IOCVS
2025
Conference

The 1st International Online Conference on Veterinary Sciences

Veterinary Virology in the New Era:
Comprehensive Research from Identification to Prevention

3–5 December 2025 | Online

Program and Abstract Book

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The 1st International Online Conference on Veterinary Sciences

03–05 December 2025 | Online

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Welcome from the Chair

Dear Colleagues,

We are delighted to announce **the 1st International Online Conference on Veterinary Sciences (IOCVS 2025)**, set to take place **online** from **3-5 December 2025**, promoted by the open access MDPI journal *Veterinary Sciences* (ISSN: 2306-7381; Impact Factor: 2.3). This virtual event provides an invaluable platform for researchers, clinicians, and experts in veterinary sciences to gather, discuss, and exchange insights on the latest developments in the field.

This conference will focus on, but is not limited to, the following five sessions:
- Identification and Detection of Novel Animal Viruses;
- Development and Optimization of Animal Vaccines;
- Veterinary Epidemiology;
- Antiviral Therapy;
- Virology in One Health.

We invite the community to join us in making the first International Online Conference on Veterinary Sciences a successful and impactful event. Let's engage, collaborate, and push the boundaries of veterinary science together!

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

Lastly, we would like to express our sincere gratitude for your unwavering support and participation, which will make this conference a great success!

Prof. Dr. Wentao Li
Conference Chair
Director, Animal Disease Diagnostic Center at Huazhong Agricultural University, China
National Key Laboratory of Agricultural Microbiology, College of Veterinary Medicine, Huazhong Agricultural University

veterinary sciences
an Open Access Journal by MDPI

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).

Impact Factor: 2.3 (2024); 5-Year Impact Factor: 2.4 (2024)

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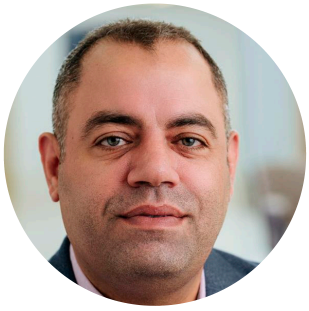

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National & Local United Engineering Laboratory of Natural Biotoxin, Apitherapy Research Institute, College of Bee Science and Biomedicine of Fujian Agriculture and Forestry University, Fuzhou, China

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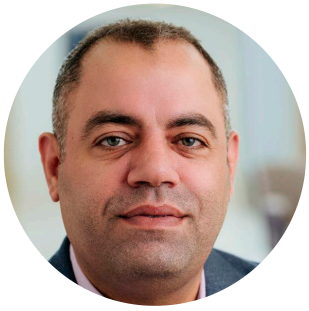
Prof. Dr. Yongtao Li

Department of Preventive Veterinary Medicine, Henan Agricultural University, Zhengzhou, China

Keynote Speakers



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Invited Speakers

Dr. Francesco Mira

Istituto Zooprofilattico Sperimentale della Sicilia, Palermo, Italy
Department of Veterinary Sciences, University of Messina, Polo Universitario dell'Annunziata, Messina, Italy

Dr. Lifang Yan

College of Veterinary Medicine, Mississippi State University, Starkville, Mississippi State, USA

Dr. Mahmoud Naguib

Institue of Infection, Veterinary & Ecological Sciences, Faculty of Health and Life Sciences, University of Liverpool, Liverpool, United Kingdom

Dr. Shen Wang

Department of Preventive Veterinary Medicine, Henan Agricultural University, Zhengzhou, China

Prof. Dr. Levon Abrahamyan

Department of Pathology and Microbiology, Faculty of Veterinary Medicine, University of Montreal, Montreal, Canada

Young Investigator Speaker

Ms. Ramya Smithaveni Barre

Luis Martinez-Sobrido
Laboratory, Texas Biomedical
Research Institute,
San Antonio, USA

Program Overview

	Day 1	Day 2	Day 3
Morning	**Session D:** Antiviral Therapy	**Session C:** Veterinary Epidemiology	**Session C:** Veterinary Epidemiology
Afternoon	**Session B:** Development and Optimization of Animal Vaccines	**Session A:** Identification and Detection of Novel Animal Viruses	**Session E:** Virology in One Health

IOCVS 2025 Program

3rd December 2025 (Wednesday)

Session D: Antiviral Therapy

Time: 9:00 (CET)| 3:00 (EST, New York) | 16:00 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
9:00–9:05	*Welcome from the Event Chair* *Prof. Dr. Wentao Li*	
9:05–9:10	*Welcome from the Session Chair* *Prof. Dr. Yongtao Li*	
9:10–9:30	**Prof. Dr. Dengguo Wei** Keynote Speaker	Tilmicosin Inhibits The Infections of Currently Prevalent PRRSV Isolates via the Downregulation of CD163 Expression
9:30–9:50	**Dr. Shen Wang** Invited Speaker	Microfold Cells: A Promising Target for Drug Delivery
9:50–10:30	**Prof. Dr. Nanhua Chen** Keynote Speaker	Discovery of Antiviral Molecules via AI and Novel Targets
10:30–10:55	**Ms. Ramya Smithaveni Barre** Young Investigator Speaker	A Bioluminescent H5N1 Virus for Real-Time Tracking of Viral Infection and Identification of Therapeutic Interventions
10:55–11:15	**Rosa Giugliano** Selected Speaker	Scorpion-Derived Peptides as Antiviral Agents in Veterinary Medicine
11:15–11:35	**Zbigniew Wyżewski** Selected Speaker	Ectromelia Virus Infection Decreases Bid Protein Level and Impairs Apoptosis in L929 Fibroblasts
11:35–11:55	**Muhammad Safdar** Selected Speaker	Polyphenol-Mediated Inhibition of SIGLEC15 to Block Newcastle Disease Virus Binding and Enhance Immunity in Chickens

Session B: Development and Optimization of Animal Vaccines

Time: 14:30 (CET)| 8:30 (EST, New York) | 21:30 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
14:30–14:35	*Welcome from MDPI conference team* *MDPI conference team*	
14.35–14.55	**Sen Zhang** Selected Speaker	Cross-Genotypic Immunity Achieved: A M. bovis-BoHV-1 Combined Vaccine Confers Universal Protection Against Diverse Bovine Herpesvirus Type 1 Strains
14:55–15:15	**Yu-Chieh Chen** Selected Speaker	Effective Induction of Cellular Immunity in Piglets Using a Single-Dose Bivalent Vaccine Against CSFV and PCV2
15:15–15:35	**Mónica Sánchez Segovia** Selected Speaker	Assessment of a Live Attenuated African Swine Fever Vaccine Produced in a Stable Cell Line: Immunogenicity and Protective Potential in Wild Boar
15:35–15:55	**Marta Díaz de Frutos** Selected Speaker	Dissecting ASFV Immune Responses: Insights from Hemadsorption Inhibition and Wild Boar Vaccination Studies
15:55–16:35	**Dr. Ahmed Mostafa Elsayed** Keynote Speaker	The Expanding Challenge of H5N1: Driving Innovation in Avian Influenza Vaccine Development
16:35–17:15	**Prof. Dr. Muhammad Munir** Keynote Speaker	Challenges in NDV Control and Solutions Ahead
17:15–17:55	**Prof. Dr. Francis Eko** Keynote Speaker	Harnessing the Power of Ghosts in Animal Vaccine Development
17:55–18:00	*Closing Remark from the Session Chair* *Prof. Dr. Francis Eko*	

4th December 2025 (Thursday)

Session C: Veterinary Epidemiology

Time: 9:00 (CET)| 3:00 (EST, New York) | 16.00 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
9:00–9:05	*Welcome from the Committee Member* *Prof. Dr. Beibei Li*	
9:05–9:45	**Dr. Yin Li** Keynote Speaker	Understanding The Epidemiology of Swine Influenza in South China
9:45–10:15	**Dr. Mahmoud Naguib** Invited Speaker	Avian Influenza Virus: Insights from Southeast Asia and The Middle East
10:15–10:35	**Gheorghe Solcan** Selected Speaker	Generalized Notoedric Mange Following Feline Immunodeficiency Virus (FIV) Infection in Cats
10:35–10:55	**Gianmarco Ferrara** Selected Speaker	Serological and Molecular Evidence of Canine Enteric Coronavirus in Campania Region (Italy)
10:55–11:15	**Md. Nazmul Islam** Selected Speaker	Feasibility of On-Farm Somatic Cell Count Screening for Subclinical Mastitis: Prevalence and Risk Factors in a Commercial Dairy Herd in Bangladesh
11:15–11:35	**Turin Afroz** Selected Speaker	The Bla TEM ESBL E. Coli Gene's Current State in Bangladesh's Poultry Industry
11:35–11:55	Flash Poster Presentation (5 mins per person)	**Davide Pepe** Introduction of Non-Autochthonous Cattle into a Farm in the Madonie Park (Sicily, Italy) and the Impact of Endemic Tick-Borne Diseases: A Serological, Molecular, and Entomological Study **Santina Di Bella** Serological Survey of Rickettsia, Anaplasma, Ehrlichia, Babesia, and Flaviviruses in Dogs from Western Sicily (Italy) **Dario Bonomo** Serological and Molecular Investigation of Rickettsia spp. and Anaplasma spp. in Domestic Cats from Sicily, Italy **Virginia Talarico** Molecular and Serological Investigation of Tick-Borne Pathogens in Equines in Sicily, Italy

Session A: Identification and Detection of Novel Animal Viruses

Time: 15:00 (CET)| 9:00 (EST, New York) | 22.00 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
15:00–15:05	*Welcome from the Session Chair* *Prof. Dr. Leyi Wang*	
15:05–15:45	**Prof. Dr. Leyi Wang** Keynote Speaker	Application of Next Generation Sequencing for Viral Identification and Challenge
15:45–16:15	**Dr. Lifang Yan** Invited Speaker	Genomic Characterization of Avian Infectious Bronchitis Virus Using a Probe-Capture Enrichment Approach
16:15–16:35	**Valeria Rodríguez Villavicencio** Selected Speaker	Identification of Rotavirus and Concurrent Enteropathogens in Foals from Mexico
16:35–16:55	**Frederikke Juncher Høeg** Selected Speaker	Discovery and Detection of Novel Parvoviruses in Danish Wild Red Foxes (Vulpes Vulpes)
16:55–17:15	**Vadym Zaluzhnyi** Selected Speaker	Discovery and Characterization of a Novel, Highly Divergent Paramyxovirus in Bearded Seals, a New Branch in North Atlantic Virology
17:15–17:35	**Nefeli Vasileiou** Selected Speaker	Known and Novel Nairoviruses in Ticks (Order Ixoidea) Collected from Danish Wild and Domestic Animals

5th December 2025 (Friday)

Session C: Veterinary Epidemiology

Time: 9:00 (CET)| 3:00 (EST, New York) | 16:00 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
9:00–9:05	*Welcome from the Session Chair* *Prof. Dr. Yingyu Chen*	
9:05–9:45	**Prof. Dr. Yingyu Chen** Keynote Speaker	Bovine Leukemia Virus (BLV) at a Crossroads: Global Decline Amidst Local Resurgence in China
9:45–10:15	**Dr. Francesco Mira** Invited Speaker	Decoding Host–Virus Interactions to Predict Spillover
10:15–10:35	**Antonia Mataragka** Selected Speaker	One Health And Non-Communicable Diseases: Animal Interconnection to Human Non-Communicable Diseases
10:35–10:55	**Zihan Tian** Selected Speaker	Mapping Risks: A Value Chain Approach to Brucellosis Introduction in Zhijiang's Cattle Population, China
10:55–11:15	**Iván Mazuecos** Selected Speaker	Characterization of BTV-3 (SPA/2024) Transmission in Mammalian and Insect Cells and in the IFNAR(-/-) Mouse Model.
11:15–11:35	**Nnenna Ekwunife** Selected Speaker	Strengthening Veterinary Biosecurity and One Health Approaches for Zoonotic Disease Prevention in Sub-Saharan Africa

Session E: Virology in One Health

Time: 15.00 (CET)| 9:00 (EST, New York) | 22.00 (CST, Asia, Beijing)

CET (Central European Time)	Speaker	Title
15.00–15.05	*Welcome from the Session Chair* *PD Dr. El-Sayed M. Abdel-Whab*	
15.05–15.45	**PD Dr. El-Sayed M. Abdel-Whab** Keynote Speaker	Influenza Virus: One Health
15.45–16.15	**Prof. Dr. Levon Abrahamyan** Invited Speaker	Decoding Host–Virus Interactions to Predict Spillover
16.15–16.35	**Maria Perra** Selected Speaker	Genetic variability of the Influenza A H5N1 virus
16.35–16.55	**Hasbi Saltik** Selected Speaker	Hemagglutinin-Esterase Gene Variation Drives Adaptive Evolution in Bovine Coronavirus (BCoV)
16.55–17.15	**Ignacio Vargas-Castro** Selected Speaker	From Skin to Brain: Herpesvirus in Cetaceans as an Emerging Systemic Pathogen and Ocean Health Sentinels
17.15–17.30	Flash Poster Presentation (5 mins per person)	**Marko Popovic** Biothermodynamics of Virus-Host Interactions: the Role of Gibbs Energy in Antigen-Receptor Binding and Virus Multiplication in Host Cells **Maria Julia Judson** Meta-Analysis of Bacteriophage Use in Managing Mastitis and Diarrhea in Cattle Infected with E. coli **Arif Ansori** Circulating Bovine Leukemia Virus Cell-Free DNA as a Promising Biomarker for Enzootic Bovine Leukosis
17.30–17.35	*Closing speech by Conference Co-Chair* *Dr. Ahmed Mostafa Elsayed*	

Session A. Identification and Detection of Novel Animal Viruses

sciforum-119726: Evaluation of Clinical, Analytical, and Genotyping Performance of Hex L1 PCR Coupled with High-Resolution Melting Curve Analysis for Outbreak Investigation in Morocco

Amina Kardoudi [1,*], Siham Fellahi [1], Faouzi Kichou [1] and Benani Abdelouheb [2]

[1] Department of Avian Pathology and Public Health, Hassan II Institute of Agronomy and Veterinary Medicine, Rabat, B.P. 6202, Rabat-Instituts, Morocco
[2] Virology Department, Pasteur Institute of Morocco, 1, Place Louis Pasteur, Casablanca, Morocco

Fowl adenoviruses (FAdVs) are widespread viruses in poultry populations, responsible for several severe diseases, including Inclusion Body Hepatitis (IBH), Adenoviral Gizzard Erosion (AGE), and Hepatitis-Hydropericardium Syndrome (HHP). These diseases have significant economic and health impacts on poultry industries globally. In this study, we aimed to evaluate the clinical, analytical, and genotyping performance of the Hex L1 PCR combined with High-Resolution Melting (HRM) Curve analysis for investigating recent IBH and AGE outbreaks in Morocco. The study involved 26 clinical samples collected from broiler and layer poultry farms suspected with IBH and AGE. These samples were amplified using conventional PCR, real-time PCR/52K test, and the Hex L1 PCR/HRM test. Field isolates were also sequenced and compared with HRM curve analysis results to validate the genotyping accuracy of the Hex L1 PCR/HRM method. Phylogenetic analysis of the sequenced samples revealed several FAdV genotypes, including FAdV-11 and FAdV-8b in IBH cases, and FAdV-1 and FAdV-8a in AGE cases, highlighting the genetic diversity of circulating strains. The Hex L1 PCR/HRM method successfully amplified all 12 FAdV serotypes, demonstrating excellent reproducibility and repeatability, with coefficients of variation ranging from 0.19% to 1.82%. Moreover, this method showed a strong correlation with the real-time PCR/52K method, achieving a high correlation coefficient of 0.9077. The HRM curve analysis reliably genotyped all the field isolates, and the results matched exactly with the sequencing outcomes. In conclusion, this method offers a fast, sensitive, and reliable alternative for FAdV detection and genotyping. It provides universal detection, quantification, and genotyping in a single step, overcoming the limitations of traditional techniques, making it a perfect tool for epidemiological studies and outbreak investigation.

sciforum-142663: Discovery and characterization of a novel, highly divergent paramyxovirus in bearded seals, a new branch in North Atlantic virology

Vadym Zaluzhnyi [1,*], Joost T. P. Verhoeven [2], Garry B. Stenson [3], Andrew S. Lang [1], Suzanne C. Dufour [1] and Marta Canuti [4]

[1] Department of Biology, Memorial University of Newfoundland, St. John's, NL A1C 5S7, Canada
[2] Centre for Evolutionary Hologenomics, The Globe Institute, University of Copenhagen, 1353 Copenhagen, Denmark
[3] Bidesuk Consulting, St. John's, NL A1A3N2, Canada
[4] Department of Veterinary and Animal Sciences, University of Copenhagen, Frederiksberg, 1870, Denmark

Introduction: Seals are important animals for Arctic and subarctic environments and a valuable resource for indigenous communities, but their virome remains poorly understood. During an effort to identify viruses circulating among North Atlantic seals, we discovered a new member of the *Paramyxoviridae*, a family including important RNA animal pathogens. This study aimed to characterize the novel virus and investigate its evolutionary relationships with other paramyxoviruses.

Methods: We conducted a metagenomic survey on paired tracheal and colon swabs collected from 59 seals — bearded (*Erignathus barbatus*, N=7), ringed (*Pusa hispida*, N=6), harp (*Pagophilus groenlandicus*, N=42), and harbour (*Phoca vitulina*, N=4) seals — from the northwest coast of Newfoundland, Canada. Virus-enriched nucleic acids isolated from each sample were subjected to reverse transcription and second-strand synthesis. Obtained dsDNA were pooled (N=9) according to species and location, and outsourced for Illumina sequencing. An in-house bioinformatics pipeline was used to identify viral contigs, and virus presence was confirmed by PCR and Sanger sequencing. *Paramyxoviridae*-wide phylogenetic analysis was performed with maximum likelihood methods on core protein concatenated alignments using a partition model.

Results: The complete genome of a novel paramyxovirus was identified in a pool from 7 bearded seals and confirmed to be present in one sample. We named the new virus bearded seal-associated paramyxovirus (BSAPV). The genome (15,989-nt) encoded five core paramyxoviral proteins — nucleoprotein, matrix, fusion, hemagglutinin-neuraminidase, and polymerase — and two proteins with no identifiable homologues. Phylogenetic analysis, including BSAPV and all 153 currently known paramyxoviral species, positioned BSAPV in a long-branched clade with Wenzhou pacific spadenose shark paramyxovirus (*Scoliovirinae*, *Scoliodonvirus scoliodontis*), its closest relative (pairwise identity of the L protein: 32.2%).

Conclusions: According to ICTV criteria, BSAPV is likely the first member of a novel paramyxoviral subfamily. This study expands our knowledge about marine paramyxoviruses, and future studies should investigate BSAPV ecology, spread, and host spectrum.

sciforum-142697: Discovery and detection of novel parvoviruses in Danish wild red foxes (*Vulpes vulpes*)

Frederikke Juncher Høeg [1,*], Nefeli Vasileiou [1], Anne Sofie Vedsted Hammer [1], Anne Cecilie Boldt Eiersted [1], Joost Theo Petra Verhoeven [2], Lars Erik Larsen [1], Tim Kåre Jensen [1], Marta Canuti [1]

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[2] Centre for Evolutionary Hologenomics, The Globe Institute, University of Copenhagen, 1353 Copen-hagen, Denmark

Introduction: *Parvoviridae* includes multi-host viruses of health relevance for canids. Wild species inhabiting human-dominated landscapes (e.g., foxes) can facilitate parvovirus transmission between wild and domestic animals. However, data on parvoviruses in wildlife remains limited. This study aimed to identify which parvoviruses circulate among Danish red foxes (*Vulpes vulpes*) and investigate their molecular epidemiology.

Methods: One stool and 81 spleen samples from foxes were included. Initially, metagenomic sequencing with a method designed to enrich for parvoviruses was performed on the stool sample. DNA was then extracted from spleen samples and screened using a pan-amdoparvovirus PCR and PCRs targeting viruses identified by metagenomics. Sanger sequencing was used to confirm positives and study virus diversity in Denmark. Global phylogenetic analyses were performed by maximum likelihood.

Results: Two complete parvoviral genomes were recovered from the metagenomic analysis: a novel hamaparvoviral species (48.7% non-structural (NS) protein 1 identity to its closest relative) that was, however, not detected in spleen samples, and the recently described fox parvovirus (*Protoparvovirus carnivoran4*) detected also in two spleens (virus prevalence: 3.7%). Additionally, we identified fragments of the recently discovered newlavirus (*Protoparvovirus carnivoran5*), later detected with a prevalence of 37.8% (31/82). Finally, a novel amdoparvoviral species (74.3% NS1 identity to its closest relative) was discovered via pan-genus PCR and detected with a prevalence of 6.1% (5/82). Danish amdoparvoviruses and fox parvoviruses were highly conserved (94.4-99.9% and 96.7-100% pairwise identities, respectively), while newlaviruses were highly variable (identities: 73.2-96.0%). Interestingly, newlaviruses clustered by country of origin within NS1 phylogenies, but no geographical clustering was observed with capsid sequences.

Conclusions: Our multi-method parvovirus discovery approach allowed us to discover two novel species and identify two other recently discovered parvoviruses. This suggests that additional, uncharacterized parvoviruses could be circulating. Further research is needed to thoroughly study parvovirus epidemiology in canids and examine cross-species transmission.

sciforum-138353: Emerging Technologies for Virus Detection in Livestock: From CRISPR-Based Diagnostics to Portable Genomic Sequencing

Muhammad Usman, Muhammad Nasir Bhaya *, Riffat Maqsood, Muhammad Imran

Department of Pathology, Faculty of Veterinary Science, University of Agriculture, Faisalabad-38040, Pakistan

Abstract

Introduction: The emergence and re-emergence of viral pathogens in livestock pose a significant threat to global food security and public health. The use of some molecular diagnostic techniques, such as ELISA and PCR, in the detection of viral nucleic acid is limited due to lack of efficiency, adaptability, and scalability.

Methods: Recent technological advances in CRISPR-based diagnostics, particularly CRISPR-Cas12 and Cas13 systems, have proven to be rapid, sensitive, and portable techniques for the detection of viral pathogens, especially when integrated with lateral flow assays or fluorescent readouts. Furthermore, some other CRISPR-based diagnostic tools like SHERLOCK and DETECTR have been proven effective in the detection of various viruses like African swine fever virus (ASFV), foot-and-mouth disease virus (FMDV), and avian influenza viruses in livestock. The combined use of CRISPR-based diagnostic tools with portable genome sequencing approaches enables rapid detection and detailed genomic insight within a few hours in the field. Portable genomic sequencing technologies, such as Oxford Nanopore Technologies' MinION, have been effectively used in the surveillance of peste des petits ruminant virus (PPRV) and bovine viral diarrhea virus (BVDV) in the field without any laboratory.

Results: Additionally, diagnostic approaches are shifting toward digital and decentralized diagnostics by integrating CRISPR with smartphone-based readers, AI-driven analysis tools, and cloud-linked biosurveillance platforms to enhance diagnostic throughput and usability.

Conclusions: Despite the intense revolution, the diagnosis of the virus is still challenged by ensuring regulatory validation, maintaining assay specificity in complex field samples, and reducing production costs for large-scale deployment. This review emphasizes the current trends of emerging diagnostic technologies for detecting viral diseases in livestock by analyzing their advantages, limitations, and integration potential in veterinary health systems.

sciforum-147738: Establishment of a Recombinant Vero Cell Line Expressing Canine SLAM Receptor for Efficient Canine Distemper Virus Propagation

Serkan Kökkaya [1,*], Ayşe Gençay Göksu [2], Muhammed Arif Toy [3], İbrahim Sözdutmaz [2] and Gamze Kandefer [4]

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Canine distemper virus (CDV), a highly contagious morbillivirus, continues to pose a major threat to domestic and wild carnivores worldwide. Efficient isolation of field strains is often limited by the lack of viral entry receptors in conventional cell culture systems such as Vero cells. To overcome this limitation, we established a recombinant Vero cell line stably expressing the canine signaling lymphocyte activation molecule (SLAM/CD150) receptor, the primary lymphoid entry receptor for CDV. The canine SLAM gene was amplified from peripheral blood mononuclear cells, cloned into the pTargeT mammalian expression vector, and transfected into Vero cells. SLAM expression was confirmed at the molecular level by PCR and further validated functionally using a Turkish field isolate (CDV-34388). Infected Vero-DogSLAM cells exhibited pronounced cytopathic effects (CPE), including extensive syncytium formation, while control Vero cells showed no evidence of CDV infection or detectable CPE. Importantly, immunofluorescence microscopy using anti-CDV polyclonal antibodies demonstrated specific intracellular viral antigen localization, providing protein-level confirmation of CDV entry and replication in SLAM-expressing cells. These findings demonstrate that the Vero-DogSLAM cell line markedly enhances the susceptibility of Vero cells to CDV infection, ensuring earlier detection of CPE and stable virus propagation for at least five passages. This recombinant system offers a robust platform for the isolation of field strains, diagnostic assay development, and potential vaccine research. Incorporation of immunofluorescence validation further strengthens its utility by providing visual evidence of virus–receptor interaction. In conclusion, engineering Vero cells to express canine SLAM significantly improves CDV isolation efficiency and provides an essential tool for advancing research in veterinary virology and immunodiagnostics.

sciforum-147640: Identification and Detection of Novel Animal Viruses: A Genome-First Surveillance and CRISPR Diagnostic Workflow

Muhammad Shahbaz Gul *, Alameen Mohammad Ibrahim Alnogomi

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Emerging animal viruses threaten livestock and human health, yet many circulate undetected because most diagnostics target known agents. We evaluated an end-to-end workflow for rapid identification and field-ready detection of novel animal viruses by conducting cross-sectional surveillance at 18 livestock-wildlife-peri-domestic sites. Oropharyngeal, rectal, and serum samples (n=1,964) underwent metatranscriptomic sequencing (Illumina/Nanopore) and pan-viral consensus PCR, with read quality control, host depletion, and taxonomic assignment using k-mer based classifiers, de novo assembly, and protein-level homology searches. Novelty was defined as 90% amino acid identity in conserved proteins; relationships and divergence were inferred with maximum-likelihood and relaxed-clock phylogenies. For priority clades, we designed CRISPR-Cas12 and SYBR qPCR assays and assessed analytical sensitivity, cross-reactivity, and blinded diagnostic performance. We detected sequences from 312 viral taxa across 24 families; 27 lineages met novelty criteria. Ten near-complete genomes were recovered (median coverage 47x). Newly identified paramyxoviruses clustered within Orthorubulavirus (fruit bats), and two coronaviruses formed distinct subclades within Alphacoronavirus. CRISPR assays for four representatives achieved limits of detection of 10–100 copies per uL with no cross-reactivity to 42 heterologous viruses; in blinded panels, sensitivity was 93–97% and specificity 98–100% (AUC 0.96). These findings show that a genome-first surveillance pipeline coupled to rapidly deployable CRISPR diagnostics can reveal and confirm previously unrecognized animal viruses with high accuracy; integration into routine One Health monitoring could accelerate risk assessment, guide targeted mitigation, and narrow the window between viral emergence and detection.

sciforum-148093: Identification of rotavirus and concurrent enteropathogens in foals from Mexico

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Equine rotavirus is the second leading cause of diarrhoea in foals under six months of age worldwide. This viral agent causes clinical alterations and lesions that compromise the immune system, facilitating colonisation by secondary bacterial enteropathogens. These agents are associated with deformities, digestive syndromes, endotoxemia, sepsis and, in severe cases, death, resulting in significant economic losses and limiting population growth in the equine industry. Despite its clinical relevance, there are few reports on the presence of concomitant pathogens in cases of diarrhoea associated with equine rotavirus, as well as on the clinical presentation when two or more enteropathogens coexist in the same animal.

The objective of this study was to identify the presence of rotavirus and concurrent bacterial enteropathogens, describe and compare the clinical signs associated with each individual agent and in co-infection, and evaluate bacterial resistance profiles. To this end, samples were collected from sick, deceased, and healthy foals on ranches in central Mexico. A detailed medical history was taken for each specimen to gather clinical and background information, and molecular, bacteriological, parasitological, and pathological diagnostic tools were used to confirm the presence of aetiological agents.

A total of 33 samples were analysed, of which 11 tested positive for rotavirus. In each of these cases, at least three different bacterial species were isolated concomitantly, all with profiles of multi-resistance to antibiotics commonly used in equine practice.

In conclusion, the use of complementary tests revealed the circulation of pathogens that are rarely reported or have no previous records, whose impact transcends animal health by generating economic losses in the productive stage of the equine sector and representing a potential risk to public health due to their zoonotic capacity. These findings highlight the need to strengthen preventive medicine, especially vaccination, and to apply more specific and effective treatments against co-infections.

sciforum-142609: Known and novel nairoviruses in ticks (order Ixoidea) collected from Danish wild and domestic animals

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Introduction: Climate change is perturbing ecological niches, contributing to animal distribution shifts. Disease vectors, like ticks, are expanding their habitat, contributing to arbovirus spread to new locations and hosts. It is, therefore, important to monitor arboviruses and identify them before they become a problem. *Orthonairovirus* (*Nairoviridae*) comprises significant tick-borne RNA viral pathogens (e.g., Crimean-Congo hemorrhagic fever andNairobi sheep disease viruses). Since orthonairovirus ecology is understudied, we investigated these viruses among ticks from Denmark, a previously unexplored territory for nairoviruses.

Methods: Viruses were detected using a pan-orthonairovirus hemi-nested RT-PCR (primers available on request), amplifying a conserved region (347bp) of the RNA-dependent RNA polymerase (RdRp) gene using RNA from 20 pools of ticks (n=228, mostly *Ixodes ricinus*) collected from Danish animals or the environment. Positives were Sanger sequenced, Blast was used to identify the closest relatives of the detected viruses, *Nairoviridae*-wide maximum-likelihood phylogenetic analysis was performed with partial RdRp protein alignments.

Results: Five samples were positive. A pool of ticks from European bison (n=45) and wild birds (n=16) contained a close relative (96.3-97.3% nt identity) of a Latvian Sulina virus (*Orthonairovirus sulinaense*) identified in *Ixodes ricinus*. Two pools of ticks from ungulates (horse, n=20; roe deer, n=15) contained viruses similar to members of *Norwavirus grotenhoutense*, previously identified in *Ixodes ricinus* across Europe (96.3- 98.6% nt identity). Finally, 2 pools of ticks from wild mink (n=39) contained a novel virus, whose closest relative was an unclassified virus from Spanish *Ixodes simplex* (nt=77.0%, aa=90.3%). Phylogenetic analysis placed it on a long branch in a clade with norwaviruses.

Conclusions: The method succeeded in identifying two genera of nairoviruses, discovering a probable new virus genus. Our results highlight that several nairoviruses circulate in Denmark, with more viruses likely awaiting discovery. Further analyses are required to fully characterize the identified viruses and assess their host tropism among vertebrates.

Session B. Development and Optimization of Animal Vaccines

sciforum-142884: Safety assessment of Rift Valley fever vaccine candidate 40Fp8 reassortants rescued by reverse genetics

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Rift Valley fever virus (RVFV; Genus Phlebovirus, Family Phenuiviridae, Order Hareavirales) is a mosquito-borne arbovirus that affects ruminants and humans. RVFV genome consists of three single-stranded, negative-sense RNA segments: S (Small), M (Medium) and L (Large). The lack of a licensed vaccine with an optimal safety profile remains a major challenge for disease control. Previously, we generated an attenuated RVFV variant, 40Fp8, through random mutagenesis of the virulent South African strain 56/74. This variant showed a hyper-attenuated phenotype and an optimal safety profile in both mice and pregnant sheep, making it a strong candidate for a live attenuated vaccine (LAV). However, LAVs may pose risks in nature due to potential reversion to virulence and/or reassortment events in the case of segmented viruses. In this study, we analyzed the contribution of each 40Fp8 genomic segment to attenuation using a reverse genetics system. Recombinant viruses were generated by replacing one genomic segment of 56/74 with the corresponding segment from 40Fp8. In vitro, viruses carrying the 40Fp8 M segment displayed a small-plaque phenotype and higher replication kinetics like 40Fp8, whereas those with the 40Fp8 S or L segments behaved like parental 56/74 strain. In vivo, sex-dependent differences were observed, with male mice more susceptible than females, likely due to hormonal, immunological, and genetic host factors. Notably, the virus carrying the 40Fp8 S segment conferred complete protection in both sexes and at all tested doses. Our data indicate that the 40Fp8 S segment is the primary determinant of attenuation, followed by the M and L segments, which provided partial protection, suggesting that coinfection events of circulating virulent RVFVs with 40Fp8 would likely preserve an attenuated phenotype, and supporting the notion that the use of the 40Fp8 as a LAV would carry minimal risk in the event of reassortment in nature.

sciforum-121523: A M. bovis-BoHV-1 Combined Vaccine Confers Protection Against Diverse Bovine Herpesvirus Type 1 Strains

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Mycoplasma bovis (*M. bovis*) and bovine herpesvirus 1 (BoHV-1) are two major infections that seriously impair cattle's reproductive and respiratory systems. We created a *M. bovis*-BoHV-1 combined vaccine and assessed its safety and effectiveness in our earlier work. This study evaluated a novel combined vaccine comprising attenuated *M. bovis* and marker BoHV-1 antigens for its immunogenicity and efficacy in protecting cattle against diverse BoHV-1 genotypes. The cattle were divided into four groups: *M. bovis*-BoHV-1 combined vaccine, inactivated vaccine, non-immune challenge and blank control groups. The results demonstrated that the combined vaccine group prompted a high degree of production of cytokines, B cells, and T cell-associated signaling pathways and was able to elicit considerably greater antibody titers (p 0.01). Subsequently, RT-PCR was used to assess viral shedding after the groups challenged with either the BoHV-1 1.1a or 1.2b strains. Under experimental challenge conditions, the combined vaccine reduced BoHV-1 viral shedding by 70% in vaccinated cattle compared to controls, shorter duration of virus shedding was also observed in the vaccinated groups compared to the non-immune challenge group for different BoHV-1 strain challenges, about 6-8 day earlier clearance of virus shedding compared to the non-immune challenge group. Notably, the combined vaccine provided cross-protection against multiple BoHV-1 genotypes, demonstrating its potential as a broad-spectrum solution for controlling bovine respiratory disease. These findings providing important insights into effective disease control strategies for cattle herds.

sciforum-140247: Assessment of a Live Attenuated African Swine Fever Vaccine Produced in a Stable Cell Line: Immunogenicity and Protective Potential in Wild Boar

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Introduction

African Swine Fever (ASF) is a severe, highly contagious hemorrhagic disease affecting both domestic pigs and wild boar, causing major losses to animal health and the global swine industry. Since its spread across Europe (2007), Asia (2018), and the Americas (2021), the need for effective control measures has become critical. Although live attenuated vaccines have shown potential, their production depends on primary cell cultures, which limits scalability and standardization.

Methods

This study evaluated the in vivo efficacy and safety of the attenuated ASFV strain Lv17/WB/Rie1-ΔCD after its adaptation to the stable MA104 cell line. Eighteen wild boar piglets were orally vaccinated on days 0 and 21 and challenged on day 37 with the virulent Armenia 2007 strain. Clinical signs, rectal temperature, immune response, and viremia levels were monitored over a 62-day period.

Results

Oral vaccination with the adapted strain led to partial clinical protection. Vaccinated wild boar exhibited a delay in the viremia onset and a reduction in the severity of fever compared to controls. Clinical scores were lower in the vaccinated group. Additionally, viremia levels post-challenge were significantly reduced in vaccinated animals, and viral genome detection was delayed, suggesting a containment effect. However, the proportion of protected animals (i.e., surviving without severe clinical signs) was lower than that reported in previous studies using the same vaccine propagated in primary cells. Seroconversion was inconsistent, and overall antibody titters were lower, indicating a weaker humoral response. These findings point toward a potential loss of immunogenicity following adaptation to the stable cell line.

Conclusions

Adapting ASFV to a stable cell line marks progress toward scalable vaccine production. Nevertheless, these results underscore the need to optimize adaptation protocols to maintain vaccine efficacy and immunogenicity. Further refinement will be essential to achieve protection levels comparable to vaccines derived from primary cell cultures.

sciforum-128727: Bivalent protection against BTV in sheep by combination of MVA viral vectors expressing proteins VP2 of BTV-4 and BTV-8

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Bluetongue virus (BTV) is an important viral pathogen listed as a notifiable disease by the World Organization for Animal Health (WOAH). BTV, which is transmitted by biting midges of the genus *Culicoides*, affects a wide range of wild and domestic ruminants, causing a significant impact on the local, regional and global primary sector. To date, more than 29 different BTV serotypes exist, hindering control and prevention of Bluetongue (BT) disease. Currently, vaccination with live attenuated vaccines and inactivated vaccines is the main countermeasure for control of these pathogens. However, classical vaccination approaches against BTV have several drawbacks related to vaccine safety and efficacy but also to their inability to confer multiserotype protection and to differentiate between vaccinated and infected animals (DIVA strategy). Here, we developed recombinant MVA viral vectors expressing the BTV VP2 proteins of serotypes 4 and 8. After characterizing this recombinant MVAs, we evaluated their immunogenicity and protective efficacy in BTV-susceptible IFNAR(-/-) mice and sheep. Immunization of IFNAR(-/-) mice with both rMVA expressing either BTV-4 VP2 or BTV-8 VP2 elicited a strong neutralizing immune response that conferred complete protection against lethal challenge with BTV-4 and BTV-8. In sheep, combinatorial prime-boost immunization with both rMVAs induced high titers of neutralizing antibodies against both homologous BTV serotypes. Importantly, immunized sheep were fully protected against BTV-4, as no fever, viraemia or RNAemia could be observed after challenge. Similarly, sheep immunized with both recombinant MVAs displayed a high degree of protection against BTV-8 although detectable but mild RNAemia and slight increase in rectal temperatures were observed after challenge. Overall, we present a DIVA vaccination strategy that confers a high degree of protection against BTV-4 and BTV-8 in natural hosts of the disease. Further experiments will explore the unlikely protective capacity against heterologous serotypes.

sciforum-142437: Development and Characterization of Novel Swine Influenza Virus-Like Particles (VLPs)

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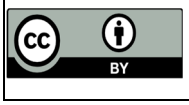
Swine influenza (SI) is an acute infectious disease of pigs caused by *Swine influenza virus* (SIV). To develop virus-like particles (VLPs) of SIV H1 and H3 subtype and determine their morphological structure and biological characteristics, this study synthesized a gene encoding lumazine synthase (LS) derived from a hyperthermophilic bacterium and introduced an immunoglobulin-binding domain sequence from streptococcal protein G (pG) to construct the pG-LS recombinant plasmid. The plasmid was then expressed in both prokaryotic and eukaryotic systems.After the conjugation of the 2 proteins, the morphology and the formation of VLP could be observed by transmission electron microscopy. Average particle diameters of the conjugated proteins were measured with dynamic light scattering method while the biological properties of the complex protein were analyzed by SDSPAGE, Western blot and hemagglutination assay. Both expression methods successfully yielded pG-LS nanoparticles, with eukaryotic expression demonstrating higher purity. The complexes formed between the two HA-Fc proteins and eukaryotic-expressed pG-LS nanoparticles exhibited a spherical morphology with an average diameter of approximately 80 nm.Further immunological analysis and particle diameter measurement both showed the successful construction of VLPs. Hemagglutination assays indicated HA-Fc alone could not agglutinate erythrocytes, while the virus-like particles prepared from 2 conjugated proteins showed exponential affinity, which could efficiently agglutinate red blood cells of different species. This study successfully constructed pG-LS nanoparticles and 2 pG-LS-HA VLPs, where HA proteins successfully displayed at the VLP surface. Both developed pG-LS-HA had stable property and biological function, with a potential of large-scale production. In the meantime, this study found that both H1 and H3 HA could be effectively displayed to form VLP, which shed light on the future use of multi-subtype influenza virus HA protein co-presentation strategy to develop novel, multivalent VLP vaccine candidates.



sciforum-142809: Dissecting ASFV Immune Responses: Insights from Hemadsorption Inhibition and Wild Boar Vaccination Studies

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African swine fever (ASF) is a highly lethal transboundary disease that severely impacts the swine industry. Because of the complexity of the ASF virus (ASFV), vaccine development remains challenging, highlighting the need to robustly evaluate immune responses induced by vaccine candidates and their efficacy against different viral strains. This study evaluates the utility of the hemadsorption inhibition assay (iHAD) as an *in vitro* method to evaluate ASFV specific immune responses, and compares its results with *in vivo* protection outcomes.

Serum samples were selected from wild boars involved in two separate *in vivo* immunization trials against the genotype II isolate Arm07. In the first trial, animals were immunized with the naturally attenuated and non-hemadsorbing strain Lv17/WB/Rie1 (Rie1), followed by a challenge with the heterologous strain Ken06.bus. In the second trial, animals were immunized with the gene-deleted vaccine candidate Lv17/WB/Rie1ΔAB (dAB). In both trials, vaccinees exhibited high protection levels against Arm07, and selected sera demonstrated high ASFV-specific antibody titers. The inhibitory activity of these sera was tested by iHAD against homologous isolates (Arm07, Rie1, dAB) and heterologous isolates (Ken06.bus, Esp70, Ken07).

90% of the animals were protected *in vivo* against Arm07, while 30% of the sera exhibited *in vitro* iHAD. For the heterologous strain Ken06.bus, 30% of the animals showed *in vivo* protection, whereas 80% of the sera demonstrated *in vitro* inhibitory activity. Sera from animals previously immunized with genotype II vaccine strains inhibited hemadsorption by the virulent strains Arm07, Ken06.bus, and the moderately virulent strain Esp70.

The iHAD correlates with the inhibitory capacity of sera from vaccinated animals but cannot be considered a definitive marker of vaccine efficacy for Rie1 and dAB strains. The *in vitro* results suggest the existence of complete or partial cross-protection among phylogenetically distinct ASFV strains, including Arm07, Ken06.bus, and Esp70.

sciforum-142929: Effective Induction of Cellular Immunity in Piglets Using a Single-Dose Bivalent Vaccine Against CSFV and PCV2

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Porcine circovirus type 2 (PCV2) compromises the immune system in pigs, increasing their susceptibility to co-infections of other pathogens. Classical swine fever virus (CSFV) is one of those diseases and is listed as a highly contagious disease by the World Organization for Animal Health (WOAH). Effective vaccination is one of the effective strategies to prevent diseases and requires stimulation of T helper cell-mediated immune responses to enhance the effectiveness of vaccines. We developed a bivalent subunit vaccine containing PCV2 ORF2 and CSFV E2 antigens, formulated with a porcine-specific CpG adjuvant. Those specific pathogen-free piglets were immunized with only a single dose and challenged with virulent strains of PCV2 or CSFV four weeks post-vaccination. Vaccinated piglets had significantly higher neutralizing and ELISA antibody titers against both viruses. Improved cellular immunity is demonstrated by increasing percentages of $CD3^+CD4^+CD8^+$ T cells and significantly upregulated mRNA expression of IL-2, IFN-α, and IFN-γ in peripheral blood mononuclear cells in vaccinated pigs after a challenge. No clinical signs or lesions were observed in vaccinated pigs, and viral loads in serum and tissues were markedly reduced or undetectable. In conclusion, a single dose of the PCV2/CSFV bivalent subunit vaccine induces both robust humoral and cellular immune responses, offering strong protection against infection. These findings highlight its potential as a practical and effective strategy for swine disease control.

sciforum-141753: MVA-NS1 vaccine candidate confers protection in IFNAR (-/-) mice against a homologous challenge with EHDV-8

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Epizootic hemorrhagic disease (EHD) is an important disease that severely affects wild and domestic ruminants, and causes substantial economic losses in the livestock industry. The etiological agent, epizootic hemorrhagic disease virus (EHDV), is an arbovirus of the genus *Orbivirus*. The virus is transmitted through the biting of infected *Culicoides* midges to susceptible hosts. EHDV has a worldwide distribution and recently, it has expanded to Europe from 2022. To date, seven different EHDV serotypes have been described and no effective DIVA (Differentiating Infected from Vaccinated Animals) vaccines against EHDV are available. The aim of our research is to explore vaccine candidates expressing a single EHDV antigen to develop an efficient, marker and safe vaccine candidate. Recombinant Modified Vaccinia Ankara virus (MVA) viral vector vaccines are effective, safe and DIVA-compatible candidates against EHDV. In this study, we designed and generated novel vaccine candidates against EHDV based on recombinant MVAs that express the non-structural protein NS1 from EHDV serotype 8. The potential vaccine was evaluated in IFNAR (-/-) mice, which are susceptible to EHDV infection and reproduce certain features of EHDV infection in natural hosts. IFNAR (-/-) mice were immunized with two doses of MVA-NS1 and subsequently challenged with EHDV-8 or EHDV-6. Immunized mice did not show viremia or clinical signs after EHDV-8 challenge, and showed reduced RNAemia titers against the virus. Therefore, vaccinated mice were completely protected against a homologous challenge with EHDV-8 after two doses of the vaccine candidate. MVA-NS1 did not confer complete protection against a heterologous challenge with EHDV-6, although it delayed the onset of clinical signs and death. These data shows that MVA-NS1 vaccine candidate is safe and efficient against a homologous challenge and compatible with a DIVA strategy.

Session C. Veterinary Epidemiology

sciforum-146987: Sarcoptic Mange in a Crab-eating fox (*Cerdocyon thous*) roadkill on BR-135 road in Bahia, Brazil – A Case Report

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Sarcoptic mange in wild canids poses important challenges for both species conservation and public health, primarily due to the risk of cross-species transmission, including to humans. *Cerdocyon thous* is widely distributed across Brazil, except for the Amazon lowlands. This species occupies a range of habitats, including forests, savannas, grasslands, and areas altered by human activity, such as agricultural lands, pastures, and regenerating zones. Despite its broad distribution, there is limited documentation of sarcoptic mange in wild canid roadkill specimens, particularly involving *Cerdocyon thous* in Brazil. This case report describes the findings from an adult male *Cerdocyon thous* specimen found dead during a roadkill monitoring campaign. Upon examination of the carcass, extensive skin lesions were observed, primarily on the face, ears, and extremities. These lesions were characterized by areas of hair loss, dandruff, and crust formation. Skin samples from the affected regions were carefully collected, preserved in a container with 70% alcohol, and submitted to the Veterinary Parasitology Laboratory at PUC-PR (Pontifical Catholic University of Paraná) for analysis. Microscopic examination confirmed the presence of Sarcoptes scabiei, with both eggs and adult mites identified. Notably, live mites were still present on the carcass, underscoring the zoonotic potential of sarcoptic mange and the risk of transmission to other mammals, including domestic animals, wildlife, and humans. This also highlights its potential impact on species conservation. These findings emphasize the importance of enhanced epidemiological surveillance, environmental education, and integrated One Health strategies to monitor and mitigate the spread of sarcoptic mange in wildlife populations.

sciforum-140614: Parasitic Monogeneans in Chrysichthys nigrodigitatus in the Bagré River, Burkina Faso: Diversity, Infestation Factors and Impact on Fish Health

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Background: Chrysichthys nigrodigitatus is a catfish of great economic value, abundantly exploited in the artisanal fisheries of Burkina Faso. Despite its importance, few studies have been devoted to the parasites that affect it, in particular monogenes, which are known to impact fish health and compromise aquaculture productivity. The objective of this study is to identify the monogeneans present in this species and to evaluate the factors influencing their infestation, from a sustainability and food security perspective. Methods: This study was conducted from February 2021 to July 2022 in the Bagré River, covering a period of 18 months during which samples of C. nigrodigitatus were collected and their gills analyzed in the laboratory according to morphological criteria. Data were examined in terms of size, sex of fish, distribution of parasites on the gills, as well as seasonal variations. Results: Three species of Monogenes of the genus Protoancylodiscoides were identified for the first time in Burkina Faso: P. spirovagina (the most dominant), P. valentini and P. sanagaensis, all specific to C. nigrodigitatus. Infestation is correlated with fish size, with males being more exposed to P. sanagaensis, and more frequent during the rainy season. Conclusion and outlook: These results call for increased monitoring in aquaculture. Research extended to other areas and species is needed to better understand the diversity and distribution of Monogeneans and support sustainable fish farming.

sciforum-142628: Characterization of BTV-3 (SPA/2024) transmission in mammalian and insect cells and in the IFNAR(-/-) mouse model.

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Bluetongue, caused by bluetongue virus (BTV), is a widespread arthropod-borne disease of livestock that entails a recurrent threat to the agricultural primary sector. In 2023, serotype BTV-3 emerged in the Netherlands and spread rapidly to neighboring countries including Spain. This new strain of BTV-3 courses with more severe clinical signs and faster spread of the virus than other serotypes that caused outbreaks in Europe. To better understand these aspects of the new BTV-3 strain, we have analyzed viral replication of BTV-3 (SPA/2024), BTV-4 (MOR/2009) and BTV-8 (BEL/2006) in mammalian (Vero and BSR) and insect (KC) cells. Growth kinetics showed significant differences in viral titers at 48 and 72 hpi in BSR and Vero cells, with higher viral titers in the supernatants of cells infected with BTV-3 than in those infected with BTV-4 or BTV-8. At 72 hpi, a greater cytopathic effect and a decrease in BTV-3 viral RNA in Vero cells were observed. In contrast, no significant differences were observed at other timepoints and in BSR cells. Interestingly, neither viral titers nor viral RNA showed significant differences among serotypes in KC cells.

In addition, BTV-3 virulence was analyzed *in vivo* in the IFNAR(-/-) mouse model. Mice infected with 10 PFU of virus developed clinical signs, RNAemia and viraemia between days 5 and 7 post-infection and all the animals died between days 7 and 10. For other BTV serotypes analyzed, lethal doses were established at 10^2 PFU for BTV-1 (ALG/2006) and BTV-8 (BEL/2006) and $5x10^2$ PFU for BTV-4 (SPA/2005), indicating that this BTV-3 (SPA/2024) is also more virulent in the mouse model than other serotypes of BTV, as observed in the natural host.

These data suggest that BTV-3 presents greater transmissibility and virulence than other BTV serotypes in the mammalian host, but these dynamics are not altered in the vector cells.

sciforum-145950: Generation and characterization of replication-competent rBTV-3 expressing fluorescent and luminescent reporter genes using a reverse genetics system

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Bluetongue virus (BTV) is a widespread vector-borne pathogen of major concern for animal health, mainly affecting both wild and domestic ruminants. This virus stands out for its ability to cause significant disease and its impact on livestock production. In 2023, BTV serotype 3 was detected in the Netherlands and spread rapidly to neighbouring countries. Compared to other serotypes circulating in Europe, BTV-3 shows greater virulence and transmissibility. The aim of this study is the design and rescue of reporter-expressing BTV-3 viruses using a BTV-1 (ALG2006/01) genetic backbone and the VP2 and VP5 outer capsid proteins from BTV-3 (SPA/2024). Using a plasmid-based reverse genetic system, we have designed and rescued rBTV-3 reporter-expressing viruses encoding NanoLuc luciferase (Nluc) or the fluorescent proteins Venus and mCherry. Rescue was achieved by transfecting BSR-T7 cells with plasmids encoding BTV genome segments. The reporter-expressing viruses were generated by chaining segment 5, which encodes the NS1 protein, with a Porcine teschovirus-1 (PTV-1) 2A autoproteolytic cleavage site, followed by the reporter genes. Consequently, fluorescence and luminescence signals are only detected following viral replication and expression of non-structural proteins. BSR cells were mock-infected or infected (MOI 0.1) with rBTV-3, rBTV-3/Venus, rBTV-3/mCherry or rBTV-3/Nluc. Fluorescence was detected in the cytoplasm of the cells infected with rBTV-3/Venus or rBTV-3/mCherry but not in those infected with rBTV-3 or rBTV-3/Nluc. Moreover, Nluc activity was only detected in rBTV-3/Nluc infected cells. The use of replication-competent viruses that encode a traceable fluorescent or luciferase reporter protein may be promising tools for studying BTV infectivity, transmissibility, pathogenesis, diagnostics, and vector competence.

sciforum-141628: Prevalence and characterization of hydatid cysts in sheep slaughtered at Korçë, AlbaniaPrevalence and characterization of hydatid cysts in sheep slaughtered at Korçë, Albania

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Cystic echinococcosis (CE) is a chronic parasitic disease caused by the larval stage of Echinococcus granulosus. It is considered a major zoonotic concern globally, particularly in regions where livestock such as sheep are raised in close contact with dogs, the definitive hosts of the parasite. In Albania, CE remains endemic, affecting both humans and domestic animals. The current study was conducted in the Korça region in southeastern Albania, with the aim of determining the prevalence, distribution, and characteristics of hydatid cysts in sheep slaughtered at local abattoirs. Between January and December 2024, a total of 1,072 sheep were inspected post-mortem. Organs including the lungs and liver were examined for the presence of hydatid cysts, and infected tissues underwent both macroscopic and histological evaluation. Hydatid cysts were detected in 19.8% (n = 213) of the animals. Pulmonary involvement was slightly more common (53.5%) than hepatic (46.5%). Among the identified cysts, 71% were fertile, 26.7% sterile, and 2.3% calcified. Histomorphological analysis revealed significant fibrotic and inflammatory changes in affected organs, with more advanced lesions seen in older sheep. The presence of collagen fibers surrounding the cysts was confirmed using Masson's trichrome staining. These findings provide valuable insight into the epidemiological burden of hydatidosis in southeastern Albania. Understanding the distribution and fertility of cysts is essential for evaluating the risk of transmission and for designing effective control strategies aimed at limiting the spread of this zoonosis among both livestock and human populations.

sciforum-138869: Serological and molecular evidence of canine enteric coronavirus in Campania region (Italy)

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Canine enteric coronavirus (CeCoV) is one of the most prevalent viruses in dogs, resulting in gastrointestinal signs and, in severe cases, death. Despite being a major disease, study on its spread remains limited, particularly in some geographical areas, such as the Campania region (southern Italy). This study investigated the CECoV serological and molecular occurrence, as well as the risk factors related to increased exposures. A total of 258 blood and 154 fecal samples were obtained from dogs in 71 districts, accompanied by information such as sex, breed, size, location, age, origin, lifestyle, and attitude. The serological and molecular prevalences were obtained using a commercial ELISA (also useful for evaluating the antibody titer) and a previously described real-time PCR protocol, respectively. More than half of the dogs investigated (53.9%) had been exposed to the pathogen, while only 5.8% tested positive in real-time PCR. Among the animals that tested seropositive, 57 had a titer of 1:50, 36 of 1:100, and 46 of 1:200. Univariate and multivariate studies found that hunting dogs and dogs with outdoor lifestyles had greater seroprevalence. Sex, age, breed, origin, and size were not associated with higher seroprevalences. Furthermore, dogs in some areas exhibited seroprevalences of up to 85%. The same area (Avellino and Salerno) included most of the PCR-positive animals. Among these 9 animals, only 2 were seronegative when tested by ELISA, another 5 had a titer of 1:50 and 2 of 1:200. Furthermore, 8 out of 9 animals were hunting dogs or strays, only one was a pet dog, and 7/9 lived outdoors. The study's findings highlighted the extensive prevalence of CECoV in the examined area, as well as the presence of ongoing outbreaks in many districts. More efforts are needed to offer useful epidemiological surveillance for this important canine disease, as well as to detect mutations and to anticipate possible changes in its epidemiological cycle.

sciforum-146904: Case Report on Canine Parvoviral Enteritis of *Mixed-Breed dog*

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This report describes the case of a Mixed-breed dog brought to the teaching Veterinary Clinical Complex of the College of Veterinary Science & Animal Husbandry, Jabalpur, Madhya Pradesh. Based on clinical signs, a canine parvovirus type 2 (CPV-2) infection was diagnosed. A rectal swab sample was collected and the clinical diagnosis was confirmed by the positive results obtained by a commercially available rapid antigen testing kit (Ubio QuickVet CPV antigen testing kit. The prognosis of this disease depends on the virulence of the virus strain as well as the response of the organism to the treatment. However, it is also important that the treatment is started as soon as possible, because without it, the prognosis could be fatal. The necessary Antibiotic, Anti-diarrheal, Antacid, Anti-emetic, Vitamin B & C and fluids for restoring the fluid lost and the electrolyte imbalance, were administered in proper dosages according to the level of dehydration and body weight of the dog. The treatment regimen was continued for 6 days, and the pet owner was instructed not to give food and water for 6 days and the prognosis of dog was satisfactory. After six days of intensive supportive therapy, the dog showed marked clinical improvement with cessation of vomiting and hemorrhagic diarrhea. Hydration status, mucous membrane color, and appetite gradually normalized. The overall prognosis was satisfactory with complete recovery observed.

sciforum-132138: Cutaneous Papillomaviruses in Cervids: A Hidden Threat to Wildlife Health and Conservation

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Cutaneous papillomaviruses (PVs) are small, non-enveloped DNA viruses with strict host specificity and the capacity to induce proliferative epithelial lesions in a wide range of vertebrates. In wild cervids—including red deer (Cervus elaphus), moose (Alces alces), roe deer (Capreolus capreolus), white-tailed deer (Odocoileus virginianus), and reindeer (Rangifer tarandus)—multiple species-specific PVs have been identified, including CePV1, AaPV1, CcaPV1, OvPV1, and RtPV1. These viruses typically cause papillomas and fibro papillomas on the skin and mucous membranes, presenting as rough, verrucous, and sometimes ulcerated lesions. Although often benign, PV-induced lesions can compromise animal welfare by affecting feeding, vision, mobility, or mating behaviours. In high-prevalence populations, especially among juveniles and immunocompromised individuals, these infections may have broader population-level impacts. Histopathological findings typically include epidermal hyperplasia, koilocytosis, and papillomatosis, with replication confined to keratinocytes. Transmission occurs via direct contact, microtraumas, and potentially through hematophagous ectoparasites. From a conservation perspective, PV infections in cervids are significant for several reasons. First, lesions may reduce individual fitness and contribute to population stress, particularly in fragmented or vulnerable populations. Second, the presence of papillomaviruses in cervid species cohabiting with livestock or other wildlife raises concerns about cross-species transmission, including spillover from bovine PVs. Third, these lesions may be misidentified as more serious conditions (e.g., sarcoids or neoplasia), complicating health assessments in the field. With cervids playing crucial ecological roles and serving as sentinel species in many ecosystems, understanding PV diversity, transmission dynamics, and pathology is essential for wildlife health monitoring and conservation planning. Ongoing molecular surveillance, pathology, and ecological studies are critical to assess the true burden of PV infections and to support evidence-based conservation medicine practices

sciforum-145990: Development of a Quantitative Structure–Retention Relationship (QSRR) Model for Predicting Veterinary Drug Retention Time in Food Matrices

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Quantitative structure–retention relationships (QSRR) offer a powerful approach to predict chromatographic retention times of compounds based on their molecular structures. In this study, we developed a practical and user-friendly QSRR model using multiple linear regression (MLR) to forecast the retention behavior of three classes of illicit veterinary drug additives in food matrices. A total of 95 drugs were analyzed, divided into a training set (62 compounds), a test set (30 compounds), and a real-sample validation set (3 compounds). Molecular descriptors were generated using freely available software tools, including Advanced Chemistry Development (ACD) and the Toxicity Estimation Software Tool (TEST).

The final MLR-QSRR model demonstrated excellent predictive performance, with a strong correlation between observed retention times and selected molecular descriptors (R^2 = 0.966). Key descriptors influencing retention time included ACDlogP, ALOGP, ALOGP2, Hy, Ui, ib, BEHp1, BEHp2, GATS1m, and GATS2m. Validation through four independent approaches—leave-one-out, k-fold cross-validation, external test set, and real-sample application—confirmed the robustness and reliability of the model.

These findings highlight the potential of QSRR modeling as a valuable analytical tool in food safety, particularly for detecting and monitoring illegal veterinary drug residues. By enabling accurate retention time prediction, this approach supports enhanced screening efficiency in chromatographic workflows and contributes to safeguarding public health.

sciforum-142741: Epidemiology and Molecular Identification of Intestinal Parasites of Slaughtered Sheep and Goats in Amosun Abattoir, Ibadan, Southwest Nigeria

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The study determined the epidemiology and molecular identification of intestinal parasites of these domesticated animals slaughtered in Amosun Abattoir, Ibadan, Oyo State, Nigeria in relation to nature of infection, host type, and sex of host. A total of 150 faecal samples were collected and examined for the eggs of the parasites using parasitological examination (sedimentation and microscopy) and molecular identification (PCR amplification and gel electrophoresis). Descriptive analysis was done using SPSS Package and T-test was used to compare the level of parasites of these domesticated animals at p≤0.05. A total of 89 (59.53%) samples were infected with at least one parasite type in goats (49 [32.67%]) and sheep (40 [26.67%]). Fourteen genera of intestinal parasites were encountered, these are: *Strongyloides, Eimeria*, *Haemonchus*, *Trichostongylus, Taenia*, *Ascaris*, *Monezia*, *Oesophagostomum*, *Dircocoelum*, *Nematodius*, *Enterobius*, *Fasciola*, *Trichuris*, and *Giardia* species. Single parasitic infection was 41 (88.89%) in goats while sheep had single infection of 32 (85.71%) and for mixed infection, there was a prevalence of 26 (11.11%) in goats while sheep had 22 (14.29%) parasitic prevalence. The most prevalent parasites in sheep and goats were *Strongyloides, Eimeria*, and *Haemonchus* species. *Strongyloides* had the highest parasite mean intensity in goats (3.76±0.08) and sheep (3.64±0.09), closely followed by *Haemonchus* (goats; 4.00±0.08, sheep; 3.25± 0.08), *Eimeria* (goats; 3.13±0.06, sheep; 4.00± 0.1), while *Giardia (*goats; 3.00±0.06, sheep; 0.00± 0.00), *Nemadius* (goats; 2.00±0.04, sheep; 0.00± 0.00), *Trichuris (*goats; 0.00±0.00, sheep; 2.00± 0.05), *Dircocoelum* (goats; 1.00±0.02, sheep; 0.00± 0.00), and *Enterobius* (goats; 1.00±0.02, sheep; 3.25± 0.08) had least mean intensity occurring in just one of the animal. The mean EPG of host type showed no significant difference p 0.05 (p=0.87) on the intensity between sheep and goats. Using the PCR method, only DNA of *Eimeria arloingi* from goats was amplified. Intestinal parasites encountered in the domesticated animals slaughtered in Amosun Abattoir pose a zoonotic risk to human population living in Ibadan and environs since the place is the source of meat supply.

sciforum-147939: Epidemiology of Gastrointestinal Parasites in Captive Deer Populations of Punjab, Pakistan

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Gastrointestinal parasites are a major health challenge in captive wildlife, reducing survival, reproduction, and conservation value of endangered and vulnerable species. The health and sustainability of captive deer species that are significant to the environment, culture, and economy are compromised by parasitic illnesses. Limited information is available on parasitic prevalence in captive deer species of Pakistan, creating gaps in wildlife health management. In this study, a total of 120 fresh fecal samples were collected from Hog Deer (*Axis porcinus*), Fallow Deer (*Dama dama*), and Blackbuck (*Antilope cervicapra*) housed in zoological gardens of Punjab. Samples were examined using flotation, sedimentation, and McMaster egg-per-gram (EPG) quantification techniques. Identified parasites were categorized, and infection prevalence was analyzed in relation to host factors (species, age, sex) and environmental seasonality. Overall, 65.8% of fecal samples were positive for at least one parasite species. Different parasite taxa were recorded, including protozoa (*Trypanosoma, Babesia*), cestodes (*Moniezia expansa, M. benedeni*), nematodes (*Trichuris globulosa, Strongyloides papillosus, Haemonchus contortus*), and trematodes (*Paramphistomum cervi*). *Trypanosoma spp.* had the highest prevalence (37.5%), followed by *Babesia* (20.0%). Hog Deer exhibited the greatest infection burden (50%), followed by Fallow Deer (26.6%) and Blackbuck (23.3%). Significant correlations between infection prevalence and host-related parameters were found by epidemiological study. Male deer showed a somewhat higher incidence than females, and younger animals were more vulnerable to parasitic diseases. Environmental conditions substantially encourage parasite survival and transmission, as seen by seasonal patterns showing higher parasite burdens during warm and humid months. The study highlights a high prevalence and diversity of gastrointestinal parasites in captive deer populations of Punjab. Findings underscore the need for routine surveillance, targeted deworming, and improved management of captive environments to reduce parasite loads. These measures are critical for safeguarding deer health, preventing cross-transmission to domestic animals, and strengthening wildlife conservation programs in Pakistan.

sciforum-142703: Feasibility of on-farm somatic cell count screening for subclinical mastitis: prevalence and risk factors in a commercial dairy herd in Bangladesh

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Subclinical mastitis (SCM) remains a widespread yet underdiagnosed issue in dairy herds, causing significant economic losses, particularly in low-resource environments with limited early detection tools. Somatic cell count (SCC) is a well-established and cost-effective method for detecting SCM in dairy production systems. This study aimed to estimate the prevalence of SCM and identify associated cow-level risk factors using on-farm SCC screening in a high-producing commercial dairy herd in Bangladesh. A cross-sectional survey was conducted in January 2025, involving 227 lactating cows. Milk samples were analyzed using the Ekomilk Horizon analyzer (Bulteh 2000 Ltd., Bulgaria). SCM was defined as SCC ≥200,000 cells/mL, a threshold commonly applied in both industry and research. Cow-level data—including breed, body condition score (BCS), age, pregnancy status, reproductive disorders, abortion history, retained placenta, number of calves, lactation stage, and milk yield—were recorded. Univariable and multivariable logistic regression analyses identified factors associated with elevated SCC. The overall SCM prevalence was 63.4%. Multivariable analysis showed significant associations between reproductive disorders and SCM. Anestrus cows had 2.68 times higher odds (95% CI: 1.20–5.95; P = 0.015), and repeat breeders had 3.85 times higher odds (95% CI: 1.69–8.76; P 0.001), compared to cows without reproductive issues. Additionally, cows weighing ≥345 kg had 3.26-fold higher risk (95% CI: 1.77–5.99; P 0.001). This pilot study confirms the feasibility of on-farm SCC screening for early SCM detection and identifies reproductive disorders and higher body weight as significant risk factors. These findings highlight the need for comprehensive herd health monitoring and targeted interventions. Larger-scale studies are essential to validate these results and inform effective management strategies aimed at improving dairy herd productivity and animal welfare in resource-constrained systems.

sciforum-139945: Generalized notoedric mange following feline immunodeficiency virus (FIV) infection in cats

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Notoedric mange, caused by *Notoedres cati*, affects cats and some rodent species, less commonly dogs and foxes. Young kittens are usually affected. It also causes transient lesions in humans. We report a case of generalized notoedric mange, in an adult tomcat (six years old) consequently to immunosuppression induced by infection with feline immunodeficiency virus (FIV). This is a retrovirus that causes suppression of cellular immunity. The disease manifested as extensive, very itchy crusted dermatitis, deep pyodermatitis on the limbs, and mucopurulent conjunctivitis. The disease is highly contagious. *N. cati* belongs to the family *Sarcoptidae*, with a life cycle and morphology very similar to *Sarcoptes canis*. Diagnosis can be clinically oriented. The distribution of lesions and intensity of pruritus are highly suggestive. Confirmation of mange was made by microscopic examination of the skin scrapings, the parasites being more abundant than in sarcoptic mange. Confirmation of FIV was made with Rapid Antigen FIV Ab/ FeLV Ag Test Kit, Bionote Inc. (Gentaur Group Europe). FIV infection progresses asymptomatically for a long time, being underdiagnosed. Once immunosuppression develops, it predisposes to numerous infectious or parasitic diseases. It is often associated with lymphoplasmacytic stomatitis. Reported dermatological signs include chronic and recurrent bacterial skin infections and otitis, an increased frequency of infection with *Cryptococcus neoformans, Candida albicans*, or *Microsporum canis*, and demodicosis.

sciforum-142894: Identification of co-infections of Bluetongue virus serotypes 3, 4, and 8 through animal and entomological surveillance in Sicily, Italy

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Introduction: Bluetongue virus (BTV), an Orbivirus from the Reoviridae family, is characterized by a segmented double-stranded RNA responsible for high genetic plasticity. A pathogen mainly transmitted by biting midges belonging to the Culicoides genus, it causes viral disease in ruminants with economic and health impacts on livestock and wild animals. There are more than 30 BTV serotypes that differ in antigenic and pathogenicity characteristics and can also undergo reassortment phenomena, producing new variants. The first outbreak of BTV infection in Sicily was reported in 2000 (2). In this study, we analyzed cases of co-infections in animals and insects by BTV 4-8, BTV 3-8, which occurred in Sicily (Italy) from January 2024 to May 2025, highlighting the risk of genetic reassortment between strains with different pathogenic and diffusion characteristics.

Methods: Blood, tissue sample and insect traps were collected. Insect vectors were sampled and morphologically identified at the species and aggregate levels. Insects and blood samples were then subjected to RNA extraction and amplification by real-time RT-PCR for the BTV NS3 gene. Specific Real-time RT-PCR for serotypes 1-3-4-8 were carried out on positive samples.

Results: Coinfection with BTV 4-8 was detected in 4/27 (14.81%) positive insects of the species Culicoides imicola, Culicoides new steady, and Culicoides spp. and in 2/77 (2.6%) positive blood samples from cattle. Coinfection with BTV 3-8 was identified in 2 additional blood samples and 4/32 (12.5%) sheep spleens.

Conclusions: The work carried out allowed us to the identification of BTV serotypes circulating and also documented cases of co-infections in animals and insects during the 2024-2025 transmission seasons in southern Italy. Some serotypes, such as BTV-8, have a greater impacton health and economy, so expanding epidemiological knowledge is essential to strengthen surveillance systems and methods for the early detection of new or more virulent strains.

sciforum-148136: Identification of Pathogens Causing Abortion in Sheep: Clinical Patterns

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Introduction: Abortion in sheep, a major global economic concern, causes significant losses in livestock industries, particularly in regions reliant on sheep farming. It is often caused by infectious agents like Neospora caninum, Chlamydia abortus, Listeria monocytogenes, Mycoplasma spp., and Brucella spp. These pathogens induce abortions at varying gestational stages with distinct clinical signs, such as placental damage (N. caninum), late-gestation placentitis (C. abortus), or systemic infections with mastitis or lameness (Mycoplasma, Brucella),

Methods: Samples from aborted fetuses, placentas, and maternal tissues in four affected flocks were analyzed. PCR assays targeted N. caninum (Nc-5), C. abortus (omp1), L. monocytogenes (hly), Mycoplasma spp., and Brucella spp., with primer sets validated against reference strains for specificity and sensitivity.

Results: Two flocks tested positive for N. caninum, showing mid-gestation abortions with placental lesions. Two flocks had Mycoplasma spp., linked to late abortions, mastitis, and lameness. No L. monocytogenes was detected, despite some respiratory or neurological signs in ewes.

Conclusion: Diverse pathogens cause sheep abortions, with distinct gestational timing and clinical signs aiding diagnosis. Molecular detection enables rapid pathogen identification, vital for early intervention and preventing disease spread in flocks. Targeted control reduces economic losses. Molecular tools enhance veterinary epidemiology, improving disease management in livestock.

sciforum-148319: Introduction of Non-Autochthonous Cattle into a Farm in the Madonie Park (Sicily, Italy) and the Impact of Endemic Tick-Borne Diseases: A Serological, Molecular, and Entomological Study

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Tick-borne diseases pose a serious challenge to cattle farming in Mediterranean endemic areas. In Sicily, pathogens such as *Anaplasma marginale, Babesia spp.*, and *Theileria annulata* are widespread and can impact herd health and productivity. This study was conducted on a farm in Sicily, Italy where non-native cattle imported from Austria, the Netherlands, and France showed severe clinical signs likely related to tick-borne infections.

Among the 35 cattle on the farm, 26 were tested for antibodies to *A. marginale, Babesia bigemina*, and Crimean-Congo Hemorrhagic Fever virus (CCHFV) by ELISA, and for *Babesia bovis* and *T. annulata* by indirect immunofluorescence assay (IFA). PCR was performed on whole blood and spleen (from one dead animal) for *A. marginale, B. bigemina, B. bovis*, and *T. annulata*. Ticks were identified morphologically and molecularly, and screened for *Rickettsia* spp. Amplicons were sequenced and compared to GenBank.

Serology showed 21/26 positive for *A. marginale*, 20/26 for *B. bovis*, 3/26 for *B. bigemina*, and 14/26 for *T. annulata*; none were positive for CCHFV. PCR confirmed *A. marginale* (9/26), *B. bigemina* (1/26), and *T. annulata* (1/26); *B. bovis* was not detected. The spleen tested positive for *A. marginale* and *T. annulata*. Ticks were identified as *Hyalomma lusitanicum*, PCR-positive for *Rickettsia aeschlimannii*.

The introduction of non-native cattle into tick-endemic areas increases the risk of disease. High seroprevalence of *A. marginale* and *T. annulata* indicates widespread exposure. Differences between serology and PCR reflect past exposure versus active infection. *H. lusitanicum* is a known CCHFV vector in Mediterranean regions. However, no CCHFV seropositivity was detected, suggesting no active viral circulation in the herd. Still, the established presence of this tick species in Sicily, along with climate change and animal movement, could favor local emergence. Enhanced surveillance is recommended to support early outbreak detection and protect animal and public health.

sciforum-135135: Mapping Risks: A Value Chain Approach to Brucellosis Introduction in Zhijiang's Cattle Population, China

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Brucellosis-free status in Zhijiang County, Hubei, is jeopardised by the continual inflow of live cattle from high-prevalence provinces. This study integrated participatory value-chain mapping with stochastic risk modelling to quantify where and how *Brucella* could be introduced.

Two focus-group discussions, 48 key-informant interviews and 31 site visits delineated the cattle production-to-consumption network, characterising trade volumes, stakeholder practices and biosecurity gaps. These data parameterised a scenario-tree model run in @Risk (50 000 Monte Carlo iterations), and a Latin-hypercube global sensitivity analysis ranked the influence of input variables.

Brokers dominated live-animal movements, sourcing ~80 % of imports and frequently bypassing origin-quarantine. The median probability that an individual imported feeder was *Brucella*-positive was 1.43 % (95 % CI: 0.68–2.18), yielding an annual probability >99.999 % that at least one infected animal enters Zhijiang in 95 % of simulations. Over 90 % of total risk stemmed from cattle introduced via (i) unregulated brokers or (ii) trading platforms that omitted origin-quarantine or relied on low-sensitivity pen-side tests. Origin-herd prevalence and the proportion of cattle handled by brokers were the most influential parameters.

Even under conservative assumptions, current movement controls cannot prevent brucellosis incursion. Policy priorities include enforcing origin-quarantine, accrediting brokers, instituting centralized post-entry isolation, and deploying high-specificity rapid diagnostics. By coupling qualitative value-chain insights with quantitative risk assessment, this framework offers a transferable template for evidence-based disease-freedom programmes and highlights critical intervention points for safeguarding public health and livestock economies.

sciforum-148290: Molecular and Serological Investigation of Tick-Borne Pathogens in Equines in Sicily, Italy

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Tick-borne diseases (TBDs) are significant health concerns affecting equines worldwide, causing a range of clinical syndromes and negatively impacting animal welfare and productivity. These diseases are caused by a broad spectrum of tick-transmitted pathogens, including bacteria (e.g., *Anaplasma* spp., *Rickettsia* spp.), protozoa (e.g., *Babesia caballi*, *Theileria equi*), and viruses such as tick-borne encephalitis virus. Sicily, Italy, with its Mediterranean climate and widespread ticks, represents a potentially high-risk area for equine TBDs. This study aimed to investigate the circulation of major tick-borne pathogens in equines (horses and donkeys) to improve understanding of their epidemiological status and to support targeted control strategies.

Between 2024 and 2025, blood, serum, and ticks were collected from equines. DNA was extracted from whole blood and ticks and subjected to PCR assays targeting genes of key pathogens, including *Rickettsia* spp. (*ompB*, *ompA*, *gltA*), *Anaplasma* spp. (16S rRNA), *Borrelia burgdorferi* (*OspA*), *Babesia caballi* (48 kDa rhoptry protein), and *Theileria equi* (*EMA-1*). Serum samples were analyzed by indirect immunofluorescence assay (IFA) for antibodies against *Anaplasma* spp. and *B. caballi*, and by ELISA for flavivirus antibodies.

Of the 163 blood samples tested, 16% were positive for *T. equi*, while no other pathogens were detected. A total of 29 ticks were collected: 20 *Ixodes ricinus*, 6 *Haemaphysalis punctata*, and 3 nymphs. One *Haemaphysalis* tick tested positive for *Anaplasma* spp. Among 196 equine serum samples, 12.2% were seropositive for *Anaplasma phagocytophilum*, 3.8% for *B. caballi*, and 6% for flaviviruses.

The molecular detection of tick-borne pathogens in equines from Sicily confirms the circulation of multiple TBD agents in the region. These findings highlight the need for improved surveillance and implementation of tick control measures to manage equine TBDs. Further studies are warranted to evaluate clinical relevance and local vector ecology.

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sciforum-142712: Molecular Characterisation of Fowl Adenoviruses Associated with Inclusion Body Hepatitis and Gizzard Erosion in Broiler Chickens in Sabah, Malaysia

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Inclusion Body Hepatitis (IBH) and adenoviral gizzard erosion (AGE) which are caused by fowl adenoviruses (FAdVs) have emerged as significant health concerns in poultry production in Sabah, Malaysia. Here, we present molecular surveillance data collected from 2019 to 2023 to characterise the FAdV serotypes associated with these diseases in broiler chickens. A total of 66 liver and gizzard samples were collected from birds exhibiting gross lesions consistent with IBH or AGE. Of these, 49 samples tested positive for FAdV by Polymerase Chain Reaction (PCR), and all 49 underwent partial sequencing of the hexon gene, a major capsid protein used for FAdV serotyping. We identified three FAdV serotypes over the five-year period, namely, FAdV-1 (species A), FAdV-8b (species E) and FAdV-11 (species D). We found that FAdV-8b was the most prevalent and was detected in 69.4% (34/49) of the positive samples and was present in all five years. Meanwhile, FAdV-11 (4/49) was limited to 2019 and 2020, and FAdV-1 (12/49) was detected only in 2023. We observed a notable increase in IBH cases in 2023, coinciding with a sharp rise in FAdV-8b detection. We also identified FAdV-1 only in 2023 and observed gizzard erosion during necropsy, suggesting the presence of AGE. From the sequence analysis of the Hexon gene, we identified revealed several single nucleotide variants (SNVs) within samples of the same serotype, which indicates intra-serotype genetic variation reflecting viral adaptation or local evolution. Our study provides the first molecular evidence of FAdV-1, -8b, and -11 associated with IBH and AGE cases in Sabah and demonstrates shifting patterns in FAdV serotype prevalence over time. Our findings highlight the importance of molecular surveillance and targeted farm-level biosecurity measures to control the spread and impact of FAdV infections in Sabah poultry flocks.

sciforum-143191: Molecular Epidemiology of *Mycobacterium bovis* in Sicily: Insights from Spoligotyping for Targeted bTB Control

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Introduction: Bovine tuberculosis (bTB), caused by *Mycobacterium bovis*, is a zoonotic disease with significant implications for animal health, public health, and livestock productivity worldwide. Despite the implementation of national and regional eradication plans, Sicily remains one of the areas in Italy with the highest bTB prevalence. Several epidemiological factors contribute to this persistence, including extensive and semi-free-range farming practices, shared pastures, interspecies interactions with wildlife and local pig breeds, and the island's complex geography, which fosters ecological conditions favorable to pathogen survival and transmission.

Methods: *M. bovis* isolates were obtained from pathological samples, such as lymph nodes and lung lesions, collected from cattle slaughtered due to suspected tuberculosis. Bacterial cultures were performed using standard solid (Löwenstein-Jensen and Stonebrink) and liquid (BACTEC MGIT 960) media. Genomic DNA from culture-positive samples was extracted and subjected to spoligotyping. This molecular technique was used to identify the genotypes circulating in the region and to assess their spatial distribution.

Results: In 2024, a total of 745 animals were analyzed, of which 213 tested positive for *Mycobacterium bovis*. Spoligotyping revealed that the genetic landscape of *M. bovis* in Sicily is characterized by a limited number of predominant genotypes, particularly SB0120, followed by others such as SB0134 and SB0841. A wider range of minor and sporadic genotypes was also detected. The distribution of genotypes varied geographically, with some provinces showing higher genetic diversity than others. These findings point to a combination of localized endemic transmission and sporadic new introductions, influenced by environmental, management, and ecological factors.

Conclusions: The observed genetic heterogeneity of *M. bovis* reflects the complex epidemiology of bTB in Sicily. Molecular data such as spoligotyping provide crucial insights into strain circulation, supporting the design of more effective and geographically tailored control strategies aimed at the progressive eradication of the disease.

sciforum-118736: One Health and Non-communicable diseases: animal interconnection to human non-communicable diseases

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Non-communicable diseases (NCDs) are a growing concern not only in human populations but also in animals, with significant implications for ecosystem health and human well-being. The interconnection of animal NCDs, environmental factors, and human health, highlights the role of the One Health framework in understanding and addressing these complex interactions. Animals, particularly livestock and wildlife, are increasingly affected by NCDs, such as obesity, diabetes, cancers, and cardiovascular diseases, often mirroring human health trends. Environmental factors, including pollution, climate change, and habitat degradation, are connected with the emergence and progression of these animal diseases. Exposure to environmental toxins, such as pesticides and heavy metals, has been linked to metabolic disorders and cancers in both animals and humans. Additionally, shared risk factors, such as sedentary lifestyles and poor nutrition, further link the connection between animal and human NCDs. The implications of animal NCDs extend beyond animal health, affecting food security, zoonotic disease dynamics, and ecosystem stability, ultimately impacting human health. Thus, the study and management of NCDs in animals are essential not only for ensuring animal welfare and livestock production but also for contributing to the broader One Health framework. A One Health approach is critical to address the root causes of animal NCDs, advocating for integrated strategies that promote sustainable environmental practices, improve animal husbandry, and enhance surveillance systems, ultimately leading to the development of holistic solutions to mitigate the burden of NCDs across species and ecosystems, fostering a healthier planet for all.

sciforum-142572: Pattern recognition receptors (PRRs) influence the formation and spatial organization of podosomes in murine dendritic cells *in vitro*

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Pattern recognition receptors (PRRs) expressed by immune cells play a crucial role in sensing pathogen-associated molecular patterns (PAMPs), thereby initiating innate immune responses. As professional antigen-presenting cells, dendritic cells (DCs) regulate the pericellular environment, capture antigens, and present them to T lymphocytes following their migration to secondary lymphoid organs. The migration of immature DCs is facilitated by specialized adhesion structures, such as podosomes.

Since podosome assembly and disassembly are highly associated with immunoregulatory and migratory functions of DCs, we evaluated the effects of various PRR agonists on podosome organization in mouse bone marrow-derived DCs (BMDCs).

Primary cultures of BMDCs were generated using mouse recombinant granulocyte-macrophage colony-stimulating factor (rmGM-CSF) and subsequently stimulated for 24 hours with selected PRR ligands, including TLR agonists (Pam2CSK4, Pam3CSK4, Poly I:C, LPS, flagellin, CpG ODN) and NOD agonists (C12-iE-DAP, MDP). Podosome types were morphologically classified as single, clustered or rosette structures and quantified in individual cells following immunofluorescent staining for F-actin and vinculin.

Our data demonstrate that PRR stimulation promotes podosome dissolution and significantly alters podosome organization. In unstimulated control BMDCs, more than 85% of cells exhibited podosomes, predominantly clustered (70%), followed by rosettes (10%) and single podosomes (6%). The most pronounced podosome disassembly was induced by LPS, resulting in over 80% of cells losing podosomes and an increased proportion of cells displaying single podosomes (11%). Similar effects were observed following stimulation with Pam2CSK4 and Pam3CSK4. Weaker podosome-disrupting effects were noted with flagellin, C12-iE-DAP, MDP, and Poly I:C, where podosome-negative cells accounted for 60%, 42%, 40%, and 36%, respectively.

Conclusion: PRR stimulation influences podosome dynamics in BMDCs, suggesting a regulatory role in DC maturation and functional plasticity.

sciforum-143899: Prevalence and Management of Foot-and-Mouth Disease in Cattle in Iraq: A Short Review

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Foot-and-mouth disease (FMD) is one of the most economically significant viral diseases affecting livestock globally, particularly in developing countries. This highly contagious disease causes severe productivity losses in affected animals, primarily cattle, sheep, and goats. This short review summarizes the prevalence, clinical presentation, and management strategies of FMD in cattle within Iraq. Data were obtained from published studies, governmental veterinary reports, and field observations between 2015 and 2024. The findings reveal that FMD outbreaks occur periodically, with higher incidence during the colder months when animal movements increase and biosecurity measures are often relaxed. Clinical signs observed in affected cattle include fever, excessive salivation, vesicular lesions on the mouth and feet, lameness, and decreased milk production, which collectively contribute to significant economic burdens for farmers and the livestock industry. Current management strategies in Iraq rely mainly on vaccination campaigns, quarantine measures, movement control, and supportive care for affected animals. However, challenges remain due to inconsistent vaccine coverage, limited laboratory diagnostic capacity, lack of public awareness, and unregulated animal trade practices. Strengthening vaccination programs, improving biosecurity measures, increasing farmer education, and enhancing regional cooperation are essential to reducing the impact of FMD in the region. This review emphasizes the importance of continuous surveillance and coordinated efforts among veterinary authorities to effectively control and prevent future FMD outbreaks in Iraq, ultimately supporting food security and livestock sustainability.

sciforum-148315: Prevalence and Resistance profiling of Methicillin Resistance Staphylococcus aureus in crustacean seafood, Lagos, Nigeria.

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The increasing emergence of antimicrobial-resistant pathogens including Methicillin-Resistant Staphylococcus aureus (MRSA) poses a significant threat to food safety and public health. The unhygienic handling practices combined with environmental contamination and antibiotic misuse in Lagos Nigeria's coastal communities make crustacean seafood a potential reservoir for MRSA. A total of 71 crustacean seafood samples were randomly collected from three major seafood markets across Lagos State .The Baird Parker Agar served as a medium for S.aureus isolation followed by Gram staining and biochemical tests to confirm the results. The Kirby-Bauer disc diffusion method on Mueller-Hinton agar followed CLSI guidelines to test presumptive isolates for antibiotic susceptibility. The phenotypic marker tests using Cefoxitin(30 µg) and Oxacillin(5 µg) identified MRSA strains. The presumptive S. aureus isolates from 71 samples reached 60 (84.5%) and the phenotypic resistance tests showed 22 (36.67%) and 60 (100%) isolates were resistant to cefoxitin and oxacillin respectively. Six out of 21 processed isolates showed resistance to cefoxitin and all 21 processed isolates showed resistance to oxacillin. The 39 fresh isolates showed 16 cefoxitin-resistant strains but all 39 samples displayed complete resistance to oxacillin.

The antibiotic susceptibility profile revealed that each of Augmentin (100%), Meropenem (100%), Ceftriaxone (100%) and Linezolid (100%) showed high resistance while ciprofloxacin exhibited relatively lower resistance. The research demonstrates that MRSA exists in crustacean seafood products sold in Lagos which creates potential health risks for both consumers and handlers. The high level of MDR indicates that antibiotics have been used either excessively or improperly in aquatic environments and post-harvest handling processes. The recommended measures to control resistant strain spread include regular surveillance and proper seafood handling practices together with controlled antimicrobial use in aquaculture operations. The research provides essential local findings about MRSA in seafood which supports the requirement for One Health-based AMR monitoring in Nigeria.

sciforum-148306: Serological and Molecular Investigation of *Rickettsia* spp. and *Anaplasma* spp. in Domestic Cats from Sicily, Italy

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Vector-borne pathogens such as *Rickettsia* spp. and *Anaplasma* spp. are increasingly recognized as emerging threats to human and animal health. Domestic cats (*Felis catus*) may act as sentinels, reservoirs, or incidental hosts, especially in Mediterranean areas where arthropod vectors are widespread. This study aimed to investigate exposure and infection rates of *Rickettsia* spp. and *Anaplasma* spp. in cats from Sicily (Italy), including molecular screening of their ectoparasites.

Serum samples were tested for antibodies against *Rickettsia* spp. and *Anaplasma* spp. using indirect immunofluorescence assay (IFA). DNA extracted from EDTA blood and ectoparasites (ticks and fleas) was subjected to PCR for *Rickettsia* spp. and *Anaplasma* spp. Positive PCR products were sequenced to confirm species identity.

Between 2024 and 2025, samples were collected from 80 cats. Serological testing revealed high exposure rates, with 56.3% of cats positive for *Rickettsia* spp. antibodies and 12.7% for *Anaplasma* spp. In contrast, molecular analyses detected *Rickettsia felis* DNA in only 3.8% of feline blood samples, while no *Anaplasma* spp. DNA was identified. Among ectoparasites, *R. felis* DNA was detected in one of 2 fleas (*Ctenocephalides felis*), and *Anaplasma phagocytophilum* DNA in one (*Ixodes ricinus*) of 8 ticks.

The marked discrepancy between seroprevalence and molecular detection suggests that while cats are frequently exposed to these pathogens, active infections detectable by PCR are uncommon, likely due to a transient bacteremia that limits the window of molecular detectability. The identification of pathogen DNA in ectoparasites supports their circulation in the environment, although this alone does not confirm a reservoir role for cats. These findings highlight the importance of integrated surveillance of companion animals and their ectoparasites within a One Health framework to better understand and mitigate zoonotic risks.

This research was funded by the Italian Ministry of Health (IZSSI 03/23 RC).

sciforum-142885: Serological Survey of *Rickettsia, Anaplasma, Ehrlichia, Babesia*, and Flaviviruses in Dogs from Western Sicily (Italy)

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Introduction

Tick-borne infections caused by bacterial pathogens such as *Rickettsia* spp., *Ehrlichia* spp., and *Anaplasma* spp., protozoa like *Babesia* spp., and viruses including Tick-Borne Encephalitis Virus (TBEV) represent a growing concern for both veterinary and public health, particularly in Mediterranean regions. Western Sicily (Italy), due to its favorable climatic and ecological conditions, is considered a potentially endemic area for several of these pathogens. This study aimed to evaluate the seroprevalence of *Rickettsia* spp., *Ehrlichia spp*., *Anaplasma* spp., *Babesia* spp., and flaviviruses in the canine population of this region.

Materials and Methods

Canine blood samples were analyzed using indirect immunofluorescence assay (IFA) to detect antibodies against *Rickettsia* spp., *Anaplasma* spp., and *Ehrlichia* spp. Enzyme-linked immunosorbent assay (ELISA) was employed to assess antibodies against flaviviruses and *Babesia* spp.

Results

A total of 386 dogs from various provinces of western Sicily were sampled. Seroprevalence rates were as follows: *Rickettsia* spp. – 47.08%, *Anaplasma* spp. – 21.33%, *Ehrlichia spp.* – 15.49%, and *Babesia* spp. – 32.38%. A subset of 121 samples (approximately 30%) was tested for flaviviruses, revealing a seropositivity rate of 26.45%.

Conclusions

The findings confirmed the circulation of the investigated bacterial, protozoan, and viral pathogens in the canine population of western Sicily. These results underscore the need for ongoing serological surveillance to better elucidate the epidemiology of these infections and to support the development of effective prevention and control strategies, in alignment with the One Health framework. Dogs represent effective sentinels for monitoring vector-borne diseases due to their frequent exposure to the same environmental risk factors as humans and their accessibility for sampling. Their role as sentinel species provides valuable insights for both veterinary and public health efforts aimed at early detection and management of emerging infectious threats.

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sciforum-148176: Seroprevalence and Lesion Profiles of Mycoplasma synoviae in Broiler Chickens: Evidence from District Karak, Pakistan

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Mycoplasma synoviae (MS) is a key avian pathogen that causes respiratory, joint, and reproductive issues in poultry, resulting in significant economic losses. This study aimed to determine the seroprevalence and pathological changes linked to MS infection in commercial broiler flocks in District Karak, Khyber Pakhtunkhwa, Pakistan. A total of 200 blood samples were collected from 13 broiler farms and tested using an indirect ELISA kit to detect MS-specific antibodies. Additionally, tissue samples from the trachea and lungs were taken from naturally infected birds and examined histopathologically. The serological results showed that 41 out of 200 samples (20.5%) tested positive for MS antibodies, indicating moderate pathogen circulation in the area. Risk factor analysis revealed higher seroprevalence in birds over three weeks old (23%) compared to those under three weeks (12%), and in smaller flocks (2000 birds; 25%) versus larger flocks (>2000 birds; 19%). However, statistical analysis (Chi-square test) found no significant associations ($p > 0.05$) with age, flock size, feed, or mortality. Clinical signs like respiratory distress, anorexia, ascites, and white diarrhea were weakly linked to seropositivity. Gross lesions included tracheal hemorrhages, splenomegaly, synovitis, and lung consolidation. Histopathology showed epithelial desquamation, leukocytic infiltration, hemorrhage in the trachea, and alveolar septal thickening and congestion in the lungs, consistent with septicemia progression of MS infection. The study confirms that Mycoplasma synoviae is endemic in broiler flocks of District Karak, with characteristic respiratory lesions. The findings highlight the importance of regular surveillance, biosecurity, and improved diagnostic methods to reduce the impact of MS on poultry production in Pakistan.

sciforum-146960: Strengthening Veterinary Biosecurity and One Health Approaches for Zoonotic Disease Prevention in Sub-Saharan Africa

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Introduction: Zoonotic diseases are a persistent threat to public health and veterinary systems worldwide, with sub-Saharan Africa particularly vulnerable due to high livestock density, porous borders, and limited disease surveillance capacity. Strengthening veterinary biosecurity within a One Health framework is essential for preventing, detecting, and responding to these risks.

Methods: This work draws on professional experience in biosecurity regulation at the National Biosafety Management Agency of Nigeria, combined with a review of relevant literature on zoonotic disease management. Case examples, including the spread of African swine fever and the increasing challenge of antimicrobial resistance in livestock, were examined to highlight current gaps in veterinary biosecurity systems.

Results: Findings indicate that weaknesses in laboratory infrastructure, limited access to molecular diagnostic tools, and insufficient coordination between veterinary and public health agencies hinder timely outbreak detection and response. However, targeted interventions—such as the application of molecular diagnostics, improved vector control strategies, and capacity building for veterinary professionals—show significant potential for strengthening surveillance and containment efforts.

Conclusions: Integrating veterinary biosecurity into national and regional One Health strategies offers a pathway to improve resilience against transboundary animal diseases and emerging zoonoses. Strengthening policies, enhancing international collaboration, and investing in diagnostic and biosafety infrastructure are critical to safeguarding both animal and human health. This contribution underscores the urgent need for sustainable, evidence-based approaches to protect sub-Saharan Africa from future biological threats.

sciforum-146180: Study of antibiotic resistance of *Escherichia coli* and *Staphylococcus aureus* isolated from biomaterial from chickens that died from avian influenza A (H5N1)

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Introduction. The aim of the work was to isolate bacterial microflora from chickens that died from influenza and determine their resistance profile to antimicrobial drugs.

Materials and Methods. Pathological material from five dead chickens from private households was delivered to the Laboratory. Detection of the genetic material of the virus was carried out using RT-qPCR according to the protocols recommended by WOAH. The biomaterial was sown on special nutrient media for the isolation of bacterial microflora and determination of pathogenicity for laboratory animals. The sensitivity of the isolated bacterial cultures to 44 antimicrobial drugs was determined by the disk diffusion method according to the EUCAST recommendations with disks with minimal inhibitory concentrations of antimicrobial drugs and Mueller-Hinton agar medium.

Results. In the biomaterial studied from chickens the presence of the highly pathogenic avian influenza pathogen (type A, H5N1) was confirmed. As a result of bacteriological studies, cultures of *Escherichia coli* and *Staphylococcus aureus* were isolated and identified from the bone marrow, which were pathogenic for white mice. The results of antibiotic sensitivity studies showed that the isolated culture of *Staphylococcus aureus* was resistant to antibacterial drugs from the groups of cephalosporins, macrolides, nitrofurans, and fluoroquinolones; the isolated culture of *Escherichia coli* was resistant to cephalosporins and macrolides.

Discussion. Analysis of the obtained data provided grounds to classify the studied isolates as multidrug-resistant (MDR). Importantly, the anamnesis data does not confirm the use of antimicrobials in households where the death of poultry from highly pathogenic influenza was recorded.

Conclusion. The results obtained indicate the risks of the spread of bacterial pathogens with multiple antibiotic resistance during avian influenza outbreaks, which poses an additional potential threat to personnel.

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sciforum-143722: The bla $_{TEM}$ ESBL *E. coli* gene's current state in Bangladesh's poultry industry

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Introduction : E. coli in poultry that produces extended-spectrum be-ta-lactamases (ESBLs) has emerged as a significant health concern in Bangladesh. To reduce the harmful impacts, it is urgently necessary to increase awareness and conduct scientifically based research by implementing a surveillance program on the genotypic antibiotic resistance profiles of E. coli obtained from chicken in Bangladesh.

Methods: This paper used a rigorous approach to locate scientific publications published be-tween 2014 and 2024 that addressed the prevalence of ESBL-producing E. coli genes derived from poultry in Bangladesh. Data from the Institute of Epidemiology, Disease Control & Research (IEDCR), which is part of the Ministry of Health and Family Welfare (MOH&FW) of the Government of the People's Republic of Bangladesh, was thoroughly analyzed in this research.

Results: Poultry isolates showed greater diversity in bla TEM, followed by blaSHV. Moreover, blaTEM is the most often found ESBL type in poultry, with detection rates ranging from 1% to 95%. The substantial association between the genotypes and phenotypes may suggest that the presence of specific blaTEM genes in their genomes is primarily responsible for the 83%–87% ampicillin resistance.

Conclusions: To address this ongoing public health issue and stop the spread of antibiotic-resistant bacteria across the food supply chain, cooperation between public health officials, veterinari-ans, food manufacturers, and consumers is essential.

sciforum-119242: The role of cats in MRSA transmission: Investigating *Staphylococcus aureus* in Feline Stomatitis and its Public Health implications

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Staphylococcus spp. commonly colonize the skin, mucosal surfaces, and gastrointestinal tracts of humans and animals, among which *Staphylococcus aureus*, especially methicillin-resistant *S. aureus* (MRSA), represents a pathogen of concern. Although MRSA is traditionally associated with healthcare settings, its increasing prevalence in the community has raised concerns about its transmission from animals to humans. Studies comparing domestic and feral cats demonstrate that indoor pet cats exhibit higher colonization rates of *S. aureus*, approximately 19% *vs.* 8% among feral cats, and MRSA carriage reaches about 10% in domestic cats, compared to only 1.4% in feral populations. In healthy indoor cats, MRSA prevalence averages 6.6%, with risk factors including households where owners work in healthcare, co-resident dogs, and antibiotic treatment in the past year. Although feline stomatitis has not been directly studied for MRSA prevalence, existing data show that oropharyngeal staphylococci from cats often demonstrate high resistance rates ~99% to at least one antibiotic, ~12% multidrug resistance, and frequent carriage of resistance genes including *mecA*. Microbiome research in cats with gingivostomatitis, periodontitis and chronic stomatitis reveals significant oral dysbiosis characterized by enrichment of anaerobic periodontal pathogens (*Treponema*, *Porphyromonas*) and reduced commensal taxa, thereby creating conditions favorable to opportunistic staphylococcal colonization. Behavior patterns such as self-licking and human face/hand licking, further increase the opportunity for bidirectional transmission of MRSA between cats and owners. Moreover, while MRSA prevalence in cats with stomatitis is yet to be directly quantified, the convergence of high antibiotic exposure, documented indoor MRSA carriage, and oral microbial disruption strongly suggests that cats suffering from chronic oral inflammatory diseases and undergoing repeated or prolonged antibiotic therapy may act as overlooked reservoirs of MRSA. Understanding the role of feline *S. aureus* in MRSA epidemiology is crucial for assessing potential risks to human cohabitants and improving public health strategies.

Session D. Antiviral Therapy

sciforum-142228: Antiviral Strategies Against Newcastle Disease: Current Insights and Future Directions

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Introduction:
Newcastle Disease (ND) is a highly contagious viral infection that continues to cause significant mortality, production losses, and trade restrictions in poultry worldwide. Despite widespread vaccination, outbreaks persist due to the emergence of more virulent Newcastle Disease Virus (NDV) strains and reduced vaccine efficacy under field conditions. Complementary antiviral strategies are increasingly recognized as a necessary addition to vaccination programs.

Methods:
A comprehensive literature review was conducted using databases including PubMed, Web of Science, and Scopus. Studies published in English up to 2025 were screened for evidence on synthetic antivirals, plant-derived compounds, immunomodulators, and supportive agents against NDV. Both in vitro and in vivo studies were evaluated, with a focus on antiviral efficacy, safety, cost, and practical field applicability.

Results:
Synthetic antivirals such as ribavirin and favipiravir demonstrated moderate efficacy in controlled laboratory studies but are limited by high cost, toxicity concerns, and regulatory restrictions in poultry. Plant-based compounds, notably *Curcuma longa* (turmeric), *Azadirachta indica* (neem), and *Allium sativum* (garlic), showed promising antiviral and immunostimulatory effects with better accessibility and safety profiles. Immunomodulators, including interferons, and supportive agents such as vitamins and probiotics, enhanced host resistance. However, most evidence comes from in vitro studies, with a shortage of well-designed in vivo and field trials.

Conclusions:
The literature supports integrating validated plant-based antivirals and immunomodulators with vaccination to create a more robust and sustainable ND control strategy. Priority research should focus on large-scale in vivo and field evaluations to confirm efficacy, safety, and cost-effectiveness under commercial conditions. Such integration could significantly reduce ND-related losses and improve poultry health management.

sciforum-139034: Chicken Pulmonary MicroRNAs Targeting the PB2, segment 1 of Avian Influenza Virus

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Highly pathogenic avian influenza (HPAI) is a devastating viral disease that leads to severe pulmonary damage and high mortality rates in domestic poultry worldwide. It is caused by avian influenza type A viruses from the Orthomyxoviridae family, the HPAI virus contains a genome of eight negative-sense RNA segments. Among these, the PB2(Polymerase basic protein) segment plays a crucial role in viral replication as a subunit of the viral RNA-dependent RNA polymerase (RdRp) complex. Targeting PB2 expression represents a potential strategy to control HPAI. MicroRNAs (miRNAs), which are short noncoding RNAs, play a significant role in post-transcriptional regulation of gene expression, influencing various biological processes including cell growth, tissue differentiation, apoptosis, and viral infection. Our previous research identified 200 differentially expressed pulmonary miRNAs in chickens during HPAI infection. In the current study, we screened these dysregulated miRNAs against the PB2 segment of the HPAI H5N1 virus. We evaluated parameters such as the thermodynamic stability of miRNA-mRNA complexes, complementarity of miRNA seed sequences with mRNA, conservation of the PB2 sequence, and accessibility of target sites to identify miRNAs that could potentially target the PB2 transcript of H5N1. Our findings indicate that chicken miRNAs gga-miR-17-3p, gga-miR-29a-5p, gga-miR-1718, gga-miR-16c-5p, and gga-miR-1744-5p are predicted to target the PB2 segment. This suggests that chickens possess inherent genetic potential to combat H5N1 infection, which can be leveraged to develop effective control strategies for HPAI in poultry and miRNA therapeutic potential.

sciforum-142912: Ectromelia virus infection decreases Bid protein level and impairs apoptosis in L929 fibroblasts

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Apoptosis, also known as programmed cell death type I (PCD I), is a phenomenon responsible for the proper development and functionality of animal organisms. It enables the elimination of old, damaged, malfunctioning, oncogenic, and/or infected cells. As an essential determinant of organismal health, apoptosis is subject to multi-level regulation. PCD I can be induced via two molecular pathways: the extrinsic and the intrinsic. The latter is mitochondria-dependent – the key event in this signaling cascade is the permeabilization of the outer mitochondrial membrane (OMM), leading to the release of cytochrome c, apoptosome formation, the proteolysis of caspase-9, and, finally, the activation of caspase-3, an effector enzyme of apoptosis. Bid is a member of the Bcl-2 family, which comprises proteins responsible for regulating mitochondrial integrity. Its active form, truncated Bid (tBid), can promote OMM permeabilization, partly by recruiting Bax protein to the OMM, resulting in Bax oligomerization into pores that perforate the membrane. As Bid is cleaved to tBid downstream of surface receptor activation, it serves as a link integrating the extrinsic and intrinsic apoptotic pathways. Our study aimed to determine the influence of the ectromelia virus Moscow strain (ECTV-MOS) infection of L929 fibroblast on Bid activation and the consequent events, including colocalization of Bax with the OMM, caspase-3 activation, and changes in the structure and integrity of the cell membrane, measured cytometrically using an annexin–propidium iodide kit. We used Western blot to determine the level of Bid and active caspase-3, confocal microscopy to examine the Bax-OMM colocalization, and flow cytometry to assess the percentage of apoptotic cells in control as well as in ECTV-infected and/or staurosporine (STS)-treated fibroblasts. ECTV-MOS infection did not activate Bid, but counteracted STS-induced apoptosis by decreasing intracellular Bid levels, Bax-OMM colocalization, and caspase-3 activation. The results suggest that ECTV-MOS actively inhibits mitochondria-dependent PCD I.

sciforum-147694: Isolation and identification of a novel goose astrovirus 2 and phylogenetic tree analysis

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Goose astrovirus type 2 (GAstV-2) has recently emerged as a causative agent of fatal gout in goslings, causing significant economic losses to the waterfowl industry. This study aimed to isolate and characterize a novel GAstV-2 strain to understand its genetic evolutionary characteristics.A virus strain was isolated from clinical samples of diseased geese collected from a farm in Taizhou, Jiangsu province, and the virus was isolated by inoculating chicken liver cancer cells. The virus was identified by electron microscopy and RT-PCR. The complete genome was sequenced and analyzed using bioinformatic tools for phylogenetic relationship and genetic variation.A novel GAstV-2 strain, designated as GAstV/Goose/China/TZ04/2025, was successfully isolated. Typical astrovirus-like particles were observed under an electron microscope. The complete genome was determined to be 7018 in length. Phylogenetic analysis based on the complete genome and ORF2 gene revealed that the isolate clustered within the GAstV-2 clade but formed a distinct branch. It shared 97.55% - 99.86% nucleotide identity with other known GAstV-2 strains. Notably, several unique amino acid substitutions were identified in the capsid protein.This is the first report on the isolation and genomic characterization of a novel GAstV-2 variant. The findings expand our knowledge of the genetic diversity of GAstV-2 and provide valuable information for developing diagnostic tools and vaccines against this virus.

sciforum-142380: Molecular mechanism of BST2 suppresses SADS-CoV replication by degrading N protein

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Swine acute diarrhea syndrome coronavirus (SADS-CoV), an emerging alphacoronavirus, leads to fatal diarrhea in piglets and exhibits broad cross-species transmission potential. Bone marrow stromal cell antigen 2 (BST2) is an IFN-induced host protein known to restrict a wide range of enveloped viruses. Previous studies have shown that BST2 inhibits Porcine epidemic diarrhea virus (PEDV) replication through the selective autophagy pathway, suggesting a novel mechanism for its antiviral activity. Given that SADS-CoV and PEDV are phylogenetically related alphacoronaviruses, we hypothesized that BST2 may employ a similar mechanism to antagonize SADS-CoV infection.

To test this hypothesis, we employed TurboID-based proximity labeling combined with co-immunoprecipitation and Western blot analysis. Our results demonstrated that BST2 binds to the SADS-CoV nucleocapsid (N) protein and promotes its degradation, resulting in significant reduction of viral replication. Further virological assays showed that overexpression of BST2 significantly reduced viral titers, whereas BST2 knockout enhanced viral replication.

These findings establish BST2 as a key host restriction factor against SADS-CoV and reveal a novel antiviral mechanism targeting the viral nucleocapsid. This work advances our understanding of innate immune defenses against coronaviruses and highlights BST2's potential as a target for developing interventions aimed at enhancing antiviral responses in swine and mitigating zoonotic risks.

sciforum-135220: One Health Virtual Screening and Molecular Dynamics Identify Saquinavir as a Lead Against Porcine Enteric Coronaviral 3CLPRO

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Introduction:
Porcine delta coronavirus (PDCoV) and porcine epidemic diarrhoea virus (PEDV) continue to pose a threat to global swine health, animal welfare, and food security. These enteric coronaviruses are associated with severe diarrhoea, dehydration, and high mortality in neonatal piglets. Despite significant economic losses, no antiviral treatments are currently approved, and vaccine control remains suboptimal due to viral evolution and incomplete protection. Repurposing clinically approved drugs that target conserved viral proteases represents a rapid and cost-effective therapeutic strategy aligned with the principles of One Health.

Methods:
We retrieved high-resolution crystal structures of PDCoV and PEDV 3CL proteases (PDB IDs: 4XFQ and 8E7C). Following validation of docking protocols using AutoDock Vina and PyRx software, compound libraries from DrugBank and ZINC15 were virtually screened. Top-ranking hits were prioritised based on docking scores and interaction profiles. These candidates were subjected to molecular dynamics simulations to evaluate complex stability over time. In silico pharmacokinetic and toxicity predictions were performed using SwissADME and pkCSM tools to assess oral bioavailability and safety profiles.

Results:
Saquinavir, an FDA-approved HIV protease inhibitor, demonstrated consistently favourable docking interactions with conserved catalytic residues in the viral protease active sites. Molecular dynamics simulations confirmed the stability of binding conformations over 100 ns, supporting the robustness of the predicted interactions. Pharmacokinetic profiling indicated acceptable oral absorption and low predicted toxicity.

Conclusions:
This integrated virtual screening and simulation pipeline identifies saquinavir as a promising repurposed candidate against porcine enteric coronaviruses. These findings justify urgent in vitro validation and illustrate how drug repurposing can accelerate antiviral discovery in veterinary medicine within a One Health framework.

sciforum-113379: Polyphenol-Mediated Inhibition of SIGLEC15 to Block *Newcastle Disease Virus* Binding and Enhance Immunity in Chickens

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SIGLEC15, a critical immune receptor in chickens, plays a crucial role in immune responses to infections, including Newcastle Disease (ND). This study aims to explore the potential of polyphenols as inhibitors of SIGLEC15-mediated *Newcastle Disease Virus* (NDV) binding, to enhance immunity in chickens. Polyphenols are bioactive plant-derived compounds known for their ability to modulate immune receptors and influence signaling pathways. Molecular docking was conducted on 12,000 polyphenols to identify those with high binding affinity for SIGLEC15. Among the screened compounds, Quercetin and Resveratrol demonstrated superior docking scores (-9.45 kcal/mol and -8.79 kcal/mol) and lower RMSD values (0.58 and 0.71, respectively) compared to synthetic SIGLEC15 inhibitors. These polyphenols effectively disrupted the binding sites of NDV on SIGLEC15, inhibiting critical receptor-ligand interactions necessary for viral entry. The NF-κB signaling pathway, activated by SIGLEC15-ligand interactions, was identified as a key pathway modulated by polyphenols. Molecular dynamics simulations (MDS) confirmed the stability of polyphenol-SIGLEC15 complexes, indicating sustained interactions that block NDV invasion. Pharmacokinetic analysis showed favorable profiles, including non-toxicity, high bioavailability, and potential for immune enhancement. By targeting SIGLEC15 and interrupting NDV binding through the NF-κB pathway, these findings provide a novel strategy to improve immunity and protect chickens from *Newcastle Disease Virus*.

sciforum-142439: Scorpion-derived peptides as antiviral agents in veterinary medicine

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Introduction: Canine distemper virus (CDV) and canine coronavirus (CCoV) are two highly contagious viruses that primarily affect dogs, causing disease in the gastrointestinal and respiratory systems, and sometimes the neurological system. Despite advances in vaccines and antiviral therapies, many viruses remain difficult to treat, underscoring the need for innovative control strategies. This study explores the antiviral activity of two antimicrobial peptides, pantinin-1 and pantinin-2, derived from the venom of the scorpion *Pandinus imperator,* against CDV and CCoV.

Methods: The peptides were prepared via solid-phase peptide chemical synthesis and assessed for their cytotoxicity in canine fibrosarcoma cells (A-72), and Vero/hSLAM cells, using MTT assay. Non-cytotoxic concentrations of both peptides were tested for antiviral activity primarily through plaque reduction assays and tissue culture infective dose ($TCID_{50}$), alongside quantification of viral N gene expression levels. Furthermore, peptide conformations were examined in aqueous buffer and in a membrane/mimetic environment (trifluoroethanol (TFE)/H_2O) using circular dichroism (CD) and NMR analyses.

Results: The results show that both pantinins exert antiviral effects within a concentration range from 6 μM to 50 μM against both viruses. Peptides affect viral particles by exerting a virucidal effect and preventing the fusion and entry of the virus into host cells. These results were confirmed by qPCR showing a complete suppression of N viral gene expression at the highest concentration of both pantinins (50 μM). In TFE/H_2O, both peptides shift to α-helical structures, which are often associated with membrane interaction and significantly influence the antiviral activity.

Conclusion: These findings show pantinin-1 and pantinin-2 have promising antiviral properties, supporting their potential as therapeutic agents against CDV and CCoV infections.

Further studies are needed to explore their mechanism, optimise antiviral potency, and assess safety in animal models.

sciforum-147455: Targeting Glutamine Metabolism Inhibits Avian Leukosis Virus Subgroup J Replication

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This study provides a comprehensive and clear investigation into the critical role of host glutamine metabolism in the replication cycle of Avian Leukosis Virus Subgroup J (ALV-J). We hypothesized that ALV-J reprograms host cell metabolism to support its replication. Using both an HD11 macrophage cell line and a chicken infection model, we demonstrated through qPCR and western blot analysis that ALV-J infection significantly upregulates key genes involved in glutamine metabolism, particularly glutaminase (GLS) and the solute carrier transporters SLC1A5 and SLC38A2. In vitro, pharmacological inhibition of GLS with the specific inhibitor BPTES, or culturing under glutamine-deprived conditions, substantially reduced viral replication (as measured by p27 antigen levels) and progeny virion production (via viral titers). Conversely, supplementing the culture medium with exogenous glutamine significantly enhanced ALV-J propagation in a dose-dependent manner. Consistent with cellular findings, in vivo experiments showed that ALV-J infection enhances glutamine metabolic activity—evidenced by increased enzyme activity and metabolite levels—in target organs such as the bursa of Fabricius and the spleen. Importantly, therapeutic administration of BPTES effectively suppressed viral loads in these tissues and alleviated virus-induced pathological damage. Our results conclusively demonstrate that ALV-J exploits host glutamine metabolism to facilitate its replication and propose that targeting this pathway with inhibitors such as BPTES represents a novel and promising therapeutic strategy against ALV-J infection and associated diseases. Further investigation into the specificity and safety of glutamine-targeting approaches will help advance their translational potential in poultry health.

Session E. Virology in One Health

sciforum-141978: Circulating Bovine Leukemia Virus Cell-Free DNA as a Promising Biomarker for Enzootic Bovine Leukosis

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Early and precise identification of illnesses linked to the bovine leukemia virus (BLV) is crucial for maintaining food safety and efficient herd management in nations like Japan, where milk and beef are staples of diets. Enzootic bovine leukosis (EBL), a B-cell lymphoma caused by BLV, emerges in approximately 5% of infected cattle after a prolonged asymptomatic phase. However, current diagnostic tools, such as serological assays and PCR detection of proviral DNA from whole blood, often lack the sensitivity and specificity needed to distinguish EBL from non-EBL cases, especially in early clinical stages. This diagnostic gap emphasizes the need for reliable, non-invasive biomarkers that reflect disease progression with greater precision. Given the increased turnover of malignant cells in EBL, we investigated the potential of plasma-derived circulating cell-free DNA (cfDNA) as a novel biomarker. Proviral loads (PVL) in whole blood and plasma were quantified using qPCR targeting the BLV LTR and pol regions in cattle at different clinical stages. Although PVL in whole blood was generally higher in EBL cases, significant overlap with non-EBL animals limited its diagnostic reliability. In contrast, BLV-derived cfDNA in plasma was significantly elevated in clinically diagnosed EBL cattle and effectively distinguished between disease states. These findings highlight cfDNA as a promising tool for liquid biopsy-based approaches in veterinary virology, with the potential to enhance early diagnosis, surveillance, and control of BLV-associated malignancies in livestock populations.

sciforum-148033: Ectoparasites as viral vectors in veterinary medicine: prevalence in companion animals

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Ectoparasites in companion animals are not only a clinical problem, but also a major epidemiological factor, being vectors for the transmission of pathogens, including some viruses of zoonotic importance. In particular, *Rhipicephalus sanguineus*, the brown dog tick, is recognized as a vector involved in the transmission of Crimean-Congo hemorrhagic fever virus (*Nairoviridae*) and some viruses of the Flaviviridae family. This species thus acquires particular relevance for veterinary medicine and public health, in the light of the One Health concept. The present study evaluated 100 clinical cases of dogs, cats and other companion animals presented to the Medicrisvet clinic (Fălticeni, Romania) in 2024, with the objective of determining the prevalence of ectoparasites and analyzing the associated risks. The results showed a prevalence of 54.8% for *R. sanguineus*, 26.9% for *Demodex cati*, 11.5% for *Otodectes cynotis* and 6.7% for *Sarcoptes scabiei var. canis.* Infestations were more frequent in the warm season, indicating a period of increased vulnerability for the transmission of pathogens, including viral ones. These results highlight the importance of ectoparasites as vectors with viral relevance in veterinary medicine and public health. The high prevalence of *Rhipicephalus sanguineus* in companion animals suggests a major epidemiological potential, with direct implications for zoonotic risk and the emergence of viral agents. The integration of these data in the current context of veterinary virology supports the strengthening of surveillance and control programs and emphasizes the need to develop health policies based on the One Health concept. Therefore, the study contributes to the understanding of the role of ectoparasites in viral ecology and to the substantiation of interdisciplinary preventive strategies, from risk assessment to limiting the transmission of pathogens.

sciforum-135766: Hemagglutinin-Esterase Gene Variations Drive Adaptive Evolution in Bovine Coronavirus (BCoV)

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Bovine Bovine coronavirus (BCoV) represents a significant etiological agent of enteric disease, exhibiting widespread endemicity and imposing substantial economic burdens on livestock industries through its pronounced pathogenicity in neonatal calves. Within the betacoronavirus lineage A, several species including human coronaviruses (HKU1, OC43), equine coronavirus (ECoV), murine hepatitis virus (MHV), canine respiratory coronavirus (CRCoV), and porcine hemagglutinating encephalomyelitis virus (PHEV) demonstrate phylogenetic relatedness to BCoV. As an enveloped RNA virus with a positive-sense, single-stranded genome, BCoV expresses the hemagglutinin-esterase (HE) glycoprotein, which functions as an auxiliary receptor-binding protein and potentially influences viral evolution through modifications in host range determination and tissue tropism.

This investigation analyzed fecal specimens (n=188) obtained from diarrheic calves to assess HE gene variability. Total RNA was extracted following standardized protocols, and HE-specific amplification was performed using targeted primers yielding 497-bp amplicons. Electrophoretic visualization confirmed successful amplification, with molecular detection revealing BCoV prevalence of 15.42% (29/188 samples). Bidirectional Sanger sequencing was conducted on selected positive isolates, and comparative sequence analysis was performed using BLAST algorithms against established betacoronavirus databases. Molecular characterization identified distinct amino acid polymorphisms in isolates designated HE1, HE10, HE30, and HE40. Phylogenetic reconstruction demonstrated that isolates HE1, HE10, and HE40 exhibited monophyletic clustering, whereas isolate HE30 displayed divergent evolutionary positioning, clustering proximally with SARS-CoV-2 variants of Chinese, Israeli, and American origin.

Our investigation into the effects of the identified mutations in the HE gene is currently ongoing.

sciforum-146972: Meta-Analysis of Bacteriophage Use in Managing Mastitis and Diarrhea in Cattle Infected with E. coli

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Calf diarrhea and bovine mastitis caused by Escherichia coli represent globally significant diseases that impose substantial economic burdens on the dairy industry. The widespread and indiscriminate use of antibiotics has accelerated the emergence of multidrug-resistant bacterial strains, posing serious threats to both animal health and ecological stability. This study aimed to explore the therapeutic potential of bacteriophages as a viable and innovative alternative to conventional antibiotics for managing these infections in cattle. A meta-analysis was conducted to evaluate the current status of bacteriophage therapy in this field. An initial screening and review of 1,148 articles were performed, drawing from PubMed, Scopus, and Web of Science databases, spanning the years 1983 to 2021. Based on the inclusion criteria, 15 articles were selected for detailed meta-analysis. In vivo assessments covered a total of 126 cattle treated with bacteriophages in seven different studies. Of these, six focused on treating calf diarrhea, while one addressed bovine coliform mastitis, with all treated animals achieving clinical recovery. Furthermore, eight in vitro experiments analyzed 738 E. coli strains subjected to bacteriophage lysis, resulting in an overall microbiological cure rate of 84.20%. These results highlight the promising efficacy, safety, and potential of bacteriophages as an alternative therapeutic strategy to control E. coli-induced diarrhea in calves and bovine mastitis, offering a sustainable option against traditional antimicrobial treatments.

sciforum-136285: Biothermodynamics of virus-host interactions: The role of Gibbs energy in antigen-receptor binding and virus multiplication in host cells

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Viruses are among the simplest pathogens and rely on host cell metabolic machinery for multiplication. However, viruses also represent complex macromolecular assemblies and can therefore be analyzed as biothermodynamic systems. This means that virus-host interactions represent processes that proceed in accordance with the laws of physics and chemistry. The biothermodynamic methodology has been extensively applied in science and engineering to analyze microorganisms, which include bacteria, yeasts, filamentous fungi and algae. Gibbs energy represents the driving force of metabolism and multiplication of microorganisms. In this research the computational and theoretical methodology of biothermodynamics is applied to analyze virus particles, which include the atom counting method, Patel-Erickson-Battley model and biosynthesis reactions. Based on the determined chemical and thermodynamic properties of virus particles, a mechanistic model of virus-host interactions is developed, based on chemical and nonequilibrium thermodynamics. Virus-host interactions at the cell membrane (antigen-receptor binding) and in the cytoplasm (virus multiplication) are analyzed. Antigen-receptor binding represents a chemical reaction that is driven by Gibbs energy. Virus multiplication can be analyzed as a chemical reaction in which precursors like amino acids are combined to form new virus particles. This process is performed by the metabolic machinery, which is also used by the host cell for reparation. This means that the processes of virus replication and host cell reparation are competitive chemical reactions. According to phenomenological equations of nonequilbrium thermodynamics, the reaction with more negative Gibbs energy change will dominate in the competition. Therefore, more negative Gibbs energy of biosynthesis contributes to the ability of viruses to hijack the metabolism of their host cells and multiply. Furthermore, the methodology of biothermodynamics is applied to analyze virus evolution.

sciforum-131201: From skin to brain: Herpesvirus in cetaceans as an emerging systemic pathogen and ocean health sentinels

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Introduction

Herpesvirus (HV) infections in cetaceans are increasingly recognized as indicators of health disturbances due to their association with immunosuppression, stress, and co-infections. However, its full clinical and ecological significance remains underexplored.

Our research in this field compiles and analyzes findings from stranded cetaceans in the Western Mediterranean, offering critical insights into herpesvirus tropism and pathology, emergence in new hosts, and its relevance in One Health frameworks.

Methods

Over 1,000 post-mortem tissue samples from 49 cetaceans, representing five different species, stranded between 2010 and 2022 were analyzed using conventional PCR, sequencing, and histopathology. HV RNA detection was employed to assess viral replication.

Results

Ecological expansion:

an overall prevalence of 80.85% was reported in a 2021 cohort of 47 stranded cetaceans in the Valencian Community, which was the highest recorded to date. Additionally, Alphaherpesvirus (AHV) was identified in a Mediterranean-stranded humpback whale (

Megaptera novaeangliae

)—the first such report in the region and only the second globally. These findings suggest both wide circulation and an expanded host range.

Tropism:

HV was detected in diverse tissues—skin, genital mucosa, and notably, the central nervous system (CNS). Gammaherpesvirus (GHV) sequences were associated with CNS inflammation and meningitis, representing the first evidence of neurotropism in odontocetes.

Clinical pathology:

HV-associated lesions ranged from proliferative to ulcerative and inflammatory changes. Some animals exhibited histological lesions with active HV replication in the absence of overt clinical signs.

Genetic diversity and replication:

most sequences belonged to GHV, while AHV showed greater genetic heterogeneity. RNA detection confirmed active replication, particularly in juveniles and neonates—supporting age-related susceptibility.

Conclusions

Our integrated assessment identifies HV as a complex, multi-organ pathogen with underrecognized impacts on cetacean health and conservation. Integrating HV surveillance within a One Health framework will enhance our capacity to detect early signs of marine ecosystem disruption through sentinel species like cetaceans.

sciforum-142271: Genetic Variability and Evolution of CsRV1 in *Callinectes sapidus*

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In recent decades, there has been a significant increase in epizootic events in aquatic species. Moreover, a notable number of pathogens typically associated with human infections have been reported in these environments, some of which are causative agents of mortality in aquatic animals. This alarming trend underscores the urgent need for comprehensive research and mitigation strategies.

In this context, we present a study focused on *Callinectes sapidus* reovirus 1 (CsRV1), a pathogenic virus spreading along the Atlantic coast of the Americas that may influence the distribution of its host populations, the blue crab *Callinectes sapidus*. CsRV1 has a double-stranded RNA genome, organized into 12 segments, and is characterized by high mutation rates, segment recombination and reassortment.

Our study investigates the genetic variability of CsRV1, aiming to understand how it is evolving along the Atlantic coast of the Americas, its area of origin. To achieve this goal, we conducted phylodynamic reconstruction using all available genomes and segments from the NCBI Virus database. Molecular dating based on whole-genome data suggests that CsRV1 emerged approximately 40 years ago, with a notable increase in genetic diversity and viral population size occurring around a decade ago.

These results not only provide an overview of the genetic variability of CsRV1 in the Americas but may also prove valuable should the virus be detected in *C. sapidus* specimens from other geographic areas, given that its host is a highly invasive alien species. In this context, we are currently screening *C. sapidus* specimens, primarily collected from Sardinia, but also from other areas of the Mediterranean Sea.

Moreover, these findings underscore the importance of monitoring aquatic pathogens, particularly when invasive alien species such as *C. sapidus* may serve as vectors for previously undetected pathogens that pose potential threats to native species and local ecosystems.

sciforum-142193: Genetic variability of the Influenza A H5N1 virus

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Influenza A H5N1 virus represents a global zoonotic threat, capable of infecting a wide range of hosts, including (besides birds) non-human mammals and, occasionally, humans. In recent years, the virus has exhibited unprecedented geographic expansion and genetic diversification, with numerous documented cases of infection in non-avian species, particularly those associated with clade 2.3.4.4b. The primary aim of this study was to evaluate the potential of the H5N1 virus to adapt to human hosts. In pursuit of this goal, all available nucleotide sequences of the genes encoding Hemagglutinin (HA) and Neuraminidase (NA) from the H5N1 strain—isolated from birds, non-human mammals, and humans and accessible via the GISAID platform—were analysed. Evolutionary dynamics and adaptive potential were assessed across the resulting datasets. The results reveal a significant expansion of clade 2.3.4.4b, along with the presence of mutations known to promote infection and replication in mammals. However, no distinct genetic signature was identified that would indicate spillover or confirmed adaptation to the human host. These findings suggest that, although the H5N1 virus has infected numerous mammalian species in recent years and several human cases have been reported, there is currently no evidence of sustained human-to-human transmission, and birds still remain the main hosts. Rather, humans appear to be incidental hosts, acquiring infections from strains typically circulating in avian or bovine populations, depending on geographic region, sanitary conditions, and lifestyle factors.

sciforum-142674: Investigations on the Biological Activity of Bovine Herpesvirus Type 1 on Copper, Zinc and Stainless Steel Surfaces

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ABSTRACT

Introduction

The increasing prevalence of viral diseases highlights the need for the destruction or inactivation of viruses on diverse material surfaces. While extensive research exists for human viruses, the interaction between metal surfaces and animal pathogens like BoHV-1 is not well understood. This study investigated the impact of copper (Cu), zinc (Zn), and iron (Fe) surfaces on the biological activity, virus and viral DNA half-life time, of BoHV-1.

Methods

MDBK-adapted BoHV-1 (strain 4016) was used to investigate the virucidal effect of copper, zinc, and iron surfaces. The virus was exposed for 1 and 24 hours under humid and dry conditions. Inactivation was evaluated by measuring the reduction in $TCID_{50}$ log_{10}, real-time PCR Ct values, and calculating half-lives for both the virus and it's DNA.

Results

Herpesviruses were inactivated most rapidly on copper-coated surfaces in all cases. The virucidal effect after 1 hour of contact under humid and dried conditions was highly effective (3.25±0.29 log_{10} $TCID_{50}$ and 4.5±0.1 log_{10} $TCID_{50}$; p0.01, p0.05), with similar results after 24 hours under both conditions (4.5±0.25 log_{10} $TCID_{50}$ and 4.5±0.1 log_{10} $TCID_{50}$; p0.05). Inactivation half-live time for the virus and viral DNA after 1 hour were shorter under dry conditions (4 minutes and 27 minutes) compared to humid conditions (6 minutes and 10 minutes). However, after 24 hours, inactivation half-live time were shorter under humid conditions (1 hour 31 minutes and 6 hours 20 minutes) compared to dry conditions (1 hour 36 minutes and 4 hours 7 minutes). Viral activity studies in cell culture correlated with real-time PCR, confirming copper's strong effect on viral DNA under both conditions.

Conclusion

Copper surfaces demonstrated the highest virucidal activity against herpesviruses. The kinetics of inactivation were biphasic: while the immediate efficacy was higher after 1 hour under humid conditions, the long-term effect considering both half-life measurements, proved to be superior in a dry environment.

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