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Title of the Abstract:

Expression and Characterization of recombinant ORF2 Protein of Swine Hepatitis E Virus for Potential Application in Serodiagnostic Assays

ABSTRACTS

Hepatitis E virus (HEV), an enterically transmitted, single-stranded RNA virus belonging to the family Hepeviridae is a major cause of acute viral hepatitis globally. Paslahepevirus balayani is considered the most important species comprising eight genotypes among which genotypes 3 and 4 are zoonotic and largely associated with swine reservoirs. Despite the recognized zoonotic importance, robust data on HEV prevalence in Indian swine populations remain limited. In view of the growing One Health significance of HEV, the present study aimed to clone, express, purify, and evaluate the immunoreactivity of a recombinant ORF2 protein of Hepatitis E Virus for its potential application in serodiagnostic assays. Due to the immunodominant and conserved nature of the ORF2 region encoding the capsid protein, a truncated ORF2 fragment (510 bp) was selected, cloned, and expressed in E. coli BL21 (pLysS) cells. The recombinant ORF2 protein (~25 kDa) was purified under denaturing conditions using Ni-NTA affinity chromatography followed by SDS-PAGE analysis. The recombinant protein demonstrated strong immunoreactivity with anti-His antibodies and HEV-positive swine sera in Western blot analysis. These findings indicate the potential utility of the recombinant ORF2 protein as a candidate antigen in the development of serodiagnostic assays for HEV surveillance in swine populations.

Keywords: Hepatitis E Virus, Immunoreactivity, Recombinant ORF 2, Swine, Zoonotic

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Title of the Abstract:
One Health monitoring of Lumpy Skin Disease Virus across clinical and environmental matrices using multiplex diagnostics and nanopore genomics

ABSTRACTS

Lumpy Skin Disease is an emerging infectious disease of dairy cattle and buffaloes in India. This disease is caused by the LSD virus (LSDV), which spread in India within the last decade and has become a major threat to cattle health and the livestock-dependent economy. Studying genetic variation in the virus is important for understanding disease progression and severity, assessing vaccine efficacy, and detecting the virus for diagnosis and surveillance. Furthermore, since LSDV is a poxvirus (belonging to the Capripoxvirus genus) and closely related to human poxviruses, it is of utmost importance to monitor it for its zoonotic potential.

In this study, protocols for clinical and environmental sampling, LSDV detection, and genotyping is developed. Hundreds of samples were analysed to obtain comprehensive data on method validation and virus profiling. Positive detection of LSDV from cattle was seen in skin lesions and nasal swabs. In environmental samples, drinking and wastewater from farms with infected animals showed high positivity. Multiplex nested PCR detection of LSDV across various sample types demonstrates the method's suitability for surveillance. To enable wider use and availability, the assay was optimised for qPCR to provide specific, sensitive detection and differentiation of LSDV from other capripoxviruses. From LSDV-positive clinical samples, the viral genome was amplified and sequenced using the Oxford Nanopore platform. Whole-genome sequencing of LSDV revealed conserved mutations and phylogenetic clustering indicative of a distinct circulating lineage in India.

This study has enabled the development of molecular methods for clinical and environmental surveillance of LSDV and has highlighted the value of genomic surveillance for studying circulating viral variants, disease prevalence, and vaccine efficacy. Detection of viral DNA in environmental samples underscores the need to incorporate environmental monitoring into national disease surveillance programs. The proposed approach supports scalable, field-adaptable one-health strategies to improve the management of livestock infectious diseases.

Keywords: Infectious Disease Surveillance, Lumpy Skin Disease Virus, Multiplex PCR detection, Oxford Nanopore Sequencing, One Health

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Title of the Abstract:
Gastropods can act as bioindicators of pollutants in drainage systems of coastal cities

ABSTRACTS

Globally, ocean disposal has been the preferred method to dispose of sewage generated by humans. Discharge of wastewater into coastal areas leads to pollutant loading and is a major conservation concern. In Mumbai, an urban metropolis on the west coast of India, interconnections between stormwater and sewage disposal systems cause untreated or partially treated sewage to enter the intertidal zone. This has led to degradation of habitat quality, with the consequent ecological effects being unevaluated. To assess the effects of stormwater effluent on intertidal habitat quality, we used gastropods as bioindicator organisms.

7 impact sites and 2 control sites were sampled for 14 marine intertidal gastropod species. Two types of shell alterations were examined: (1) Blackening due to high organic matter content, and (2) Loss of periostracum caused by ocean acidification. Quadrats were laid at 20m, 70m, and 120m distances on both sides of a stormwater outfall across three horizontal spatial scales in the intertidal zone, with some sites extending to 220m.

Generalised linear models showed a correlation between the proportion of altered shells and the presence of outfall. The proportion of blackened shells was found to be higher at impact sites, with no observable difference in the proportion of shells showing loss of periostracum across control and impact sites. Gastropod abundance was strongly correlated with environmental and habitat variables. However, individual plots show that at impact sites, a higher number of gastropods are found closer to the point of discharge of stormwater effluent, showing that release of stormwater effluent is changing the natural environmental conditions.

Our study shows that gastropod shell alterations can serve as valuable bioindicators to detect such changes in coastal habitats, and highlights stormwater effluent as a threat to marine environments, causing changes in the distribution of gastropods across the intertidal zone.

Keywords: Bioindicator, Gastropods, Marine pollution, Shell alterations, Stormwater.

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Title of the Abstract:

Development of Environmental Surveillance Protocol for Molecular Detection of FMDV, LSDV, and Influenza A Virus in Gujarat, India

ABSTRACTS

Environmental surveillance is emerging as a powerful, non-invasive approach for the early detection of infectious diseases. This study aimed to develop a robust method for environmental surveillance of three important animal pathogens: Foot and Mouth Disease Virus (FMDV), Lumpy Skin Disease Virus (LSDV), and Influenza A Virus (IAV). The objectives included developing and standardizing molecular detection protocols and testing feasibility of implementing systematic environmental surveillance strategies for routine surveillance of viruses. The project integrates multi-matrix sampling, molecular detection, and genomic analysis to assess pathogen circulation.

For FMDV and LSDV, sampling was conducted across seven major livestock zones, which includes nine dairy cooperative networks and three livestock markets. IAV, sampling spanned nine ecologically significant wetlands and adjacent poultry farms. Environmental samples for LSDV and FMDV surveillance included pooled milk, slurry/run-off water, air, drinking water, dung pile, leftover feed, and manger swab, while bird's cage swab, wetland water, wetland sediment, birds dropping, molted feathers, litter, and air were evaluated for IAV surveillance.

The results demonstrate that environmental surveillance can effectively detect viral presence even in the absence of clinical cases, and the data correlated with findings during outbreaks. Sample types such as leftover feed, drinking water, manger swab, and slurry showed the highest positivity for surveillance of LSDV. While, samples such as manger swab, left-over feed and slurry demonstrated good positivity for FMDV surveillance. Pooled milk was also proved to be an efficient sample type for large-scale surveillance tool. For IAV surveillance, wetland water and sediment showed highest positivity whereas the trend observed between wetlands and nearby poultry farms remained consistent.

The study highlights the utility of environmental surveillance as a promising indicator of pathogens (LSDV, FMDV, and IAV) circulation enabling the detection of virus circulation even in subclinical form which potentially enables authority to take advance prevention and control measures and supports their integration into routine surveillance systems. Challenges remain in genome sequencing due to degraded nucleic acids in the environmental samples. Overall, this work provides a scalable framework for environmental surveillance and underscores its potential to strengthen the early warning systems, inform public health interventions, and guide policy for animal and zoonotic disease management.

Keywords: Environmental surveillance, One Health, LSDV, FMDV, IAV

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Title of the Abstract:

Atmospheric pollution crosses borders but governance does not: implications of PM2.5 emission–concentration decoupling for one health in India

ABSTRACTS

Air quality policies often assume that reducing emissions within administrative boundaries will directly improve ambient air quality. This assumption can fail when atmospheric processes redistribute pollution across space, decoupling local emission trajectories from observed concentration trends and creating a structural mismatch between pollution sources, exposure, and governance responsibility. Here, we analyse long-term changes in PM2.5 concentrations and emissions across Indian states and union territories from 1998 to 2023, focusing on their tempPoster dynamics rather than absolute levels. Using generalised additive mixed models we estimate annual rates of change in both PM2.5 emissions and concentrations across India. Across most Indian states and union territories, concentration growth rates decline or stabilise while emission growth rates exhibit an N-shaped trajectory, indicating systematic decoupling between concentration and emission dynamics. While the timing and magnitude of this decoupling varies across states, the overall pattern is consistent. This divergence intensified post-2015, with concentration growth rates continuing to decline while emission growth rates rebounded. The divergence between PM2.5 concentration and emission growth rates suggests that population exposure to PM2.5, a major environmental health risk, is not determined solely by local emissions. Air pollution therefore needs to be addressed as a transboundary health risk, likely requiring coordinated, multi-scalar governance approaches that align with the spatial dynamics of atmospheric processes. Without such alignment, communities may continue to experience pollution burdens that are not fully explained by their own emissions, posing a challenge for equitable and effective air quality governance.

Keywords: air pollution, emission–concentration decoupling, environmental governance, india, PM2.5, transboundary pollution

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Title of the Abstract:

Environmental surveillance and sequencing of low pathogenic avian influenza virus in live bird markets

ABSTRACTS

Introduction: The threats to the poultry industry and the ongoing potential of zoonotic transmission to humans make avian influenza a serious global issue. Live bird markets (LBM) are especially high risk hotspots since they provide the ideal environment for viral reassortment and adaptability due to high levels of human-poultry interaction.

To overcome the limitations of conventional invasive sampling techniques in high turnover markets, we used environmental surveillance to track the circulating influenza subtypes and identify genetic drift indicative of potential zoonotic spillover.

Objective: To assess avian influenza virus presence and genetic characteristics through environmental sampling and sequencing in live bird markets.

Methods: Environmental samples such as air samples, wash water, bird fecal matter, cage swabs, and chopping board swabs were collected from LBM. Cloacal and Poster swabs were obtained from live birds for comparative analysis. Avian influenza virus detection and whole genome sequencing (Oxford Nanopore Technologies) were performed on positive samples collected during May 2025-July 2025 and December 2025-January 2026 to characterize the circulating strains and identify unique genetic mutations.

Results: We successfully detected avian influenza through environmental sampling, despite negative results from individual cloacal and Poster bird swabs. Notably, the H9 subtype was identified consistently throughout the study period, and four of the five sequenced samples had high depth coverage (>100x) across all eight genome segments. Our sequence analysis revealed specific mutations associated with altered receptor binding affinity, and we are currently performing phylogenetic analyses to determine the viral clustering patterns.

Conclusion: Live bird markets represent dynamic environments for avian influenza circulation. The identification of receptor binding mutations highlights the evolving zoonotic threat. These results prove that environmental sampling is a powerful way to keep track of these viral changes, reinforcing the need for ongoing surveillance and better biosecurity to mitigate pandemic risks.

Keywords: avian influenza, environmental sampling, live bird markets, one health, viral sequencing

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Title of the Abstract:

Interconnected Futures: One Health, Ecological Change, and Sustainable Conservation in the Anthropocene

ABSTRACTS

Abstract

The twenty-first century has witnessed unprecedented ecological transformations driven by climate change, biodiversity loss, industrial expansion, and rapid technological development. These interconnected crises demand interdisciplinary approaches capable of integrating environmental, agricultural, and public health perspectives. This paper examines the evolving relationship between humans, animals, and ecosystems through the framework of One Health, emphasizing the necessity of collaborative global responses to emerging ecological and health challenges in the Anthropocene.

The study explores how chemical pollutants, habitat fragmentation, and unsustainable resource extraction have reshaped ecological interactions, particularly within vulnerable pastPoster and coastal communities. By analysing changing pastPoster socio-ecologies, the paper highlights the socio-economic pressures faced by traditional livelihoods under conditions of environmental instability and technological transition. Simultaneously, it investigates the transformative potential of precision agriculture in promoting sustainable food systems through data-driven farming practices, efficient resource management, and climate-resilient agricultural strategies.

Special attention is given to neglected tropical diseases in India and Africa, demonstrating how environmental degradation, poverty, and inadequate healthcare infrastructures contribute to the persistence of zoonotic and vector-borne diseases. The paper further argues that effective responses require integrated monitoring systems ranging from micro-level biological surveillance to macro-scale ecological observation. Such approaches enable early detection of environmental disruptions and strengthen conservation planning.

In addition, the study addresses the ecological significance of marine and mangrove ecosystems as critical buffers against climate change, coastal erosion, and biodiversity decline. It advocates for conservation models that combine indigenous knowledge, scientific innovation, and policy intervention. Ultimately, the paper argues that sustainable futures depend upon reimagining ecological ethics beyond disciplinary boundaries, fostering resilient socio-ecological systems that balance human development with environmental stewardship.

Keywords: One Health, Anthropocene, Climate Change, Biodiversity Loss, Ecological Transformation, Precision Agriculture, Sustainable Food Systems, Environmental Degradation, Zoonotic Diseases, Neglected Tropical Diseases, PastPoster Socio-Ecologies, Ecosystem Monit

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Title of the Abstract:

Title: Understanding Public Health through a One Health Approach

ABSTRACTS

Abstract:

The One Health approach explains that human health, animal health, and the environment are closely connected. Today, many health problems are not separate, but linked with nature and animals. Diseases like COVID-19 and Nipah virus show how infections can spread from animals to humans.

In India, especially in places like Kerala, changes in the environment such as deforestation and urban growth increase contact between humans and animals. This raises the chance of new diseases. Another serious problem is the overuse of antibiotics in both humans and animals, which leads to antimicrobial resistance.

To solve these problems, experts from different fields must work together. Doctors, veterinarians, and environmental scientists need to cooperate. Better disease monitoring, protecting nature, and increasing public awareness are important steps.

In conclusion, the One Health approach is very important for protecting public health and preventing future diseases. It helps build a safer and healthier future for everyone.

Keywords: Zoonotic Diseases,Public Health,Environmental Health,Antimicrobial Resistance,Sustainability

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Title of the Abstract:
Integrated Phenotypic and Genomic Insights of Milk Microbiome Reveals Multidrug Resistance in Dairy Cattle from Maharashtra

ABSTRACTS

Antimicrobial resistance (AMR) in dairy ecosystem is a growing concern with significant implications for animal health, food safety, and public health. Milk antimicrobial susceptibility testing (AST), which is routinely used for detection of resistance, does not identify the causative pathogens or the underlying genetic mechanisms responsible for resistance and its spread via mobile genetic elements.

In this study, we have carried out sequencing analysis of DNA from milk samples from normal and mastitis animals to detect microbial pathogens and comprehensive identification, by whole genome sequencing, of all antibiotic resistance genes (ARG). Our approach used a combination of AST for phenotypic testing and sequencing for understanding the genetic basis for resistance.

AST on 317 milk samples collected from dairy farms across Maharashtra, India, revealed widespread resistance to commonly used antibiotics, particularly β-lactams, macrolides, and aminoglycosides. Subsequently, selected samples were subject to culture enrichment followed by Oxford Nanopore sequencing and comprehensive genomic analysis. Taxonomic profiling identified major mastitis-associated pathogens, including Staphylococcus aureus, Escherichia coli, and Streptococcus agalactiae. Resistome analysis revealed a diverse array of antimicrobial resistance genes, including β-lactamases, aminoglycoside-modifying enzymes, and multidrug efflux systems such as acrAB-tolC and mdfA. In addition to the presence of chromosomally encoded ARGs, the presence of a significant number of ARGs associated with mobile genetic elements indicate active horizontal gene transfer within the milk microbiome.

These findings demonstrate that dairy milk serves as a complex reservoir of antimicrobial resistance, where mobile and stable genetic elements collectively sustain multidrug resistance. This study underscores the importance of integrating genomic approaches with phenotypic assays to fully understand resistance mechanisms and to develop effective One Health strategies for AMR surveillance and control.

Keywords: antimicrobial resistance, milk microbiome, horizontal gene transfer, Oxford N2anopore sequencing, resistome

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Title of the Abstract:
Lineage-Linked Biofilm Formation and Widespread Multidrug Resistance among Indian Acinetobacter baumannii Clinical Isolates

ABSTRACTS

Aims: This study aimed to investigate the diversity and determinants of biofilm formation among clinical Acinetobacter baumannii Indian isolates and assess their relationship with antimicrobial resistance profiles, biofilm-associated genes, and genetic lineages revealed through whole-genome analysis.

Methods and Results: 230 A. baumannii clinical isolates across India (2015–2022) were tested for antibiotic susceptibility using the VITEK 2 system. Biofilm formation was quantified via the Tissue Culture Plate method. Whole genome sequencing (Illumina MiSeq) and bioinformatic analysis were performed to identify biofilm-associated genes, antimicrobial resistance genes and sequence types. Statistical associations were assessed using Kruskal-Wallis, Spearman's, and Fisher's tests. 85.22% of isolates were multidrug-resistant (MDR), and 100% exhibited biofilm formation, with 52.17% strong, 39.57% moderate, and 8.26% weak biofilm producers. Genes including ompA, bfmR, pgaA, pgaB, and pgaD were universally present. No significant association was observed between biofilm formation and antibiotic resistance ($P = 0.55$), specimen type ($P = 0.54$), or the presence of specific biofilm-related genes ($P > 0.05$). 21 sequence types (STs) were identified, with ST2 being the most prevalent (51.73%). Strong biofilm formation was more common in ST164, ST1, and ST575.

Conclusions: This study demonstrates a high prevalence of MDR and strong biofilm-forming A. baumannii isolates in India. Biofilm formation appeared independent of resistance or gene carriage but showed lineage-linked variation across sequence types. Impact Statement: These findings underscore the need for enhanced surveillance and targeted strategies against infections caused by strong biofilm-forming A. baumannii, which may exhibit lineage-linked persistence and resistance.

Keywords: Acinetobacter baumannii, Antibiotic resistance, Biofilm formation, Biofilm-associated genes, Whole genome sequencing

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Title of the Abstract:

From Embryo to Ecosystem: Standardizing Zebrafish Embryos as a NAM Platform for Biocompatibility and Chemical Safety under One Health”

ABSTRACTS

The zebrafish (Danio rerio) has emerged as a powerful vertebrate model bridging developmental anatomy and translational screening. However, broader regulatory acceptance requires rigorous standardization of developmental endpoints to ensure reproducibility, inter-laboratory comparability, and predictive reliability. This study aimed to establish a structured developmental anatomical framework as a New Approach Methodology (NAM), aligned with Replacement, Reduction, and Refinement (3Rs), for biocompatibility assessment and chemical safety evaluation.

Zebrafish embryos (0–72 hours post-fertilization; hpf) and early larval stages were systematically evaluated under controlled laboratory conditions following Institutional Animal Ethics Committee approval and in compliance with Committee for the Control and Supervision of Experiments on Animals (CCSEA) and Organisation for Economic Co-operation and Development (OECD) Fish Embryo Toxicity guidelines. Developmental progression was mapped using defined morphological landmarks including cleavage, gastrulation, segmentation, organogenesis, cardiac initiation (~22 hpf), hatching, swim bladder inflation, and early behaviPoster responses. Quantitative morphometric parameters such as body length, yolk sac utilization, pigmentation index, cardiac rhythm, and fin development were recorded using high-resolution imaging to generate a reproducible anatomical dataset.

The influence of the chorion as a barrier to chemical exposure was evaluated, and optimized dechorionation improved exposure uniformity and assay sensitivity. The standardized framework demonstrated high reproducibility and enhanced detection of subtle alterations. Translational screening confirmed that extracellular matrix-based scaffolds and decellularized xenografts did not induce developmental toxicity, supporting their biocompatibility.

This study establishes zebrafish embryos as a robust, scalable, and ethically aligned NAM for high-throughput screening, enhancing regulatory relevance under the One Health paradigm.

Keywords: Biocompatibility, Chemical safety, NAM, One Health, Zebrafish embryos

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Title of the Abstract:

Environmental Surveillance of LSDV and FMDV- Towards Integrated and Scalable Detection Systems

ABSTRACTS

Effective surveillance of transboundary animal diseases such as Lumpy Skin Disease Virus (LSDV) and Foot-and-Mouth Disease Virus (FMDV) is essential for early detection, outbreak mitigation, and informed disease control strategies. Conventional surveillance systems, which rely primarily on clinical case reporting, often have limited sensitivity for detecting subclinical infections and early transmission events. In this context, environmental surveillance provides a complementary, non-invasive, and scalable approach for monitoring pathogen circulation at the herd and ecosystem levels.

In the present study, we developed and implemented an integrated environmental surveillance framework for LSDV, with potential applicability to FMDV, across selected livestock-intensive regions. The approach involved systematic collection of environmental samples, including drinking water, wastewater, soil, feed, and milk, alongside targeted clinical sampling. Standardized protocols were established for sample collection, processing, and metadata capture, supported by digital tools for real-time data acquisition, site mapping, and integration of field and laboratory datasets.

Molecular detection was carried out using optimized DNA extraction methods and a nested PCR assay to enhance sensitivity. Among the environmental matrices tested, LSDV detection was successfully observed in drinking water and wastewater, while soil and feed samples showed comparatively lower positivity. These findings identify drinking water as a key indicator matrix for environmental monitoring of LSDV.

The results demonstrate the feasibility of detecting viral signals from environmental sources, providing early evidence of pathogen circulation within affected areas. The integration of environmental surveillance with field epidemiology and digital data systems enables improved situational awareness, facilitating timely and targeted interventions.

Overall, this study highlights the utility of environmental surveillance as a cost-effective and scalable strategy to strengthen livestock disease monitoring systems. The proposed framework offers a transferable model that can be extended to other transboundary and zoonotic pathogens within a One Health paradigm, supporting enhanced disease preparedness and response.

Keywords: Environmental surveillance, Lumpy Skin Disease Virus (LSDV), Foot-and-Mouth Disease Virus (FMDV), Molecular diagnostics, One Health

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Title of the Abstract:

Linking Ecosystem Recovery, Human Well-Being, and Livelihood Resilience: A One Health Perspective from Manganese Ore India Limited, Dongri Buzurg, Maharashtra, India

ABSTRACTS

Open-cast-mining of Manganese in Dongri-Buzurg has extensively altered surrounding pristine ecosystem via heavy metal enrichment, deposition of extraneous lithogenic material, dust pollution, and landscape degradation. Mining-induced degradation affects various trophic levels of the ecosystem, disrupts trophic networks by affecting vegetation structure, ecological processes, lower and higher-level-organisms including livestock and humans. In the context of land-degradation, climate change, ecological-restoration of mining landscapes has appeared as an important environmental and One Health challenge in India. The present investigation examines ecological restoration of Mn mine landscapes as a One Health intervention linking ecosystem recovery, environmental quality, human wellbeing, and ecosystem resilience. The study evaluates the outcomes of a 10-year-old restored Mn mine landscape, where active restoration involving plantation of native-trees and bamboos was initiated in 2012. Restoration assessment was carried out through assessment of soil-physicochemical- properties, heavy-metals, vegetation-structure, ecological-succession, within the restored-mine-landscape. In addition, the study examines the influence of ecological restoration on ecosystem-linked livelihood vulnerability and the environmental vulnerability of surrounding communities dependent on dryland ecosystem resources. Results of the investigation infer that by 2024 restored mine landscapes exhibited showed improved ecological recovery, reduced soil metal concentrations (Mn, Fe, etc.), and reduced soil erosion. Further results indicate improved environmental quality, and reduced ecosystem-linked livelihood vulnerability among livestock and communities. Restored mine landscapes exhibited lower Ecological Risk Index (ERI = 36) and Human Health Risk Index (HHRI = 0.67), indicating reduced ecological and human health risks following restoration. Ecological restoration of mining landscapes supports One Health resilience strategy by improving ecosystem stability, environment quality, and livelihood-linked ecosystem services, thereby contributing to long-term human, livestock and ecosystem resilience.

Keywords: ecosystem health, human health, manganese mining, native flora regeneration, restoration, toxicity

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Title of the Abstract:

Antibacterial activity of bacteriophage and biosynthesized nanomaterials against carbapenem-resistant Shigella: a One Health approach

ABSTRACTS

Antimicrobial resistance (AMR) is a critical global health challenge that threatens the effective treatment of infectious diseases, particularly those caused by enteric pathogens such as Shigella spp., which are major causes of bacillary dysentery. The emergence of multidrug-resistant (MDR) strains, including those harboring blaNDM-mediated carbapenem resistance, underscores the urgent need for alternative therapeutic strategies within a One Health framework that integrates human, environmental, and microbial health. This study evaluated the antibacterial potential of bacteriophages and biosynthesized nanoparticles derived from Holarrhena antidysenterica against clinical Shigella isolates.

Clinical isolates were characterized based on their antimicrobial susceptibility and resistance gene profiles. Silver nanoparticles were synthesized using plant extracts and assessed for antibacterial activity, whereas Shigella-specific bacteriophages were isolated and evaluated for lytic efficacy. The combined effects of the nanoparticles and bacteriophages were further investigated.

The results indicated that both bacteriophages and biosynthesized nanoparticles exhibited significant antibacterial effects against MDR Shigella isolates. Notably, the combination approach demonstrated enhanced inhibitory activity compared to individual treatments, suggesting an improved antibacterial efficacy.

This study highlights the potential of integrating phage therapy with green nanotechnology as a sustainable and effective alternative to conventional antibiotic therapy. From a One Health perspective, these strategies offer promising solutions for combating AMR while minimizing environmental impact. Further studies are required to validate these findings and explore their clinical applicability.

Keywords: Antimicrobial resistance, Bacteriophage, Nanoparticles, One Health, Shigella

Mode: Poster Presentation

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Title of the Abstract:

Extraction and detection techniques for avian influenza virus environmental surveillance across high-risk locations in Hyderabad

ABSTRACTS

Introduction: Highly pathogenic avian influenza virus has caused significant economic and biodiversity losses globally therefore, an efficient surveillance method is required to predict and contain outbreaks. In this study, we address this need by standardizing extraction and detection methods for Avian Influenza virus across diverse environmental sample types.

Objective: To standardize and test methods for extraction and detection of avian influenza virus (AIV) in multiple environmental sample matrices.

Methods: Environmental samples (air, water, fecal material, and surface swabs) and limited clinical samples were collected from poultry farms, live bird markets, urban sewage, lakes, and wildlife-associated habitats in Hyderabad, India. Viral RNA was extracted using a total nucleic acid protocol. Detection was performed using qRT-PCR targeting the influenza A M gene using WHO recommended primers and subtype-specific assays, alongside a commercial probe-based kit. Digital PCR (dPCR) was additionally used to assess detection sensitivity in selected samples. Positive samples were subjected to sequencing using Oxford Nanopore Technologies for subtype identification.

Results: AIV RNA was detected in multiple environmental sample types, with higher detection frequencies observed in samples from live bird markets and sewage systems. Among sample types, wash water and surface swabs (cage and chopping board) from live bird markets showed relatively higher viral loads, while water and fecal samples showed lower but detectable positivity. Air samples from enclosed environments also yielded detectable viral RNA. dPCR demonstrated higher sensitivity compared to qRT-PCR in same samples. Detection of viral RNA in environmental samples corresponded with detection in nearby clinical or tissue associated samples within live bird market.

Conclusion: Environmental sampling combined with sensitive molecular detection methods enables consistent detection of AIV RNA across diverse sample types and settings. These findings support the utility of environmental surveillance as a complementary approach to existing surveillance systems, particularly in high-risk interfaces such as live bird markets.

Keywords: avian influenza, environmental surveillance, one health, wastewater

Mode: Poster Presentation

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Title of the Abstract:

Molecular surveillance of antimicrobial resistance genes in Hospital wastewater

ABSTRACTS

Background: Antimicrobial resistance (AMR) is an increasingly significant global threat to human health, accounting for over one million deaths annually due to resistant infections. It is recognised as a quintessential One Health problem that encompasses human, animal, and environmental health. Hospital wastewater serves as a critical reservoir of AMR genes, facilitating their dissemination. Monitoring hospital wastewater enables early detection of resistance trends in the community, provides insights into environmental dissemination, and informs integrated strategies to mitigate AMR transmission.

Methods: Wastewater samples were collected fortnightly under sterile conditions from the inlet of the hospital sewage treatment plant at NIMHANS, Bengaluru (June 2025- March 2026), using a grab sampling technique during peak flow hours (6-10 am). Samples were inactivated onsite with 0.1% sodium hypochlorite and transported to the laboratory at 4°C. Concentration was performed using PEG-based precipitation with overnight incubation at 4°C, followed by centrifugation. The pellet was resuspended, and nucleic acid was extracted using the Huwel wastewater extraction kit. A customised real-time PCR panel (Quantiplus AMR kit) targeting 21 AMR genes, including carbapenemases, ESBLs, methicillin resistance, vancomycin resistance, and mobilised colistin resistance genes, was used.

Results: Multiple AMR genes were detected in hospital wastewater, with the highest prevalence observed for carbapenemase genes (NDM, VIM, KPC, IMP, and OXA), followed by ESBL genes (CTX-M, SHV, CMY). Vancomycin resistance genes (vanA and vanB) were also identified. Among mobilised colistin resistance determinants, mcr3, mcr4, mcr8, and mcr5/9/10 were detected. In contrast, genes Van M, mcr8, mcr1/2/6, and Mycobacterium tuberculosis were not detected in the samples.

Conclusion: Hospital wastewater harbours a high burden of clinically relevant AMR genes, reflecting local antibiotic usage and selective pressure. These findings emphasize its role in AMR dissemination and underscore wastewater surveillance as a critical tool for guiding AMR mitigation strategies.

Keywords: Antimicrobial resistance, Environmental surveillance, Hospital wastewater, Resistome

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Title of the Abstract:

Biomimetic Design and Performance Evaluation of a Decentralized 30 KLD Sewage Wastewater Treatment System for Sustainable Water Reuse

ABSTRACTS

Growing freshwater scarcity and increasing sewage generation due to rapid urbanization have intensified the need for sustainable wastewater treatment technologies with low energy consumption, minimal maintenance, and reduced operational costs. Conventional sewage treatment plants (STPs) often depend on continuous electricity, chemical dosing, and skilled manpower, which limits their applicability in decentralized settings. This study evaluates the design and treatment performance of a 30 KLD biomimetic sewage wastewater treatment system (ECOSTP) installed at Koramangala Club, Bengaluru, India. The system was developed by mimicking natural purification mechanisms observed in wetlands through anaerobic digestion, aggregate filtration, plant biofiltration, and sand filtration processes. The treatment includes primary anaerobic treatment, secondary aggregate filtration, and tertiary polishing using a Plant Bio Filter (PBF) and sand filter. Wastewater samples collected between February 2025 and July 2025 were analyzed using APHA standard methods. The treated effluent achieved pH values of 7.1–7.38, total suspended solids (TSS) of 5.6–8.6 mg/L, biochemical oxygen demand (BOD) of 3.8–4.2 mg/L, chemical oxygen demand (COD) of 18–44 mg/L, total nitrogen (TN) of 3.6–6.4 mg/L, ammoniacal nitrogen (NH3) of 1.6–3.2 mg/L, and fecal coliform levels of 32–33 MNP/100 mL, complying with Karnataka State Pollution Control Board standards (KPCBS). Regression analysis confirmed stable long-term performance. The findings highlight the potential of biomimetic decentralized systems for sustainable water reuse applications.

Keywords: decentralized wastewater treatment, nature-based solutions, sewage treatment plant, plant biofilter, sustainable water reuse, anaerobic filtration, wastewater management.

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Title of the Abstract:

Rabies Prophylaxis Gaps: Missed Opportunities to Save Lives

ABSTRACTS

Background: Rabies is a fatal zoonotic disease and a major public health concern in India. Timely and appropriate post-exposure prophylaxis (PEP), including wound washing, anti-rabies vaccination, and rabies immunoglobulin (RIG) for severe exposures can prevent disease onset. However, deviations in PEP implementation continue to result in preventable deaths.

Objective: To assess deviations in PEP practices among human rabies cases.

Methods: This retrospective study analysed adherence to PEP protocols following animal-exposure in laboratory-confirmed human rabies cases from 2023–2025 at NIMHANS, Bengaluru.

Results: Sixty-nine confirmed cases of rabies were analysed. Dogs accounted for 88.4% of exposures, followed by wild animals (8.7%) and cats (2.9%). Most patients (85.5%, n=59) had Category III (severe) exposures.

Wound care was performed in 23 (33.3%) cases; an equal proportion did not receive or had unknown wound care status. Thirty-one (45.6%) cases did not receive any vaccination, 23 (33.8%) received incomplete vaccination, and the vaccination status was unknown in 8 (11.8%) cases. Only 6 (8.8%) cases received all vaccine doses. Among Category III exposures, RIG was administered in 16 (27.1%) cases, not administered in 34 (57.6%) cases and unknown in 9 (15.3%) cases.

Overall, only 3 (5.1%) cases received complete PEP, 16 (23.2%) received none, and 50 (72.5%) received incomplete PEP.

Conclusion: Most rabies deaths were linked to deviations in PEP, often misinterpreted as vaccine failure. Inadequate wound care, incomplete vaccination, and lack of RIG highlight critical gaps in care. Strengthening awareness among healthcare providers and communities on essential PEP practices is key to preventing these avoidable deaths.

Keywords: Animal Exposure, PEP Deviation, Post Exposure Prophylaxis, Rabies

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Title of the Abstract:

Reuse of Treated Wastewater for Water Security and One Health: A Case Study of the K&C Valley Initiative in India

ABSTRACTS

The One Health framework recognizes the interlinkages between human, animal, and environmental health, particularly in water resource management. The Koramangala–Challaghatta (K&C) Valley Project in southern India represents a large-scale urban wastewater reuse intervention aligned with this approach. Initiated in 2018, the project diverts 440 MLD of treated wastewater from Bengaluru to a network of 142 lakes in water-scarce regions such as Kolar and Chikkaballapur, facilitating indirect groundwater recharge and hydrological restoration. The system employs a Soil Aquifer Treatment (SAT) approach, wherein treated wastewater percolates through soil layers, enhancing water quality through natural filtration.

Environmentally, the project has revitalized lake ecosystems, improved aquifer recharge, and enhanced biodiversity. Groundwater levels have increased by 65–70%, accompanied by improved quality, including conversion of hard water to softer forms through dilution. The Water Quality Index improved from "very poor" to "good," indicating substantial ecological recovery. These hydrological improvements have supported agricultural transformation, increasing cropping intensity from 1 to 6 crops per year, reducing eucalyptus plantations, and enabling reverse migration toward farming, floriculture, horticulture, dairy, and fisheries. Enhanced water availability has also improved sanitation, hygiene, and rural livelihoods, with a benefit–cost ratio of ~4.34, demonstrating strong economic viability.

From a human and animal health perspective, the project provides a reliable alternative water source, reducing dependence on overexploited aquifers. Studies indicate no adverse impacts on soil, crops, livestock, or public health. Notably, a 67% reduction in waterborne diseases was observed, including declines in typhoid (85%), bacillary dysentery (70%), and diarrhea–gastroenteritis (68%). In livestock, disease prevalence decreased by 38% (from 18,504 to 11,365 cases) and mortality reduced by 43% (from 431 to 244 cases).

Overall, study demonstrates a successful One Health model by integrating wastewater reuse, groundwater sustainability, and ecosystem restoration, highlighting the potential of circular water management strategies for resilient and sustainable water systems.

Keywords: Groundwater Sustainability, One Health, Soil Aquifer Treatment (SAT), Wastewater Reuse, Water Security

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