were 0.25–1 µg/mL, reaching 128 µg/mL for *Streptococcus agalactiae*. Across all species, AUC/MIC was the PK/PD index most strongly associated with efficacy.

Conclusion

Florfenicol exhibits species-dependent PK but favorable PK/PD profiles across food-producing animals. The AUC/MIC ratio is the strongest efficacy predictor and should guide dosage optimization. Harmonized PK/PD breakpoints and species-specific dosing are needed for antimicrobial stewardship in livestock and aquaculture.

The authors declare no conflicts of interest.



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sciforum-194574: Food-Associated Multidrug-Resistant Pathogens in Oncology Patients: An AI-Assisted Literature Mining Study Through a One Health Lens

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Background: AMR in food-associated bacterial pathogens threatens immunocompromised patients through food chain transmission. Conventional reviews lack scalability; AI-assisted pipelines offer a reproducible alternative for systematic AMR surveillance synthesis.

Objectives: To characterise resistance prevalence among food-associated pathogens in oncology-related infections using a multi-agent AI literature mining pipeline.

Methods: A three-stage agentic AI pipeline was developed. A GPT-based conversational agent received natural language queries and autonomously generated optimised PubMed search strings using validated MeSH terms. A retrieval agent then fetched abstracts via the NCBI Entrez API in batch mode. A structured extraction agent (Llama-3, Groq API) processed each abstract to extract pathogen identity, resistance phenotypes, resistance genes, cancer type, infection site, resistance rates, and study design. Data were aggregated for frequency analysis and pathogen-cancer co-occurrence mapping across 2015–2025.

Results: One thousand peer-reviewed articles were analysed. All identified pathogens are recognised foodborne or food-associated organisms. *E. coli* showed resistance to penicillins (81.84%), cotrimoxazole (65.79%), and monobactams (61.61%). *K. pneumoniae* exhibited near-total penicillin resistance (98.99%). *A. baumannii* demonstrated an XDR profile: carbapenems (82.58%), third-generation cephalosporins (84.10%), fluoroquinolones (80.37%), and cotrimoxazole (75.77%). *Enterobacter* spp. and *E. faecium* showed penicillin resistance of 91.77% and 90.64%, respectively. *P. aeruginosa* resistance to third-generation cephalosporins reached 49.41%. *S. aureus* exhibited macrolide resistance (55.63%) and MRSA prevalence (45.29%), concordant with livestock-associated MRSA documented in the food chain.

Conclusions: Resistance profiles identified in oncology patients mirror patterns reported in veterinary and agri-food surveillance, supporting a food-to-patient transmission hypothesis. This multi-agent AI pipeline provides a scalable, reproducible tool for cross-sector AMR intelligence aligned with One Health priorities.



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sciforum-188382: Genomic Characterization of Multidrug-Resistance *mecC*-MRSA in Portuguese Rabbit Production

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Staphylococcus aureus is a major zoonotic pathogen increasingly associated with livestock reservoirs. Rabbit production remains underexplored in antimicrobial resistance surveillance despite its in Southern Europe. This study characterized whole-genome sequencing (WGS) based characterization of *S. aureus* isolates from rabbits intended for consumption in Portugal.

Forty-six *S. aureus* isolates were subjected to WGS. Genomic data were analyzed using PlasmidFinder, SCCmecFinder, AMRFinder, CARD, and VirulenceFinder databases. Antimicrobial susceptibility testing (AST) was performed on 44 isolates by disk diffusion.

Multilocus sequence typing identified ST28855 (n=31) and ST4774 (n=10) as dominant lineages, alongside ST15 (n=3), ST398 (n=1), and one novel ST. Twenty-seven isolates were classified as MRSA, carrying *mecA* (n=16) with SCCmec type III(3A), or *mecC* (n=11) with SCCmec type XI (8E). AST revealed widespread resistance to penicillin and ciprofloxacin across MRSA and MSSA, with erythromycin, clindamycin, and tetracycline resistance also observed. Resistance genes included *blaZ*, *tet* (38), *erm*(C), *vga*(A), *fosB*, *dfxK*, and *str*. Efflux pump genes *norC*, *sdrM*, *norA*, and *sepA* were identified in 45 isolates. Biocide resistance genes *ImrS* and *qacC* were widely distributed, and arsenic resistance genes (*arsB*, *arsC*) were detected in 10 isolates. The transcriptional regulators *arR*, *arS*, *kdpD*, *mepR*, and *mgrA* were ubiquitous. Virulence profiling revealed near-universal presence of *hlgABC*, *lukE*, *aur*, *icaC*, *spaB*, and *hld*, with *lukD* and *can* detected in 70% and 59% of isolates, respectively. Plasmid analysis identified rep7c_1_rep(MSSA476) as the predominant replicon.

These findings reveal that rabbits for consumption harbor multidrug-resistant *S. aureus* with diverse resistance mechanisms and substantial virulence potential. The detection of *mecC*-MRSA in dominant livestock-associated lineages, combined with widespread biocide and metal resistance determinants, underscores the importance of integrating rabbit farming into One Health AMR surveillance frameworks.

Acknowledgements:

This work was supported by the project UID/00772/2025 DOI <https://doi.org/10.54499/UID/00772/2025> funded by the Portuguese Foundation for Science and Technology (FCT).



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sciforum-188576: Global genomic analysis revealed first emergence of *mcr-10.1* carrying *Enterobacter cloacae* ST1 clone from retail pork in Jiangsu, China.

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The emergence, persistence, and spread of resistance to last-resort antibiotics such as colistin is of critical concern globally which can pose a potential threat to public health due to limited treatment options. In this study, we first identified and characterized the genomic features of a food-acquired *Enterobacter (E.) cloacae* strain harboring *mcr-10.1* gene through antibiotic susceptibility testing and whole genome sequencing, followed by global comparative analysis of *Enterobacter cloacae* genomes submitted in the National Center for Biotechnology Information (NCBI) database. *E. cloacae* LYG_2_2AN exhibited resistance to colistin and multiple other antibiotics. The genomic analysis revealed that LYG_2_2AN belong to sequence type 1 and harbored 8 antibiotic resistance genes (ARGs) conferring resistance to five antimicrobial classes including *tet(A)* [tetracycline], *bla_{LAP-2}* and *bla_{CMH-4}* [β-lactam], *qnrS1*, *oqxA10*, and *oqxB9* [fluoroquinolone], *mcr10.1* [colistin], and *fosA* [fosfomycin]. The plasmid analysis revealed that LYG_2_2AN acquired three plasmids types including IncR (73,948 bp), rep_cluster_2335 (12,949 bp), and IncFIB (94,014 bp). The *mcr-10.1* was found to be located on 94 Kb IncFIB plasmid. Further, comparative phylogenomic analysis identified this strain showed close homology with other *mcr*-harboring *E. cloacae* strain from clinical settings and environment. This may indicate the expanding source distribution and independent transmission potential of these critical resistance genes across bacterial species or settings in One Health framework. Therefore, the current study recommends the continuous genomic surveillance of bacterial strains in food supply chain and other One Health settings to monitor and prevent their further dissemination. Moreover, the emergence of critical resistance genes in food-origin bacteria can pose a direct threat to human health.



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sciforum-181857: Global Prevalence of Antimicrobial Resistance in ESKAPE Pathogens Causing Canine Otitis Externa (1995-2025): A Systematic Review and Meta Analysis

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Introduction: Canine otitis externa (COE) remains a clinical challenge due to frequent treatment failures. The ESKAPE pathogens (*Enterococcus faecium*, *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Enterobacter* spp.) are major contributors to COE. This study aims to provide a comprehensive global estimate of antimicrobial resistance prevalence across drug classes and to identify resistance trends within these bacterial species.

Methods: Following PRISMA 2020 guidelines, a comprehensive systematic search was conducted across the Scopus, ScienceDirect, PubMed, and ProQuest databases. Ultimately, 37 studies published between 1995 and 2024 comprising 58,223 clinical isolates, met the predefined inclusion criteria. Random-effects model was employed to determine pooled resistance rates for each antimicrobial class using meta package in R software. Heterogeneity was evaluated using the I^2 statistic.

Results: The pooled prevalence of antimicrobial resistance (AMR) among ESKAPE pathogens in COE was 33.13% (95% CI: 30.80–35.54%). Resistance varied significantly by antibiotic class ($p < 0.01$), with the highest robust rates observed for beta-lactams ($n = 388$; 34.36%), aminoglycosides ($n = 196$; 29.17%), and fluoroquinolones ($n = 169$; 20.67%). Subgroup analysis by antibiotic type identified highest resistance were observed in second-generation cephalosporins (74.15%), followed by amoxicillin (69.54%) and neomycin (58.58%). At the genus level ($p < 0.01$), *Staphylococcus* spp. exhibited significant resistance across multiple antibiotic classes, particularly to beta-lactams (38.82%), and aminoglycosides (32.55%), however *Pseudomonas* spp. showed very high resistance to amphenicols (91.26%). High heterogeneity ($I^2 > 85\%$) indicated substantial global variation in AMR patterns.

Conclusion: The escalating resistance of ESKAPE pathogens, particularly against frontline treatments like neomycin and amoxicillin, signals a growing crisis in veterinary dermatology. These findings provide a critical baseline for the development of targeted therapeutic protocols to manage multidrug-resistant infections and to strengthen global antimicrobial stewardship in veterinary field.



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sciforum-188963: Healthy Livestock as Silent Reservoirs of Enterococci with Vancomycin Resistance Determinants in Sabah, Malaysian Borneo

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Introduction: Antimicrobial resistance in food-producing animals is a growing One Health concern because clinically healthy livestock may harbour resistant bacteria without obvious signs of disease. In Sabah, Malaysian Borneo, information on enterococcal reservoirs and vancomycin resistance determinants in livestock remains scarce. This study investigated the carriage of *Enterococcus* species and vancomycin resistance genes in healthy cattle and poultry, with the aim of identifying potential silent reservoirs of resistance within local food-animal systems. **Methods:** A total of 256 faecal samples were collected from cattle and poultry farms in Kota Kinabalu, Sabah, between October 2019 and February 2020. Enterococcus isolates were recovered using selective culture and identified by standard bacteriological methods. Polymerase chain reaction assays targeting *vanA*, *vanB* and *vanC1/2/3* were performed to detect acquired and intrinsic vancomycin resistance determinants. **Results and Discussions:** *Enterococcus* was recovered from 85.5% of samples, confirming widespread carriage among healthy livestock. *E. faecalis* was the dominant species, followed by *E. faecium* and other *Enterococcus* species. The acquired vancomycin resistance genes *vanA* and *vanB* were not detected in any isolate, suggesting that high-level transferable vancomycin resistance was not evident in the sampled farms. However, three *E. casseliflavus* isolates from poultry carried the intrinsic *vanC2/3* gene, demonstrating that vancomycin resistance determinants are present within the gut microbiota of apparently healthy poultry. **Conclusions:** This study provides evidence that healthy livestock in Sabah can carry enterococci with vancomycin resistance determinants, even in the absence of acquired *vanA* and *vanB* genes. The detection of *vanC*-positive *E. casseliflavus* in poultry highlights a low-level but biologically relevant reservoir of glycopeptide resistance within the food-animal microbiota. Rather than representing routine surveillance alone, these findings establish an important early-warning baseline for One Health antimicrobial resistance monitoring in Malaysian Borneo and support more targeted molecular tracking of enterococci across livestock, food, environmental and human interfaces.



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sciforum-186038: High Prevalence of Multidrug-Resistant and Extended-Spectrum Beta-Lactamase-Producing *Escherichia coli* in Equine Uterine Infections: A One Health Concern

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Introduction: Antimicrobial resistance (AMR) represents a major One Health challenge at the human–animal–environment interface. Although *Escherichia coli* from humans and livestock has been extensively studied, equine reproductive tract infections remain an underrecognized reservoir of resistance determinants. This study aimed to characterize the molecular features, antimicrobial resistance genes, and phenotypic resistance patterns of *E. coli* isolated from equine uterine infections, with emphasis on One Health implications.

Methods: A total of 67 uterine lavage samples were collected from mares with reproductive disorders prior to antibiotic therapy. *E. coli* isolates were identified using culture, biochemical assays, and 16S rRNA PCR. Molecular analysis targeted O-serogroups (including O157), virulence genes (stx1, stx2, eae, ehly), and 11 AMR genes (aadA1, sul1, aac(3)-IV, blaSHV, cat1, cmlA, tetA, tetB, dfrA1, qnr, CITM) using multiplex and simplex PCR. Antimicrobial susceptibility was assessed by disk diffusion against 13 antibiotics according to CLSI guidelines.

Results: *E. coli* was confirmed in 42/67 samples (62.7%). The most prevalent AMR genes were aac(3)-IV (95.2%), blaSHV (73.8%), tetB (71.4%), sul1 (66.7%), and aadA1 (66.7%). High phenotypic resistance rates were observed for enrofloxacin (95.2%), ciprofloxacin (73.8%), tetracycline (71.4%), and trimethoprim (69.0%). Serogroup O157 was detected in 16.7% of isolates. Significant variation was observed in AMR gene distribution (p 0.001) and phenotypic resistance patterns (p 0.05).

Conclusions: Equine uterine infections harbor a high prevalence of multidrug-resistant *E. coli*, including ESBL-associated blaSHV. Detection of O157 and resistance to critically important antimicrobials highlights potential risks for environmental dissemination and interspecies transmission. These findings emphasize the need for integrated AMR surveillance within a One Health framework encompassing equine health, environmental pathways, and food safety.



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sciforum-188517: ISOLATION, IDENTIFICATION, AND ANTIBIOGRAM OF MASTITIS PATHOGENS FROM MILK SAMPLES OF DAIRY BOVINE IN KATHMANDU VALLEY, NEPAL

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ABSTRACT

Background and Aim: Bovine mastitis remains one of the most economically significant infectious diseases of dairy production worldwide and is increasingly associated with antimicrobial resistance (AMR). Monitoring pathogen distribution and cumulative resistance patterns (antibiogram) is essential for disease management and rational antibiotic use. This study aimed to identify mastitis pathogens and develop an antibiogram from isolates recovered from bovine milk samples in the Kathmandu Valley, Nepal.

Materials and Methods: A total of 422 bovine milk samples suspected of mastitis were screened using the California Mastitis Test (CMT) and processed for bacterial culture and identification. Antimicrobial susceptibility testing used the Kirby–Bauer disc diffusion method per standard guidelines, and cumulative data were compiled into an antibiogram. Associations between microbial growth and risk factors (age, parity, species, breed) were analyzed using appropriate statistical tests.

Results: Of 422 samples, 324 (76.8%) yielded microbial growth, comprising 320 bacterial and 4 fungal (*Candida* spp.) isolates. *Staphylococcus* spp. (36.7%) predominated, followed by *Klebsiella* spp. (27.5%), *Escherichia coli* (8.6%), *Pseudomonas* spp. (8.6%), and *Streptococcus* spp. (7.4%), with Enterobacteriaceae (38.8%) and Staphylococcaceae (37.2%) the leading families. Microbial growth was significantly associated with age ($p = 0.016$) and parity ($p = 0.001$). The cumulative antibiogram indicated high susceptibility to trimethoprim–sulfamethoxazole, marked ampicillin resistance among Enterobacteriaceae, and emerging β -lactam resistance in *Staphylococcus* spp. Multidrug resistance was observed in major isolates, including *Staphylococcus* spp. (17.6%), *Escherichia coli* (20.7%), and *Klebsiella* spp. (15.7%).

Conclusion: Bovine mastitis in the Kathmandu Valley was largely bacterial in origin, dominated by *Staphylococcus* spp. and Enterobacteriaceae, with age and parity as significant risk factors. Beyond herd-level treatment failure, the spread of resistant pathogens through milk threatens animal clinical management and dairy supply-chain safety, a public health concern. The high prevalence of ampicillin resistance, emerging β -lactam resistance, and multidrug resistance among key isolates highlights the urgency of antibiogram-guided antimicrobial stewardship in dairy herds.



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sciforum-187037: *Lactobacillus* Cell-Free Supernatants as Clean-Label Biopreservatives for Carabeef: Antimicrobial, Antioxidant, and Quality-Sustaining Efficacy under Refrigerated Storage

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Buffalo meat (carabeef) is a nutritionally superior red meat and a globally significant commodity, with India contributing approximately 37% of world production and serving as the largest exporter. However, microbial spoilage and lipid oxidation remain persistent challenges that compromise carabeef quality and safety during storage and export. Growing consumer demand for clean-label, natural preservation alternatives has intensified interest in postbiotic-based biopreservation strategies. This study evaluated the biopreservative potential of cell-free supernatants (CFS) derived from *Lactobacillus plantarum* MTCC 9496, *Lactobacillus rhamnosus* MTCC 12920, and *Levilactobacillus brevis* MTCC 13243 – individually (AB-CFS) and in combination (ABC-CFS) – on the quality and shelf life of carabeef under refrigerated storage for six days.

The minimum inhibitory concentration of both AB and ABC extracts was determined as 32 AU/mL against *E. coli* ATCC 25922, *Listeria monocytogenes* ATCC 19118, and *Staphylococcus aureus* ATCC 6538 using a microtiter broth dilution assay. CFS-treated carabeef maintained significantly lower total plate counts compared to untreated controls and ascorbic acid (0.05%) groups throughout storage, demonstrating superior antimicrobial efficacy attributable to bacteriocins, organic acids, and bioactive peptides. Colour stability was preserved, with b* values – an indicator of lipid-associated discolouration – effectively controlled in CFS-treated groups. CFS treatments maintained pH within the acceptable fresh carabeef range (5.4–5.8) across the storage period. TBARS values remained well within safe limits throughout storage, with ABC-CFS achieving antioxidant efficacy comparable to synthetic ascorbic acid ($p > 0.05$), attributed to phenolic metabolites and metal-chelating organic acids produced during LAB fermentation.

These findings collectively establish that *Lactobacillus* CFS, particularly the tri-species combination, is a highly promising, GRAS-compliant, clean-label biopreservative capable of extending carabeef shelf life without compromising sensory or physicochemical quality, with significant implications for sustainable meat preservation during cold chain export.



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sciforum-180772: Mechanistic In Silico Evaluation of ABCG2-Mediated Drug–Drug Interactions in Lactating Animals: Implications for Efflux Modulation, Milk Excretion, and Antimicrobial Exposure

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Drug disposition in lactating animals is critically influenced by active transport processes that regulate the transfer of xenobiotics into milk. The efflux transporter ABCG2/BCRP is a key determinant of this process; however, its modulation by co-administered veterinary drugs is not routinely considered in pharmacokinetic assessment. This study investigates the mechanistic basis of transporter-mediated drug–drug interactions and their potential impact on drug excretion dynamics in lactating systems. A structure-based computational framework was applied using an ovine ABCG2 homology model with high structural confidence. Molecular docking was performed to evaluate binding affinity and interaction profiles of representative veterinary drugs within the transporter cavity. Docking scores were analysed comparatively, and ligand–residue interactions were mapped to identify key binding determinants. Spatial overlap analysis was conducted to assess potential competitive inhibition. Ivermectin demonstrated a strong binding affinity within the ABCG2 cavity (predicted binding energy ≈ -10.2 kcal/mol), stabilised by hydrophobic interactions with residues such as Phe and Leu lining the binding pocket, and by polar contacts with Arg residues involved in substrate coordination. Marbofloxacin exhibited moderate affinity (≈ -7.6 kcal/mol) with partial spatial overlap within the binding region. Structural alignment revealed that ivermectin occupies a substantial portion of the efflux pathway, suggesting a potential inhibitory effect on substrate transport. The overlap in binding regions supports a competitive interaction mechanism, whereby ivermectin may reduce transporter-mediated efflux of co-administered compounds. Differences in physicochemical properties further indicate altered distribution and retention behaviour under co-administration scenarios. This study provides mechanistic evidence that ABCG2-mediated drug–drug interactions may significantly modulate efflux capacity and influence drug excretion into milk in lactating animals. Such modulation of antimicrobial excretion may contribute to sub-therapeutic residue levels in the food chain, potentially influencing the selection pressure for antimicrobial resistance at the human–animal interface.



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sciforum-187744: Meta-Analysis of Mycotoxin-Induced Alterations in Gut Microbiota and Fermentation in Livestock: Implications for Animal Health and Productivity

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Mycotoxins are secondary metabolites of fungi which contaminate animal feed worldwide and pose a serious risk to animal health and agricultural productivity. This meta-analysis systematically reviewed evidence on the effects of six major mycotoxins on the gut flora, namely deoxynivalenol (DON), aflatoxin B1 (AFB1), zearalenone (ZEN), fumonisin B1 (FB1), T-2 toxin and ochratoxin A (OTA) in the main animal species, pigs, poultry and rabbits. Following the PRISMA guidelines, a comprehensive search of the web-based database of peer reviewed studies between 1997 and 2026 identified 47 eligible studies, including in vivo, in vitro, ex vivo and review designs. Data collection focused on the type of mycotoxin, animal species, study design, gut microbial taxa concerned, fermentation results and impacts on productivity in the animals. Statistical comparison showed that DON was the most extensively studied mycotoxin (23 studies, 49 patients) and primarily affected pigs and poultry by reducing Firmicutes, increasing Proteobacteria and disrupting the intestinal barrier. AFB1 showed the largest organ involvement including intestinal reproductive axis disruption in sheep, while ZEN had a unique effect on Akkermansia abundance and lipid metabolism. The FB1 has consistently reduced the total microbial diversity. Combined exposures to mycotoxins induced synergistic dysbiosis beyond the effects of individual toxins. Probiotic (*Lactobacillus* spp., *Saccharomyces cerevisiae*) and mycotoxin binding agents have been shown to have a partial protective effect against microbial disturbances. These findings underline the critical need for integrated mycotoxin management strategies in livestock production in order to protect both intestinal health and productivity



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sciforum-187806: Microbiological quality, molecular characterization, and antimicrobial resistance profiling of foodborne bacterial pathogens in donkey milk and associated environmental sources in Maharashtra, India

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Introduction: Donkey milk has attracted increasing attention because of its compositional similarity to human milk and its nutritional and therapeutic potential for infants, adults, and elderly individuals. However, the occurrence of foodborne pathogens and antimicrobial-resistant bacteria in donkey milk poses a potential public health concern. The present study evaluated the microbiological quality, occurrence of selected bacterial pathogens, and antimicrobial resistance patterns in donkey milk and its associated environment in Maharashtra, India.

Methods: A total of 50 raw donkey milk samples and 100 environmental samples, including udder swabs, utensils, farmers' hand swabs, and drinking water, were analyzed using standard microbiological methods for the detection of *Escherichia coli*, *Salmonella* spp., *Listeria* spp., and *Staphylococcus* spp. Total bacterial counts were determined by standard plate count methods. Isolates were characterized by biochemical assays, PCR, and MALDI-TOF MS/VITEK® MS. Antimicrobial susceptibility testing was performed to assess multidrug resistance (MDR) patterns and multiple antibiotic resistance (MAR) indices.

Results: The total bacterial count in donkey milk ranged from 3.95 to 5.02 log CFU/mL, with a mean count of 4.39 ± 0.02 log CFU/mL. *Escherichia coli* was detected in 6% of milk samples, whereas *Salmonella* spp. and *Listeria* spp. were absent in all samples analyzed. Overall occurrence of *Staphylococcus* species was 5.33%, including *Staphylococcus sciuri* and *Staphylococcus aureus*. Molecular and MALDI-TOF MS identification showed strong concordance with microbiological findings. All bacterial isolates exhibited notable MDR patterns, with resistance to multiple commonly used antibiotics and MAR index values ranging from 0.32 to 0.56.

Conclusions: The detection of multidrug-resistant *E. coli* and *Staphylococcus* species in donkey milk and related environmental sources highlights potential public health risks associated with raw milk consumption. Implementation of strict hygiene measures, pasteurization, Good Dairy Farming Practices, and prudent antimicrobial use is essential to ensure the microbiological safety of donkey milk and limit the spread of antimicrobial resistance.



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sciforum-188057: Molecular Epidemiology and Dissemination of Extended-Spectrum Beta-Lactamases (ESBL)- producing *Escherichia coli* of European Wildlife: A Systematic Review and Meta-Analysis

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Antimicrobial Resistance (AMR) in wildlife threatens public health globally, particularly concerning extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* (*E. coli*). European wildlife populations can contribute to the dissemination and persistence of ESBL-producing *E. coli* in the environment. Our aim of study was to conduct a comprehensive analysis of *E. coli* and AMR profiles in the various wild birds and animals within the European continent. A systematic review and meta-analysis were conducted on studies published from 2000 onwards to 2025, focusing on ESBL-producing *E. coli* in wildlife across European countries. From more than 500 initially identified records, nearly 120 studies met the eligibility criteria, and 93 studies were included in the final quantitative synthesis. Pooled prevalence estimates were calculated using a random-effects model to estimate the inter-study variability. The comprehensive meta-analysis presented the pooled prevalence of 39.9% (95% CI: 31.1%-49.5%) for ESBL-producing *Escherichia coli* in the wildlife in Europe, with substantial heterogeneity among the studies included ($I^2=61.57\%$). Molecular characterisation indicated that *bla*_{CTX-M}, *bla*_{TEM}, *bla*_{SHV} and *bla*_{CMY} classes were the most frequently reported ESBL genes. Polymerase Chain Reaction (PCR)-based assays were the dominant diagnostic approach across studies, while more recent publications increasingly incorporated whole-genome sequencing (WGS), enabling detection of plasmid-associated resistance genes. A rising trend in publication output was observed over the last eight years, with the highest number of studies reported in 2021. While geographically, Italy accounted for the highest number of eligible studies. Wildlife populations in Europe represent an important reservoir of ESBL-producing *Escherichia coli*, with CTX-M-type enzymes predominating. The increasing use of genomic tools highlights the role of mobile genetic elements in cross-species dissemination. These findings support the need for coordinated One Health standardised monitoring and surveillance strategies across Europe to mitigate the consequences of AMR.



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sciforum-189045: Multidrug-resistant bacterial pathogens associated with surgical site infections in veterinary medicine: an evidence-based systematic review

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Background

Surgical site infections (SSIs) are among the most common postoperative complications in veterinary medicine and are increasingly driven by antimicrobial-resistant (AMR) pathogens. These infections result in prolonged hospitalization, treatment failure, increased healthcare costs, and represent a significant One Health concern due to the potential spread of resistant bacteria and resistance genes across animal, human, and environmental interfaces.

Objectives

This systematic literature review aimed to synthesize current evidence on the bacterial etiology of veterinary SSIs and to characterize antimicrobial resistance patterns among the isolated pathogens.

Methods

A comprehensive search was conducted in PubMed, Web of Science, Scopus, and CAB Abstracts from database inception to May 2025. Eligible studies reported culture-confirmed bacterial isolates from veterinary SSIs with antimicrobial susceptibility testing performed according to CLSI or EUCAST standards. Data on pathogen distribution, resistance profiles, multidrug resistance (MDR), animal species, and geographic origin were extracted. Thirty-two studies from Europe, North America, and Asia involving companion animals, equines, and livestock met the inclusion criteria.

Results

Staphylococcus spp., particularly *S. pseudintermedius* and *S. aureus*, were the predominant Gram-positive pathogens, while *Escherichia coli*, *Pseudomonas aeruginosa*, and *Klebsiella* spp. were most common among Gram-negative isolates. Gram-negative bacteria consistently showed higher resistance rates than Gram-positive organisms. Resistance to beta-lactam antibiotics ranged from 40% to 80%, tetracycline resistance from 30% to 70%, and the prevalence of multidrug-resistant isolates varied between 30% and 60%, demonstrating substantial heterogeneity across regions, species, and clinical settings.

Conclusions

Veterinary SSIs are frequently complicated by multidrug-resistant pathogens, posing major challenges to treatment and infection control. These findings underscore the urgent need for strengthened antimicrobial stewardship, standardized surveillance programs, and improved infection prevention and control measures in veterinary practice. Moreover, veterinary SSIs may serve as reservoirs for antimicrobial resistance with important implications for public health and food safety.



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sciforum-194317: Nanoparticle-Mediated Interventions for Antimicrobial Resistance in Dairy Farms: A Systematic Review from a One Health Perspective

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Introduction: Antimicrobial resistance (AMR) is one of the greatest public health threats, closely linked to the use of antibiotics in industrial animal husbandry, particularly on dairy farms. In recent years, nanotechnology has been proposed as an innovative approach to combat AMR, without additional selective pressure on bacteria. This systematic review aimed to assess the effectiveness of nanoparticle-based interventions in reducing the burden of resistant bacteria and inhibiting the transmission of resistance genes on dairy farms within the One Health framework.

Methods: A systematic search was conducted in PubMed, Scopus, Web of Science, and Science Direct for English-language articles published between January 2015 and December 2024. Original experimental studies that investigated metal nanoparticles (silver, copper, zinc), polymeric nanocarriers, or liposomes for the control of key dairy pathogens (e.g., *Escherichia coli*, methicillin-resistant *Staphylococcus aureus*, *Mycoplasma bovis*) were included. Of the 892 articles found, 47 studies met the inclusion criteria.

Results: Silver nanoparticles (21 studies) and zinc oxide nanoparticles (14 studies) were the most commonly used. In farm studies, intramammary injection of silver-chitosan nanoparticles resulted in a 89% reduction in the number of resistant bacteria in milk and eradication of *S. aureus* biofilms. However, concerns were raised in several studies about the cytotoxicity of nanoparticles to mammary tissue and their survival in the food chain. Furthermore, studies have shown that nanoparticles can reduce resistance genes in manure, but the environmental disposal of nanoparticles is a new challenge.

Conclusion: Nanoparticle-based interventions have great potential to reduce AMR in dairy farms, but before widespread application, dose standardization, ecotoxicity assessment, and cost-benefit analysis in a unit health framework are essential. The development of biodegradable nanoparticles and their integration into antibiotic stewardship programs is recommended.



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sciforum-194739: Non-Bacterial Microbiome Diversity and Signatures in Bovine Subclinical Mastitis

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Introduction: Bovine subclinical mastitis (SCM) is traditionally studied through a bacterial lens, leaving the archaeome and virome of the mammary microbiome largely uncharacterized. These non-bacterial components may drive key ecological shifts between udder health, disease, and post-antibiotic recovery.

Methods: Shotgun metagenomic sequencing was performed on milk samples from three bovine mammary states: SCM (n=10), healthy mammary (HM, n=10), and antibiotic-treated (ANT, n=10). Reads were analyzed for species richness, inter-group overlap, and differential abundance to identify state-specific archaeal and viral signatures.

Results: The archaeome comprised 54 species and the virome 96 species, with 40.74% and 48.96% shared across groups, respectively. SCM was defined by *Methanosarcina sp. Kolksee* (21.31%) and *Methanolacinia petrolearia* (16.30%), the latter absent in HM. The HM state had a distinct biomarker, *Halomicrobium mukohataei* (15.96%), absent in ANT samples. ANT showed a significant bloom of *Methanobrevibacter sp. YE315* (25.30%; $p=0.014$), indicating antibiotic-resilient archaeal enrichment. Virome analysis reflected bacterial dysbiosis in SCM through Streptococcus phage enrichment (5.58%). HM and ANT shared a restorative phage community; Lactococcus phage 98103 (12.22% and 12.13%) and Escherichia phage Penshu1 (6.59% and 8.86%) were both absent (1.2%) in SCM.

Conclusions: Bovine mammary health, SCM, and antibiotic intervention carry distinct non-bacterial microbiome fingerprints. Antibiotic treatment appears to suppress SCM-associated archaeal taxa and facilitate a structural shift toward the HM virome profile, marked by resilient archaea and restorative phages. These non-bacterial signatures offer candidate biomarkers for SCM diagnosis and ecological recovery assessment.



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sciforum-187672: One Health Perspective on Antibiotic Resistance in Enterobacteriaceae from Livestock in Batna, Algeria

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The resistance of *Enterobacteriaceae* to antibiotics is changing worldwide, their emergence and dissemination are due to their ability to adapt, which is manifested by their ability to appropriate new properties. The purpose of this contribution was to study the resistance of *Enterobacteriaceae* and their ability to produce biofilm, the strains were isolated from different farms spread over four municipalities (Ras El Aïoun, Boumia, Hamla) of the wilaya of Batna, and a farm located in Aïn Azel (Sétif). Bacteria were isolated using MacConkey agar supplemented with cefotaxime at a concentration of 2 µg/mL in order to selectively recover third-generation cephalosporin-resistant *Enterobacteriaceae*. The isolated strains were subsequently identified using the API 20E biochemical identification system and confirmed by MALDI-TOF mass spectrometry. Antibiotic susceptibility testing was performed using the disk diffusion method on Mueller–Hinton agar, in accordance with the recommendations of the French Society of Microbiology (CA-SFM). A total of 29 strains were isolated and MALDI-TOF identified, their distribution was as follows: 4 *Citrobacter freundii*, 4 *Enterobacter sakazaki*, 3 *Escherichia coli*, 3 *Enterobacter cloacae*, 3 *Kluyvera* spp., 3 *Proteus penerie*, 2 *Proteus mirabilis*, 1 *Pontea* spp., 1 *Pasteurilla* sp., 1 *Enterobacter amnigenus*, 1 *Enterobacter canrogeus*, 1 *Citrobacter koseri*, 1 *Yersinia enterocolitica*. The β-lactam susceptibility test showed high resistance rates to cefotaxime (100%), cefazolin (100%), ceftiofur (89.28%), ampicillin (75%), ertapenem (64.28%), amoxicillin + clavulanic acid (64.28%), imipenem (60.71%), ticarcillin (53.57%), cefepime (39.28%). Also, rates of resistance to aminoglycosides (50%) and fluoroquinolones (50%) have been observed. Towards, trimethoprim + sulfamethoxazole, colistin, chloramphenicol, the resistances were respectively (28.57%), (78.57%), and (32.14%). The trimethoprim + sulfamethoxazole combination was the most active on these strains. Biofilm production revealed that 15 *Enterobacteriaceae* were biofilm producers, 8 variable strains and 5 non-producers.



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sciforum-187625: Plant Secondary Metabolites as Adjuvants to Restore Tetracycline Efficacy Against Multidrug-Resistant Zoonotic *Escherichia coli*

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Introduction: Antimicrobial resistance (AMR) is a pressing global health threat, observed in Gram-negative bacteria, especially *Escherichia coli*, unaffected by multiple drug classes. Tetracycline efficacy has diminished, to the extent that the drug exhibits reduced effectiveness. This has led researchers to seek alternative strategies, for instance plant secondary metabolites. These compounds have natural antimicrobial effects; more significantly, they can restore antibiotic activity by disrupting bacterial defense mechanism.

Methods: A systematic review was carried out following PRISMA 2020 guidelines. Google Scholar, PubMed, and Scopus were searched using keywords 'plant secondary metabolites', 'tetracycline resistance', and '*E. Coli*'; only papers published between 2010 and May 2026 were considered. The initial search returned 558 studies. After duplicate removal, 322 abstracts were assessed for relevance including in vitro, in silico, and systematic studies. Then 253 irrelevant studies were excluded due to non-English articles or association with other bacteria, leaving 69 articles read in full and used for qualitative synthesis.

Results: Several classes of plant secondary metabolites exhibited effects alongside tetracycline against MDR *E. coli*; flavonoids, alkaloids, terpenoids, phenolic compounds, and saponins showed synergistic effects using checkerboard, fractional inhibitory concentration index (FIC), and time-kill assay. Mechanistically, in many cases they acted as efflux pump inhibitors (EPIs), which led to more tetracycline accumulating inside the bacteria and a corresponding drop in resistance. Certain phytochemicals lowered minimum inhibitory concentrations (MICs) of tetracycline – quercetin, cepharanthine, ellagic acid, propyl gallate, catechin, myricetin, thymol, carnolic acid, triterpenoid, and chlorogenic acid demonstrated this effect.

Conclusions: Plant secondary metabolites appear as genuine candidates for natural antibiotic adjuvants, and tetracycline activity against multidrug-resistant bacteria can be restored. Their synergistic effects and ability to modify bacterial susceptibility. However, due to the low bioavailability of plant metabolites under in vivo conditions, further studies in this area are still required. The authors declare no conflicts of interest.



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sciforum-194252: Prevalence and Antimicrobial Resistance Patterns of Multidrug-Resistant *Escherichia coli* in Commercial Broiler Farms in Iran: A Cross-Sectional Study

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Introduction: Antimicrobial resistance (AMR) is a major One Health challenge affecting animal and public health. Commercial broiler farms are important reservoirs of antimicrobial-resistant bacteria; however, comprehensive multicenter data on the prevalence and resistance patterns of multidrug-resistant (MDR) *Escherichia coli* in Iranian poultry remain scarce. This study aimed to determine the prevalence, antimicrobial resistance profile, and farm-level distribution of MDR *E. coli* in commercial broiler farms in Iran.

Materials and Methods: A cross-sectional study was conducted during 2025-2026 in 18 commercial broiler farms across major poultry-producing regions of Iran. Farms were selected using a multistage sampling strategy. Cloacal and fecal samples were collected from healthy and diseased flocks. A total of 412 samples were cultured, yielding 174 non-duplicate *E. coli* isolates confirmed by standard bacteriological and biochemical methods. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method according to CLSI guidelines. MDR was defined as resistance to at least three antimicrobial classes. Differences in resistance prevalence between farms were evaluated using the chi-square test ($p < 0.05$).

Results: Among the 174 isolates, 128 (73.6%) exhibited resistance to at least one antimicrobial agent, and 69 (39.7%) were classified as MDR. Resistance was highest to tetracyclines (64.4%), beta-lactams (60.3%), and sulfonamides (57.5%), followed by fluoroquinolones (32.2%) and aminoglycosides (23.0%). MDR isolates most frequently exhibited resistance to three (46.4%) or four (28.1%) antimicrobial classes. Farm-level MDR prevalence ranged from 21.7% to 56.4%, likely reflecting differences in antimicrobial usage, flock management, and biosecurity.

Conclusions: The high prevalence of AMR and MDR *E. coli* highlights commercial broiler farms as important reservoirs of resistant bacteria in Iran. These findings provide baseline data for national AMR surveillance and support antimicrobial stewardship programs, routine susceptibility testing, strengthened farm biosecurity, vaccination-based disease prevention, and prudent antimicrobial use to reduce the dissemination of resistant bacteria throughout the poultry production chain.



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sciforum-194388: Prevalence, Antimicrobial Resistance, and Genomic Analysis of *Yersinia enterocolitica* from Livestock Farms in Qinghai, China

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Introduction: *Yersinia enterocolitica* is a zoonotic foodborne pathogen that contaminates water, animal-derived food products, thereby posing a continuous threat to food safety and public health. **Methods:** In 2025, a total of 513 animal-derived and environmental samples were collected from five livestock farms in Qinghai, China. Isolates were characterized using biotyping, antimicrobial susceptibility testing, whole-genome sequencing, multilocus sequence typing (MLST), and analyses of resistance/virulence genes, plasmids, pan-genome, and phylogeny. For comparative purposes, genomic data of 60 *Y. enterocolitica* strains from other regions of China were retrieved from the NCBI database. **Results:** The overall isolation rate of *Y. enterocolitica* was 1.56%, with a higher detection rate in environmental water samples than in bovine feces or porcine anal swabs in Qinghai, China. Biotype 1A was predominant, followed by biotype 4. MLST identified six sequence types (ST5, ST18, ST3, ST404, ST278, and ST26). Antimicrobial susceptibility testing revealed high resistance rates to ampicillin (100%) and sulfisoxazole (87.5%), and most isolates exhibited multidrug resistance. Whole-genome analysis identified 116 virulence-related genes and 14 genes associated with antimicrobial or disinfectant resistance; *crp*, *vatF*, and *y56_beta-lactamase* were present in all isolates. Pan-genome and phylogenetic analyses demonstrated substantial genomic variability, and some isolates from Qinghai were closely related to strains from Ningxia, China. **Conclusions:** *Y. enterocolitica* isolates from livestock farms in Qinghai, China, exhibit a certain level of contamination and pose a risk of multidrug resistance. The high detection rate in environmental water suggests potential transmission from farm environments to the food chain. This study provides scientific evidence for regional epidemiological surveillance, food safety risk assessment, and the development of AMR control strategies in China.



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sciforum-185917: Prevalence, Antimicrobial Susceptibility Patterns, and Risk Factors for *Staphylococcus aureus* from Meat of Animal Origin in Mekelle, Tigray, Northern Ethiopia

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Background: *Staphylococcus aureus* (*S. aureus*) is well known for causing human and animal diseases, primarily through the consumption of contaminated meat.

Objective: This study aimed to determine the presence of *S. aureus*, its antimicrobial susceptibility test, and risk factors from meat of animal origin in Mekelle, Northern Ethiopia.

Method: Socio-demographic data were collected using a pre-designed questionnaire. Meat samples were collected sterily from butchers and abattoir facilities and transported in an icebox to the microbiology laboratory. An isolation, characterization, and antimicrobial susceptibility test was performed using the disc diffusion method. The data were cleaned and entered into STATA 20.0. Logistic regression models with odds ratios were used to assess risk factors and bacterial contamination. A p-value of 0.05 was considered statistically significant.

Results: During the current investigation, we collected 250 samples. The analysis revealed the presence of contamination by *S. aureus* in 88 (35.2%) of the samples. The prevalence of *S. aureus* in samples from the butcher and abattoir houses was 37.6% (n=47) and 32.8% (n=41), respectively. Significant factors included, use of gloves (COR = 0.523; 95% CI: 0.308-0.889, P-value: 0.017, AOR = 0.222; 95% CI: 0.104-0.473, P-value: 0.001), strict separation between clean and dirty areas (COR=2.48; 95% CI: 1.45-4.24), and poor handwashing practice (COR=2.93; 95% CI: 1.41-6.06), with all associated with *S. aureus* contamination. The presence of resistance to cefotaxime, ampicillin, and penicillin G was observed in all isolates of *S. aureus* from butcher and abattoir house sources. In contrast, the in vitro antimicrobial sensitivity pattern of amikacin, cephalixin, gentamicin, trimethoprim-sulfamethoxazole, and nitrofurantoin was tested.

Conclusion: This study highlights the widespread presence of *S. aureus* in meat products. Consequently, early identification of the pathogen and antimicrobial susceptibility testing for *S. aureus* are crucial to improve treatment outcomes and prevent the development of drug resistance.



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sciforum-193239: Prevalence, Geographic Distribution, and Risk Factors of Antimicrobial-Resistant Bacteria in Companion Animals in Iran: A Cross-Sectional One Health Study

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Introduction: Antimicrobial resistance (AMR) is an increasing global threat affecting human, animal, and environmental health within the One Health framework. Companion animals may serve as reservoirs of resistant bacteria because of frequent antimicrobial exposure and close contact with humans. This study investigated the prevalence, geographic distribution, and risk factors associated with AMR in bacterial isolates from dogs and cats in Iran.

Materials and Methods: A multicenter cross-sectional study was conducted between 2025 and 2026 using routine bacteriological data from veterinary clinics across Iran. A total of 428 clinical samples were collected from 312 dogs and cats with suspected infections. Among these, 186 bacterial isolates were identified and tested for antimicrobial susceptibility according to Clinical and Laboratory Standards Institute guidelines. Isolates resistant to at least one antimicrobial class were classified as AMR, while those resistant to three or more classes were defined as multidrug resistant (MDR). Risk factors were assessed using odds ratios and 95% confidence intervals.

Results: The most frequently isolated bacteria were *Escherichia coli* (33.3%), *Staphylococcus pseudintermedius* (25.8%), *Pseudomonas aeruginosa* (16.7%), and *Klebsiella pneumoniae* (12.9%). Overall, 79.0% of isolates were AMR and 42.5% were MDR. Resistance was highest against beta-lactams, tetracyclines, and fluoroquinolones. Significant MDR risk factors included recent antimicrobial use, hospitalization, older age, and chronic disease. Tehran, Alborz, and Mazandaran provinces showed the highest resistance rates.

Conclusions: AMR is highly prevalent among companion animals in Iran, highlighting the need for antimicrobial stewardship, culture-guided therapy, and integrated surveillance programs to reduce the spread of resistant bacteria.



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sciforum-194307: Surgical Site Infections in Veterinary Practice: A Systematic Review of Pathogen Transmission, Antimicrobial Resistance, and One Health Implications

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Introduction: Surgical site infection (SSI) is a common and preventable complication in veterinary medicine, which, in addition to increasing morbidity and mortality, has significant economic and public health consequences. However, patterns of pathogen transmission and antimicrobial resistance (AMR), and their links to the One Health approach, have been studied less systematically in this area. The present systematic review aimed to summarize the available evidence on the causative agents of SSI in veterinary medicine, the routes of pathogen transmission, the status of antimicrobial resistance, and its implications for human, animal, and environmental health.

Methods: A systematic search was conducted in PubMed, Scopus, Web of Science, and Google Scholar databases for articles published between January 2020 and December 2025. The keywords used were the combination of surgical site infection, veterinary, antimicrobial resistance, One Health, methicillin-resistant *Staphylococcus*, and cross-species transmission. Original observational, quasi-experimental, and cross-sectional studies that confirmed SSI in companion animals, horses, or large livestock and provided data on the microorganisms involved, antibiotic susceptibility patterns, or evidence of cross-species transmission were included.

Results: Of the 1,247 articles found, 28 studies met the inclusion criteria. The most common pathogens isolated were *Staphylococcus aureus*, *Escherichia coli*, *Enterococcus* spp., and *Proteus* species. More than 35% of staphylococcal isolates were methicillin-resistant (MRSP). Acquired resistance to fluoroquinolones and third-generation cephalosporins was observed in 12 studies. Strong evidence of transmission of the same resistant clones between surgical animals and veterinary personnel was reported in 16 studies. Only 18 studies reported shedding of resistant pathogens via clinic wastewater or animal bedding.

Conclusion: SSI in veterinary medicine is often caused by multidrug-resistant pathogens that have a high potential for interspecies and environmental transmission. Integration of antibiotic stewardship programs in veterinary medicine, along with integrated unit health surveillance, is essential to address this growing threat.



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sciforum-188097: Systematic Review on the Use of Natural Products for Ectoparasite Control in Ruminants.

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Introduction: Ectoparasites, including ticks, lice, fleas, and flies, represent a major challenge in livestock production because of their negative impact on animal health and their role as vectors of infectious diseases. Current control strategies mainly rely on synthetic ectoparasiticides; however, their extensive use has promoted the emergence of resistant strains and raised concerns regarding environmental safety and food quality. In this context, plant-derived compounds have attracted increasing attention as sustainable alternatives for ectoparasite management in ruminants. Therefore, this systematic review aimed to evaluate the efficacy of plant-based products against ectoparasites affecting ruminants.

Methods: A comprehensive literature search was performed in the PubMed database, including studies published between January 1993 and June 2023, using keywords related to phytochemicals, ectoparasites, and livestock species. Studies were selected according to predefined inclusion and exclusion criteria.

Results: A total of 615 records were identified, of which 66 studies met the inclusion criteria. Most studies focused on ticks (47/66), followed by flies (14/66) and lice (5/66), with the majority conducted in vitro (59/66). Publications increased markedly after 2014, reflecting growing interest in sustainable ectoparasite control. Overall, 136 plant species from 42 botanical families were evaluated, mainly essential oils and extracts, particularly from the Lamiaceae and Asteraceae families. Tea tree oil, cinnamon, and lemon eucalyptus showed notable insecticidal or repellent activity, likely related to bioactive terpenes and alkaloids. Plant-based products demonstrated promising activity against flies and lice, whereas efficacy against ticks was more variable, with only 45% of studies reporting $\geq 80\%$ effectiveness. Repellent activity was generally short-lived.

Conclusions: Plant-derived products represent a promising strategy for sustainable ectoparasite control in livestock systems. However, further studies are needed to improve the standardization, efficacy, and field applicability of these compounds before large-scale implementation in veterinary practice.



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sciforum-194649: The Role of Insect-Based Animal Feed in the Transmission of Antimicrobial-Resistant *Salmonella*: A One Health Perspective

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Introduction: The increasing adoption of insect-based feed ingredients as sustainable alternatives to conventional protein sources has transformed modern livestock and aquaculture production systems. However, concerns have emerged regarding the potential role of insect-derived feeds in the dissemination of antimicrobial-resistant (AMR) pathogens, particularly *Salmonella*, across animal, environmental, and human interfaces. This study investigated the potential contribution of insect-based animal feed to the transmission of antimicrobial-resistant *Salmonella* within a One Health framework and assessed associated implications for global food safety.

Methods: A multidisciplinary surveillance approach was employed to evaluate insect meal production systems, animal feed products, livestock production environments, and associated food chains. Samples from insect rearing substrates, processed insect meals, animal feces, farm environments, and food products were subjected to microbiological screening and whole-genome metagenomic analyses. Antimicrobial resistance genes (ARGs), mobile genetic elements (MGEs), and *Salmonella* serovars were identified using bioinformatic pipelines. Potential transmission pathways were assessed through comparative genomic and ecological network analyses.

Results: Diverse ARGs conferring resistance to tetracyclines, aminoglycosides, sulfonamides, and β -lactams were detected throughout the insect-feed production continuum. Several multidrug-resistant *Salmonella* strains carried plasmid-associated resistance determinants and shared genetic signatures across insect-derived feed, animal production systems, and environmental samples. Network analyses revealed potential routes for horizontal gene transfer between microbial communities associated with insect substrates, livestock microbiota, and farm environments. The persistence of ARGs following feed processing highlighted potential challenges in mitigating AMR dissemination.

Discussion: The findings suggest that insect-based feed systems may represent an underrecognized pathway for the transmission of antimicrobial-resistant *Salmonella* within interconnected food production ecosystems. While insect-derived feeds offer substantial environmental and economic benefits, robust surveillance strategies are required to minimize AMR-related risks. Integrating genomic monitoring, feed safety regulations, and One Health-based risk assessment frameworks will be essential for ensuring the sustainable and safe expansion of insect-based feed technologies.



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