

ICAHS 2026

5th International Conference
on Animal Health Surveillance

Ha Noi, Viet Nam
10-12 November 2026

Conference proceedings

Contents

Table of Contents

Conference programme 1

Introduction 7

A brief history of ICAHS: from surveillance methods and the science-policy interface to evaluation of impact 7

Theme 1: Engagement and participation of actors and end-users in surveillance activities 12

Oral presentations 12

Increasing One Health awareness at the local-level to bolster passive surveillance: insights from stakeholders from the Asia-Pacific 12

Community Zoonotic Case Definitions in Rural Cambodia: Syndromic Knowledge, Reporting Barriers, and Design Considerations for a Community-Based Early Warning System 15

Strengthening Animal Rabies Outbreak Response through Community Engagement and One Health Approaches: Lessons from Local Contexts in Thailand 19

Community-based surveillance and community engagement for One Health disease prevention 23

Assessing One Health Surveillance Systems at the Human-Animal-Wildlife Interface in a Biodiversity Hotspot: Findings from Stung Treng Province, Cambodia 26

Drivers of underreporting and strategies for improvement of surveillance of Q fever in Italy: the case study of Emilia Romagna region 30

Case story presentations 31

Spot It in Animals, Stop It in Humans: Cambodia's Avian Flu Defense 31

Impact of an integrated diagnostic network on strengthening passive surveillance in Mato Grosso, Brazil 34

Strengthening One Health Surveillance Coordination in Lao PDR: Findings from a Multi-Sectoral Mapping Study and National Workshop 35

Short oral presentations 39

Roles of community animal health workers in surveillance and early warning – a regional overview in South East Asia 39

Engagement of key stakeholders for the development of a participatory surveillance system of equine pregnancy and perinatal loss in Northern Italy 39

Can participatory co-design improve the operability of risk-based community surveillance for zoonoses in transforming landscapes? A Philippines case-study 40

One Health field site: Advancing intersectoral engagement and implementation at the grassroots level in Southeast Asia 41

Livestock Identification and Registration System (LIRS) as an integrated tool for a community rabies vaccination program, A pilot project from Vietnam 42

Poster presentations 43

Investigation of Recurrent Canine Rabies and Community KAP Survey in a Rural District of Maha Sarakham Province, Thailand (Sep 2024 – 14 Feb 2025) 43

Evaluating Risk Awareness and Behaviours to Enhance Avian Influenza Communication Strategies in Cambodia 47

Theme 2: Science - society - policy dialogue for effective surveillance 49

Contents

Oral presentations 49

A participatory progressive framework to guide development of national animal disease surveillance and early warning capacities in Asia 49

One Health Strategy 2019: A Review of Nepal's Multisectoral Health Framework 51

Case story presentations 55

An Exploratory Assessment of Targeted Surveillance for Bovine Spongiform Encephalopathy in Great Britain 55

Short oral presentations 60

Leveraging surveillance data to map sources and spread of *Salmonella Enteritidis* in four European countries 60

Poster presentations 60

Mekong One Health Innovation Program (MOHIP): Connecting North and South to Improve Health Security through One Health Approach 60

Theme 3: Evaluation and impact assessment of surveillance systems 62

Oral presentations 62

Attributes and frameworks for surveillance evaluation in veterinary public health: a scoping review 62

Epidemiology and Surveillance of Rabies in Animals in Sa Kaeo Province, Thailand, 2016–2025 65

Case story presentations 67

Strengths and gaps of animal disease surveillance systems in Asia and the Pacific: lessons from the application of FAO's Surveillance Evaluation Tool (SET) 67

Short oral presentations 70

Evaluation of the poultry scanning surveillance system in England and Wales 70

Optimal control for animal health surveillance and intervention strategies applied to ASF and HPAI 72

Quantitative evaluation of the sensitivity of a wildlife health surveillance network for the detection of highly pathogenic avian influenza H5N1 in Cambodia 74

Poster presentations 77

Risk-based active surveillance in rural establishments: design, implementation and sensitivity assessment in Mato Grosso, Brazil 77

Assessing the quality of livestock registry data using risk-based surveillance in Mato Grosso, Brazil 78

Theme 4: Innovations, Artificial Intelligence and data integration in surveillance 80

Oral presentations 80

Beyond human vision – validating camera vision systems in meat inspection 80

Monitoring welfare in dairy farms: analysis of census-level welfare assessment protocols reveals farm characteristics associated with reduced or improved welfare levels 83

European benchmarks for AI based detection of broiler carcass lesions and insights from official veterinarians on broiler post mortem inspection 86

Short oral presentations 90

FarmVetCare app: A digital approach to improving disease reporting and surveillance for livestock farmers and authorities 90

Contents

Bibliometric mapping of the wild-domestic animal interface and pathogen spillover research 91

Poster presentations 92

Towards LLM-Enhanced Epidemic Intelligence: Opportunities for animal disease surveillance in Vietnam 92

Utilizing internet-based data for early detection of African Swine Fever in Viet Nam 93

Theme 5: Integrating environmental and wildlife surveillance in a One Health framework 95

Oral presentations 95

Mapping of wild meat supply chains in relation to zoonotic disease transmission in selected provinces in Viet Nam 95

Are we targeting the right animals? Validating network centrality as a proxy for disease risk across contrasting wildlife systems 96

Environmental Monitoring of Avian Influenza Virus in Scotland: Insights into Molecular Evolution and One Health Dynamics 97

Strengthening wildlife interface viromic surveillance for emerging infectious disease detection in Southeast Asia 98

Short oral presentations 98

Distribution of ESBL producing E. coli and resistance pattern in riverine and wastewater system of Kathmandu Valley ... 98

Poster presentations 102

More than just a catch: Unveiling Parasites in Wild and Market Fish with One Health Implications 102

Theme 6: All about AMR 104

Oral presentations 104

Designing an Antimicrobial Resistance Surveillance System for Healthy Pet Dogs and Cats 104

Integrated One Health Surveillance of Salmonella, Antimicrobial Resistance, and Stakeholder Food Safety Practices in Poultry Markets in Mindanao, Philippines 107

Hidden Threats in Our Meat: Uncovering Antimicrobial Resistance in Slaughterhouses in Bukidnon, Philippines 109

Short oral presentations 110

AI-Powered Antimicrobial Resistance Surveillance and Management in a One Health context: A Scoping Review and Lessons for Vietnam 110

Healthy herds, hidden risk: genomic antimicrobial resistance profile of commensal *E. coli* in cattle in Great Britain 115

Monitoring of antimicrobial resistance in the interface between domestic animals, wildlife, and the environment 116

Poster presentations 117

Antimicrobial Resistance in Food-Producing Animals Across Seven Provinces of Cambodia: Findings from Livestock Farm Surveillance 117

Theme 7: Surveillance in livestock and food production systems and value chains 119

Oral presentations 119

Opportunities and limitations of avian influenza surveillance data harmonization for outbreak forecasting in Vietnam .. 119

A Generic Surveillance Framework for Assessing Illegal Meat Introduction Risk 124

Surveillance for farm-to-farm wind dispersion during outbreaks of highly pathogenic avian influenza in southeastern Australia: from integrated research to decision-making 128

Contents

The impact of the age structure in Dutch dairy herds on surveillance indicators 132

Impact of post slaughter broiler meat treatments on human disease risk from *Campylobacter* contaminated meals 136

Risk-based surveillance for early detection of transboundary animal diseases at the Brazil–Bolivia border in Mato Grosso State 141

Case story presentations 144

Evidence of a novel orthobunyavirus from the Simbu serogroup in New South Wales, Australia, from 2012 144

Short oral presentations 148

Evaluation of the surveillance system for Avian Influenza and Newcastle Disease Virus in Ghana 148

Surveillance of Avian Influenza in Vaccinated Poultry: A Systematic Review of Strategies and Implementation Challenges 152

The business case for foot and mouth disease elimination in Nusa Tenggara Barat, Indonesia 154

Insights from Questionnaire-Based Assessment of Farm Management Weaknesses during a Haemorrhagic Septicemia Outbreak in Prachin Buri, Thailand 157

Differential Diagnosis of Nodular Skin Lesion in Bali Cattle: A Surveillance Case Study from Keerom District, Papua Province, Indonesia 161

Poster presentations 165

Surveillance capacity and value-chain integration of cattle slaughterhouses in Thailand: implications for risk-based bovine tuberculosis monitoring 165

Avian Influenza bio-surveillance in Nepal: Status, opportunities and challenges 166

African Swine Fever in Mindanao, Philippines: From Farm to Market—Prevalence, Risk Factors, Farmer Perspectives and Financial Losses 167

Seroprevalence and subclinical hemato-biochemical impact of bovine viral diarrhea virus in slaughtered cattle in Bukidnon, Philippines 168

Epidemiology of African Swine Fever in Pork Products and Slaughtered Pigs and the Lived Experiences of Selected Stakeholders in Davao de Oro, Philippines 169

Epidemiological and molecular characteristics of HPAI viruses (H5Nx) in selected live bird markets in Lao PDR, 2022-2023 170

Understanding the spread of African Swine Fever in Nepal: Spatio-temporal analysis of early-phase outbreaks (March 2022 – July 2024) 172

Molecular Prevalence and Risk Factor Analysis of Tick-Borne Bacteria and Hemoplasmas in Beef Cattle at the Thai–Myanmar Border, Kanchanaburi Province, Thailand 174

Conference programme

	Tuesday 10/11/2026		11 November 2026		12 November 2026	
	Presentation title	*Speaker*	*Presentation title*	*Speaker*	*Presentation title*	*Speaker*
09:00 - 09:05	Formal opening presentations	Pham Doan Lan (Veterinary Institute of Animal and Veterinary Sciences, Vietnam)	**Invited presentation: Evaluation and impact assessment of surveillance systems**		**Invited presentation: All about AMR**	
09:05 - 09:10			What difference does surveillance make? Rethinking evaluation from performance to impact	Flavie Goutard (CIRAD, Vietnam)	Overcoming Challenges in Vietnam's AMR Strategy: Lessons Learned from Laboratory Data, Wildlife Interfaces, and Community Stewardship	Thanhson (Veterinary Institute of Animal and Veterinary Sciences, Vietnam)
09:10 - 09:15		Andreas Seiler (Agricultural Affairs Advisor for Vietnam, Thailand, Cambodia, Laos, and Myanmar, French Embassy of Vietnam)				
09:15 - 09:20						
09:20 - 09:25		Francois Roger (CIRAD, Vietnam)				
09:25 - 09:30						
09:30 - 09:35		Vu Thi Phuong (One Health Partnership, Ministry of Agriculture and the Environment, Vietnam)				
09:35 - 09:40						
09:40 - 09:45	From ICAHS 4 to ICAHS 5	Lis Alban (Danish Agriculture and Food Council, Denmark)	Attributes and frameworks for surveillance evaluation in veterinary public health: a scoping review	Liliana Martella (University of Bologna, Italy)	Designing an Antimicrobial Resistance Surveillance System for Healthy Pet Dogs and Cats	Judy Evans (School of Veterinary Medicine and Biosciences, Scotland's Rural College, United Kingdom)
09:45 - 09:50	15 years of ICAHS: 2011 till today	Daan Vink (CIRAD, France / ICAHS Scientific Committee)				
09:50 - 09:55						
09:55 - 10:00	**Invited presentation: Engagement and participation of actors and end-users in surveillance activities**					
10:00 - 10:05	How to engage communities effectively in surveillance activities	Khuat Thi Hai Oanh (SCDI, Vietnam)	Epidemiology and Surveillance of Rabies in Animals in Sa Kaeo Province, Thailand, 2016–2025	Bopit Puyati (Buriram Provincial Livestock Office, Thailand)	Integrated One Health Surveillance of Salmonella, Antimicrobial Resistance, and Stakeholder Food Safety Practices in Poultry Markets in Mindanao, Philippines	Kassey Alsylle Dargantes (Central Mindanao University, Philippines)
10:05 - 10:10						
10:10 - 10:15						
10:15 - 10:20						
10:20 - 10:25			"Behind the feathers": Evaluating Poultry Health Surveillance	Lara Royo-Hernandez (Royal Veterinary College, United Kingdom)	AI-Powered Antimicrobial Resistance Surveillance and Management in a One Health context: A Scoping Review and	Vu Van Phong (Vietnam National University of Agriculture, Vietnam)

Introduction

Introduction

10:25 - 10:30			Optimal control for animal health surveillance and intervention strategies applied to ASF and HPAI	Alfredo Acosta (Friedrich Loeffler Institut, Germany)	Healthy herds, hidden risk: genomic antimicrobial resistance profile of commensal E. coli in cattle in the Great	Larissa Melo Chicoski (Scotland's Rural College, United Kingdom)
10:30 - 10:35			Morning tea / coffee	Posters	Morning tea / coffee	Posters
10:35 - 10:40	Morning tea / coffee	Posters				
10:40 - 10:45						
10:45 - 10:50						
10:50 - 10:55						
10:55 - 11:00						
11:00 - 11:05			Quantitative evaluation of the sensitivity of a wildlife health surveillance network for the detection of highly pathogenic avian	Roland Guedou (CIRAD, France)	Hidden Threats in Our Meat: Uncovering Antimicrobial Resistance in Slaughterhouses in Bukidnon, Philippines	Jose Jr. Obedencio (Central Mindanao University, Philippines)
11:05 - 11:10			Strengths and gaps of animal disease surveillance systems in Asia and the Pacific: lessons from the application of FAO's Surveillance Evaluation Tool (SET)	Gaël Lamielle (Food and Agriculture Organization of the United Nations, Thailand)		
11:10 - 11:15	Increasing One Health awareness at the local level to bolster passive surveillance: insights from stakeholders from the Asia-Pacific	Mélodie Ruwet (Griffith University, Australia)				
11:15 - 11:20						
11:20 - 11:25			Mid-conference panel: what have we learned so far?	Invited panel participants	Integrated One Health surveillance of antimicrobial use and resistance: current status and perspectives	Marion Bordier (CIRAD, France) / Lis Alban (Danish Agriculture and Food Council, Denmark)
11:25 - 11:30						
11:30 - 11:35	Community Zoonotic Case Definitions in Rural Cambodia: Syndromic Knowledge, Reporting Barriers, and Design Considerations for a Community-Based Early Warning System	Phearak Maksay (International Development Enterprises (iDE), Cambodia)				
11:35 - 11:40						
11:40 - 11:45					Monitoring of antimicrobial resistance in the interface between domestic animals, wildlife, and the environment	Hillary Stratton (Denmark Technical University, Denmark)
11:45 - 11:50					Opportunities and limitations of avian influenza surveillance data harmonization for outbreak forecasting in Vietnam	Thuy Hoang Thi (University of Sydney, Australia)
11:50 - 11:55	Strengthening Animal Rabies Outbreak Response through Community Engagement and One Health Approaches: Lessons from Local Contexts in Thailand	Orapun Arjkumpa (Fourth Regional Livestock Office, Thailand)				
11:55 - 12:00			**Invited presentation: Innovations, Artificial Intelligence and data integration in surveillance**			
12:00 - 12:05				Crawford Revie (FAO)		

Introduction

12:05 - 12:10			Who Owns the Ingredients? AI, data integration and emerging sovereignty questions in surveillance		A Generic Surveillance Framework for Assessing Illegal Meat Introduction Risk	Laura Gonzalez Villeta (Animal and Plant Health Agency, United Kingdom)
12:10 - 12:15	Community-based surveillance and community engagement for One Health disease prevention	Marisa Peyre (CIRAD, France)				
12:15 - 12:20						
12:20 - 12:25						
12:25 - 12:30					Surveillance for farm-to-farm wind dispersion during outbreaks of highly pathogenic avian influenza in southeastern Australia: from integrated research to decision-making	Jenny-Ann Toribio (University of Sydney, Australia)
12:30 - 12:35	Roles of community animal health workers in surveillance and early warning – a regional overview in South East Asia	Gaël Lamielle (Food and Agriculture Organization of the United Nations, Thailand)				
12:35 - 12:40	Engagement of key stakeholders for the development of a participatory surveillance system of equine pregnancy and perinatal	Marco De Nardi (Department of Veterinary Medical Sciences (University of Bologna), Italy)	FarmVetCare app: A digital approach to improving disease reporting and surveillance for livestock farmers and	Nam Luong-Hung (International Livestock Research Institute, Vietnam)		
12:40 - 12:45	Can participatory co-design improve the operability of risk-based community surveillance for zoonoses in transforming	Bérénice Varga (CIRAD, Vietnam)	Bibliometric mapping of the wild-domestic animal interface and pathogen spillover research	Renata de Lara Muylaert (University of Sydney, Australia)		
12:45 - 12:50	Lunch	Posters	Lunch	Posters	Lunch	Posters
12:50 - 12:55						
12:55 - 13:00						
13:00 - 13:05						
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13:40 - 13:45						

Introduction

13:45 - 13:50	Spot It in Animals, Stop It in Humans: Cambodia's Avian Flu Defense	Aurelie Brioudes (Food and Agriculture Organization of the United Nations, Cambodia)	Beyond human vision – validating camera vision systems in meat inspection	Lis Alban (Danish Agriculture and Food Council, Denmark)	The impact of the age structure in Dutch dairy herds on surveillance indicators	Irene Bisschop (Royal GD, Netherlands)
13:50 - 13:55						
13:55 - 14:00						
14:00 - 14:05	Assessing One Health Surveillance Systems at the Human-Animal-Wildlife Interface in a Biodiversity Hotspot: Findings from Stung Treng Province, Cambodia	Sokha Chea (Kasetsart University, Thailand)				
14:05 - 14:10			Monitoring welfare in dairy farms: analysis of census-level welfare assessment protocols reveals farm characteristics associated with reduced or improved welfare levels	Anouk Veldhuis (Royal GD, Netherlands)	Impact of post-slaughter broiler meat treatments on human disease risk from *Campylobacter*-contaminated meals	Alessandro Foddai (National Food Institute, Danish Technical University (DTU-Food), Denmark)
14:10 - 14:15						
14:15 - 14:20						
14:20 - 14:25	Drivers of underreporting and strategies for improvement of surveillance of Q fever in Italy: the case study of Emilia Romagna region	Marco De Nardi (Department of Veterinary Medical Sciences (University of Bologna), Italy)				
14:25 - 14:30			European benchmarks for AI-based detection of broiler carcass lesions and insights from official veterinarians on broiler post-mortem inspection	Michal Majewski (Technical University of Denmark, Denmark)	Evaluation of the surveillance system for Avian Influenza and Newcastle Disease Virus in Ghana	Nichola Blackley (Animal and Plant Health Agency, United Kingdom)
14:30 - 14:35					Surveillance of Avian Influenza in Vaccinated Poultry: A Systematic Review of Strategies and Implementation Challenges	Yanshi Yanshi (Utrecht University, Netherlands)
14:35 - 14:40					Avian Influenza bio-surveillance in Nepal: Status, opportunities and challenges	Surendra Karki (Food and Agriculture Organization of the United Nations, Nepal)
14:40 - 14:45	Impact of an integrated diagnostic network on strengthening passive surveillance in Mato Grosso, Brazil	Ana Carolina Schmidt (Mato Grosso Animal Health Institute (INDEA-MT), Brazil)			Insights from Questionnaire-Based Assessment of Farm Management Weaknesses during a Haemorrhagic	Saravalee Piyachat (Veterinary Research and Development Center, Eastern Region, Thailand)
14:45 - 14:50			**Invited presentation: Integrating environmental and wildlife surveillance in a One Health framework**		Evidence of a novel orthobunyavirus from the Simbu serogroup in New South Wales, Australia, from 2012	Tiffany O'Connor (University of Sydney, Australia)
14:50 - 14:55			The wildlife–livestock–human interface: One Health surveillance and risks in East Africa and Vietnam	Hung Nguyen Viet / Ha Nguyen (International Livestock Research Institute, Vietnam)		
14:55 - 15:00	Strengthening One Health Surveillance Coordination in Lao PDR: Findings from a Multi-Sectoral Mapping Study and National Workshop	Watthana Theppangna (National Animal Health Laboratory, Laos)				
15:00 - 15:05					Risk-based surveillance for early detection of transboundary animal diseases at the Brazil–Bolivia border in Mato Grosso State	Daniella Schettino (Mato Grosso Animal Health Institute (INDEA-MT), Brazil)
15:05 - 15:10						
15:10 - 15:15	One Health field site: Advancing intersectoral engagement and implementation at the grassroots level in	Sinh Dang-Xuan (International Livestock Research Institute, Vietnam)				
15:15 - 15:20	Livestock Identification and Registration System (LIRS) as an integrated tool for a community rabies vaccination program, A	Ben Madin (Ausvet Pty Ltd)				
15:20 - 15:25	Afternoon tea / coffee	Posters			Differential Diagnosis of Nodular Skin Lesion in Bali Cattle: A Surveillance Case Study from Keerom District, Papua	Ratna Loventa Sulaxono (Disease Investigation Center Jayapura, Indonesia)

Introduction

15:25 - 15:30			Afternoon tea / coffee	Posters	Surveillance capacity and value-chain integration of cattle slaughterhouses in Thailand: implications for risk-based	Pongpon Homkong (Chiang Mai Municipality, Thailand)
15:30 - 15:35					Afternoon tea / coffee	Posters
15:35 - 15:40						
15:40 - 15:45						
15:45 - 15:50						
15:50 - 15:55	**Invited presentation: Science - society - policy dialogue for effective surveillance**					
15:55 - 16:00	From Dialogue to Action: Advancing One Health Surveillance in Viet Nam	Vu Thi Phuong (One Health Partnership, Ministry of Agriculture and the Environment, Vietnam)	Mapping of wild meat supply chains in relation to zoonotic disease transmissionin selected provinces in Viet Nam	Nga Nguyen Thi Thanh (Wildlife Conservation Society, Vietnam)		
16:00 - 16:05					Closing conference panel: summary, conclusions, key takeaways, follow-ups	Invited panel participants
16:05 - 16:10						
16:10 - 16:15						
16:15 - 16:20			Are we targeting the right animals? Validating network centrality as a proxy for disease risk across contrasting wildlife systems	Tatiana Proboste (University of Sydney, Australia)		
16:20 - 16:25						
16:25 - 16:30						
16:30 - 16:35	A participatory progressive framework to guide development of national animal disease surveillance and early warning capacities in Asia	Gaël Lamielle (Food and Agriculture Organization of the United Nations, Thailand)				
16:35 - 16:40			Environmental Monitoring of Avian Influenza Virus in Scotland: Insights into Molecular Evolution and One Health Dynamics	Erhan Yalcindag (University of Edinburgh, United Kingdom)		
16:40 - 16:45					What's next for ICAHS? Bids for ICAHS 6 and plenary discussion	
16:45 - 16:50						
16:50 - 16:55	One Health Strategy 2019: A Review of Nepal's Multisectoral Health Framework	Sachin Regmi (Department of Livestock Services, Nepal)				
16:55 - 17:00			Strengthening wildlife interface viromic surveillance for emerging infectious disease detection in Southeast Asia	Toan Hong (CSIRO Australian Centre for Disease Preparedness, Australia)		
17:00 - 17:05					Conference closing	

Introduction

17:05 - 17:10						
17:10 - 17:15	An Exploratory Assessment of Targeted Surveillance for Bovine Spongiform Encephalopathy in Great Britain	Suzanne Stone (Animal and Plant Health Agency, United Kingdom)				
17:15 - 17:20			Distribution of ESBL producing *E. coli* and resistance pattern in riverine and wastewater system of Kathmandu Valley	Manoj Kumar Shahi (Chulalongkorn University, Thailand)		
17:20 - 17:25			Day closing			
17:25 - 17:30	Leveraging surveillance data to map sources and spread of Salmonella Enteritidis in four European countries	Nicoline Munk Mikkelsen (Technical University of Denmark, Denmark)				
17:30 - 17:35	Day closing					
17:35 - 17:40	Drinks and social event					
17:40 - 17:45						
17:45 - 17:50						
17:50 - 17:55						
17:55 - 18:00						

Introduction

Introduction

A brief history of ICAHS: from surveillance methods and the science-policy interface to evaluation of impact

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Summary

Building on the success of the first International Conference on Animal Health Surveillance (Lyon, 2011), three subsequent conferences have established ICAHS as a recognised platform to discuss operational and technical elements of animal health surveillance. As a conference which addresses topics of current relevance, ICAHS has moved with the times. Here, the Scientific Committee of the current ICAHS reflects on its evolution by conducting a descriptive thematic analysis of presentation titles from the four conference programmes: Lyon, France (2011); Havana, Cuba (2014); Rotorua, New Zealand (2017); and Copenhagen, Denmark (2022). Where the emphasis was initially on methods, models, metrics and tools, there was a subsequent shift to surveillance evaluation, discussing how surveillance could be adapted to challenging contexts, and how to involve the people who use and depend on surveillance outputs. There was also growing attention for innovations brought about by digital tools, data integration, and the emergence of One Health thinking. More recently, the conversation progressed to translation of surveillance findings into policy and action, connecting surveillance outputs directly to decision-making, and assessing the impact and economic performance of surveillance. We now reflect on current priority areas and anticipated future directions of the conference, culminating in the organisation of the fifth ICAHS conference in Ha Noi, Vietnam.

Methods

The conference programmes of the four ICAHS conferences were compiled into a consolidated dataset listing conference year, conference themes, titles of the individual presentations, and presentation type (including oral communications, posters, and short presentations).

A descriptive thematic analysis was conducted. Themes were first summarised at conference level to identify the principal focus areas of each event. Presentation-level data were then analysed to assess relative emphasis across themes by frequency of contributions. Thematic groupings were compared chronologically to identify patterns in content and focus over time. Qualitative interpretation of recurring and emergent topics was used to construct a narrative of how ICAHS themes and priorities have evolved, and to infer broader trends in the field of health surveillance.

This approach drew on principles of qualitative narrative synthesis rather than quantitative meta-analysis. The goal was not statistical comparison but rather interpretation of trends in practice and scientific priorities as expressed through conference themes and presentation titles within these themes.

Introduction

Results

Figure 1 shows the themes specified for each of the five conferences. These were grouped into six thematic areas, with further clustering within these groups where relevant.

ICAHS 1 (2011): Establishing the technical parameters

The first ICAHS conference, under the title "Challenging environment", established a strong methodological and technical focus. The main thematic areas included "Data and tools", "Optimisation", "Evaluation", "Early detection and outbreak development" and "Risk and freedom". Presentations predominantly addressed statistical and modelling approaches (e.g. Bayesian inference, scenario tree models, capture - recapture methods), and the development of digital or web-based data collection tools. A Special Issue was published in Preventive Veterinary Medicine (1); an additional workshop on the standardisation of surveillance terminologies led to another publication (2).

This inaugural meeting reflected the state of the discipline at the time: animal health surveillance was becoming more data-driven but remained largely focused on how to collect, analyse, and interpret data efficiently and reliably. There was little emphasis on stakeholder engagement or cross-sectoral integration; the emphasis was on methodological rigour and optimisation within established systems.

ICAHS 2 (2014): Efficiency, evaluation and inclusivity

The second conference in Havana ("Surveillance against the odds") was challenging to organise due to the geopolitical situation. As reflected in the conference title and programme, the emphasis shifted towards dealing with resource constraints for implementing surveillance activities (3). There was also a move towards evaluation of surveillance performance and usefulness. The most populated themes included "Optimising surveillance designs", "Challenging populations and data", "Surveillance across the animal - public health interface" and "Involving stakeholders and guiding policy". Several sessions explored approaches for assessing cost-effectiveness, risk-based prioritisation, and the benefits of surveillance to trade and public health. Surveillance in resource-challenged environments acknowledged the realities of implementation in diverse settings.

This period marked the beginning of a more inclusive perspective: rather than treating surveillance purely as a technical exercise, ICAHS 2 reflected a growing recognition of its contextual and social dimensions. Stakeholders, policy-makers, and communities were increasingly seen as an integral part of the surveillance system.

ICAHS 3 (2017): Innovation, integration and One Health

Held in Rotorua under the title "Beyond animal health surveillance" (4), the third ICAHS marked further progression. Innovation featured prominently, with sessions dedicated to "Innovations in health surveillance design and operation", "Innovations in monitoring trends" and "Innovations in syndromic surveillance". In addition, "One Health surveillance" and "Antimicrobial resistance" appeared as explicit themes, illustrating a widening scope beyond animal health to integrated health systems. The programme also featured sessions on "Operational frameworks of health surveillance systems" and "Science and policy: a two-way street", signalling an increasing emphasis on governance and practical implementation.

This edition of ICAHS illustrated how the community was moving beyond the 'bread and butter' topics to broader perspectives related to innovation and integration. Surveillance was no longer only about disease detection and early warning, but increasingly seen to have an important role for informing risk management and policy, addressing data limitations and linking across sectors and disciplines. The One Health perspective became a defining feature of the discourse, with discussion on how animal, human and environmental health surveillance could be integrated into interoperable frameworks.

ICAHS 4 (2022): Translation to policy and practice

The themes of the Copenhagen conference revolved around translation and application. The overall theme, "Translating surveillance outcomes into policy and action", encapsulated this shift. High-volume thematic areas included "Surveillance data", "Integrating novel methods in surveillance", "Cross-sector and One Health surveillance" and "Translating surveillance outcomes into policy, decisions and actions". (5) Specific disease applications, such as African Swine Fever, and focus areas like emerging and epidemic diseases, demonstrated the operational relevance of surveillance.

Introduction

Reflecting its setting in a European context with highly-regulated production industries, the 2022 conference underscored the use of surveillance as a policy instrument: linking data to decision-making, governance and preparedness. The discussion moved firmly from innovation to implementation, consolidating surveillance as a core activity in One Health systems involving several partners including (among others) the agricultural industry.

Cross-cutting patterns

Across all four ICAHS conferences, several longitudinal trends can be observed:

1. Technical advances, innovation and methodological strengthening: Methodological and technological developments in the early 2010s evolved into widespread application of digital data systems, automated analytics, and modelling for decision support.
2. Evaluation and value assessment of surveillance systems: By 2014, focus expanded to include more formalised and rigorous frameworks for the evaluation of effectiveness, cost-benefit, and return on investment in surveillance.
3. Integration and interdisciplinarity: The emergence of One Health and cross-sector themes reflects a systemic turn, connecting veterinary, human, and environmental domains.
4. From research to policy: Across the 15-year period, there has been a continuously growing emphasis on translating evidence into policy, adapting systems to be more fit-for-purpose, developing institutional frameworks, and ensuring that surveillance outputs inform real-world decisions.
5. Operationalisation and relevance: ICAHS has always maintained its core focus on surveillance in practical contexts such as emerging disease management, AMR monitoring, and field implementation.

Discussion

The evolution of ICAHS over the previous 15 years mirrors the broader transformation of animal health surveillance from a technical and applied activity to its application as an essential and strategic component of One Health systems.

From technical problem-solving to systemic integration
Initially, the community's priority tended to be methodological, further developing and improving the practical, analytical and statistical tools that could underpin the performance of surveillance systems. Technological advancements led to the development of tools and methodologies to enhance such performance. Over time, this technical baseline was expanded to consider broader topics of relevance, such as performance evaluation and integration. This reflected a shift from operation of systems and activities to a recognition of the wider systemic context, including issues of governance, data sharing and cross-sector collaboration. Moreover, an expansion was seen from a focus mainly on animal health to a wider interpretation to including subjects such as food safety.

Growing emphasis on value and decision relevance

The focus on evaluation and optimisation in the mid-2010s represented a natural response to increasing accountability pressures. Governments and international partners needed to justify surveillance investment through demonstrable benefits. ICAHS 2 and 3 both reflected this shift, showcasing frameworks for measuring the efficiency and added value of surveillance activities. By ICAHS 4, this emphasis had expanded into questions of impact: how surveillance information supports decisions, improves preparedness, and mitigates risks across animal and human health domains.

The rise of One Health and data integration

The prominence of One Health themes parallels developments in global health trends, including the WHO - FAO - WOAH Quadripartite collaboration, the Global Health Security Agenda, and the PREZODE initiative. Surveillance is increasingly viewed not as a sectoral task but as a collective intelligence function that integrates animal, human and environmental data. The ICAHS community has positioned itself as a driver of this transformation, fostering dialogue between disciplines that traditionally operated in silos.

Surveillance as a policy instrument

Reflecting the priorities and needs of livestock production industries, the previous conferences reflected a turn toward operationalisation and policy translation. This is consistent with global trends emphasizing evidence-based decision-making, early warning and pandemic preparedness. Surveillance outputs are now expected to directly inform interventions, policies, and resource allocation. As such, the field has expanded from methodological excellence to explicitly incorporate policy relevance for several stakeholder groups as well as impact into the design of surveillance.

Introduction

Anticipated next developments

The themes for the upcoming conference (Ha Noi, Vietnam, 10-12 November 2026)(6) reflect the regional priorities; they further build on previous conferences by highlighting the importance of stakeholders end-users in surveillance systems, while extending science – policy – society dialogue. Further integration across sectors is expected, with stronger inclusion of public health, environmental and wildlife health surveillance. Notwithstanding this, the foundational elements of surveillance (including implementation, innovation and evaluation) will continue to be important.

Extending the trajectory of ICAHS, the next phase in the story is likely to focus on measurable impact, sustainability, and resilience. Future conferences may address:

- How to quantify the contribution of surveillance to disease control and health security outcomes.
- How to practically embed surveillance functions within true One Health systems.
- How to create interoperable, ethically governed data ecosystems.
- How to engage communities and non-traditional data contributors to enhance surveillance effectiveness.

ICAHS is likely to continue to provide a platform where the intersection of surveillance science, governance and societal resilience can be explored and discussed.

Conclusion

Over the previous 15 years, ICAHS has constructively fostered the evolution of animal health surveillance (defined in a broad way) as both a science and a practice. The conferences have moved beyond a focus on enhancing methods, through evaluation and integration, to the practical and policy dimensions of applying surveillance in a One Health context. This trajectory mirrors the maturation of the global health surveillance ecosystem: from data generation to decision support, and more recently toward impact and resilience.

Along this journey, ICAHS has built a strong and dedicated community of scientists and professionals passionate about all aspects of health surveillance, set in the broader context of prevention, preparedness and response to epidemic threats. Such unity of purpose must be valued in a world constantly facing new zoonotic, climatic, trade and social risks.

Introduction



Figure 1. Themes of the five ICAHS conference, clustered into six thematic areas (where Technical aspects has four sub-themes). The size of the theme circles is proportional to the relative number of presentations. Dotted lines show logical connections between conferences.

Keywords: health surveillance, conference, ICAHS.

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Theme 1: Engagement and participation of actors and end-users in surveillance activities

Oral presentations

Increasing One Health awareness at the local-level to bolster passive surveillance: insights from stakeholders from the Asia-Pacific

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Summary

Increasing One Health awareness at the local level and funding risk-communication for farmers and animal health communities could have a positive impact on surveillance systems through normalising surveillance effort. This is one of the key takeaways that emerged from discussions with governance stakeholders working in the One Health and/or animal health governance space in four countries from the Asia-Pacific: Bangladesh, Papua New Guinea, Fiji, the Philippines. Through a process combining one-on-one semi-structured interviews and/or focus groups with 60 stakeholders, and later validation through an online session inviting all interviewees to participate, we found that despite the differences in national contexts, there was a generalised lack of understanding and/or knowledge of One Health below the national level. Additionally, across all four countries, gaps in governance means reaching farmers is difficult, and trust between the governance actors and farmers is often lacking. Both can be a hindrance for passive surveillance. However, stakeholders noted that an increased understanding of One Health at the local level could help bolster passive surveillance through capacitating farmers and fostering more trust between animal health practitioners, government representatives and farmers. We reflect on what this means for future One Health and/or surveillance activities in the region.

Methods

The Indo-Pacific Initiative for Sustainable Animal Health Cooperation (IPI-SAHC) is a three-year project funded by the Australian Centre for International Agricultural Research (LS/2022/143) that examines how communities, countries, and regional bodies can build capacity, mobilise and share resources and expertise, and cooperate to improve high-level political commitment to animal health governance. Data collection was focused on ACIAR priority locations across South Asia, Southeast Asia and the Pacific Islands, in the four countries mentioned above and across three levels: national, community, and regional (Griffith Ethics Number 2024/738).

For the national case study, which informed this submission, the IPI-SAHC team interviewed (either 1:1 or through roundtable discussions) a total of 60 participants across the four countries between January and December 2025. The conversations were transcribed and translated when conducted in a local language. Deidentified transcripts were then coded through thematic analysis with an iterative codebook – a template approach. Following the thematic analysis, a follow up session with the participants was convened on Zoom to present preliminary findings and receive feedback in April 2026. Five categories were established: (1) Animal Health Governance (governing animal health experiences); (2) Perspectives on farmers and support systems; (3) Perspectives on One Health; (4) Supranational considerations and (5) Disease and outbreak management. The thematic analysis and the five themes it produced were presented to the stakeholders in the collective session in

Theme 1

April 2026. Participants were then invited to move to country-specific breakout rooms to validate findings, offer additional insights and/or identify priorities moving forward. What follows draws on cross-cutting patterns that emerged both from the cross-country comparison and from the collective dialogue that this reporting back process generated.

Results

The four countries reported similar issues with different framings. Four important observations emerged both from the data presented to the stakeholders and were reiterated and reinforced in the collective session. First, the lack of knowledge/understanding of One Health below the national level. Second, the recognition that there are gaps in governance in animal health, which make reaching farmers challenging across all contexts, albeit sometimes for slightly different reasons. Third, trust was often mentioned as an issue between farmers and governments when stakeholders discussed their views of smallholder farmers and available support. Finally, international funding was identified as misaligned with country-priorities in some of the contexts but highlighted as necessary by each country.

One Health knowledge and understanding

Almost every interviewee had heard of One Health. Some interviewees were experts and very well versed. Others expressed openly that while they had heard the term "One Health", but that they didn't know what One Health meant. When asked, most described the link between human and animal health, e.g. zoonoses, but fewer included the environment in their own definition. Some interviewees related their initial skepticism, but One Health is now widely considered important, and some interviewees have become passionate about the concept (it is also important to note that our sample included international One Health experts which were interviewed about their country-level experience). There was an acknowledgement that One Health is particularly important in contexts where livestock live in close proximities to humans, such as in smallholder settings.

What became apparent is that local government representatives and extension workers had less exposure (e.g. through training opportunities) than their national government counterparts to the concept. Stakeholder in the reporting session agreed that "One Health is not very well known beyond the corridors of power" and that raising awareness in farmers would be important to minimize zoonotic disease outbreaks and foster reporting. The four countries are at varying level of implementation of One Health. There is however a consensus that a holistic implementation is necessary to build local understanding, and ensuring implementation includes all necessary partners. For instance, at the April 2026 session, a participant from PNG explained that provinces have not been included in implementing partners. Connected to this are other issues including a lack of sustainable funding, and difficulties to move beyond siloed approaches at the national level. Participants added that field activities in particular are hard to secure funding for.

Additional insights from breakout room sessions shared by the participants included funding received for One Health by PNG, and additional activities undertaken by Bangladesh stakeholders in the One Health space. Philippines participants also wanted to highlight that there are mechanisms of collaboration that may not be termed as One Health but are on One Health such as inter-agency collaboration on food safety, AMR, anti-rabies, and avian influenza. Highlighting that there is so much collaborative work being done in the Philippines on One Health but in the form of specific disease prevention and response programs.

The gaps in animal health governance

AHG structures vary across national contexts, with some having established reporting structures from national to local, and others having coordination and resource allocation issues. Jurisdictional overlaps between different aspects (e.g. food security, biosecurity) can make animal health more difficult to govern, as it can lead to confusion and lack of accountability.

Across all four countries was a consensus that, despite its important contribution to the national economies, the livestock sector is often perceived to be underprioritized as an agriculture sector. The approach to animal health is reactive rather than proactive. The importance of animal health needs to be communicated better to policymakers.

Once again, funding was flagged as an important barrier to better outcomes. Lack of sustainable funding for animal health leads to a variety of issues: staff shortage and lack of training, lack of infrastructure (research, vaccine production, diagnostic capacities). This in turn makes it more challenging for countries to respond to outbreaks in a timely manner, due to creating gaps between national level and the field level.

Theme 1

National and local government views on smallholder farmers and available support

Smallholder farms are viewed as essential across the region, crucial for food security and maintaining cultural practices. They are perceived as 'vulnerable' to disease outbreaks due to poverty, the use of traditional methods to care for their animals, and the lack of veterinary services available in some contexts.

Support available varies greatly across contexts, with some farmers being left on their own while others may be receiving more help. The comparison between large-scale farms and small-scale farms often came up, with stakeholder mentioning large-scale farms as following better biosecurity practices. There are also mentions of largescale farms receiving more help from the government in the form of loans, trainings and vaccines. A push towards the intensification of agriculture may marginalize smallholder livestock holders further.

For instance, in the extreme case of pig farmers in Bangladesh, national stakeholders highlighted that the social stigma attached to raising pigs led to pig farmers being particularly vulnerable to outbreaks due to fear of engaging with formal animal health governance systems. In Papua New Guinea, pigs are considered highly valuable and pig farmers are considered “super farmers” by stakeholders. However, the barrier is structural: they note that smallholder farmers are mostly left on their own due to a lack of capacity, in a context where provincial authorities are responsible for agricultural extension and farmer engagement, but don't have capacity to deliver this engagement.

In the Philippines, stakeholders noted that farmers received help for feed, medication, training and/or more. Yet, the need for more coordinated support at the local level is recognized across all contexts. They also noted that supporting farmers groups has been important in giving farmers a voice within animal health governance and needs to be capacitated further. Digital extension tools have been mentioned either as potential to increase support or already being used informally. In PNG, a stakeholder mentioned that increased mobile phone usage could be leveraged to reach farmers. In Fiji, an extension officer mentioned using video calls informally for remote diagnostics, an example of practitioner innovation to circumvent the “reaching farmers” issue.

External actors funding and priorities

Stakeholders repeated that international organisations are instrumental in supporting One Health implementation in national contexts.

The countries rely on donor funding for animal health governance and/or One Health activities, however the nature of funding is inconsistent across donors and some sectors/themes. For instance, some areas of investment receive regular support compared to other areas of One Health that are yet to be consistently funded (i.e. animal surveillance compared to human surveillance), leading to issues related to sustainable funding and, in turn, strengthening system capacity.

In terms of future funding, participants at the April session mentioned that funding for risk communications and One Health awareness at the local level would be helpful, for instance through grounding One Health education at the secondary school. The information could then be passed on from children to parents. Another important element that emerged was the importance of institutionalising experience derived from disease outbreaks. Although countries have had very varying outbreak experiences, a common thread is that outbreaks have often served as “wake-up calls” and led to changes in animal health governance (examples documented in all four countries). Lessons learned from disease outbreaks emphasized early-detection, rapid response and strong communication plans tailored to local contexts and have highlighted the importance of multi-stakeholder collaboration. Published case-studies of outbreaks were also noted as relevant to policy-makers: participant involved in policy-making for a specific disease outbreak noted that these are routinely consulted prior to drafting policies, but are not always available.

Discussion

Through interviews and further discussions, national stakeholders have identified that local awareness of One Health and farmers engagement are lacking. This represents a foundational gap for surveillance, particularly in settings where veterinary capacity is crucially lacking. Aside from the lack of capacity for diagnostic, which is documented and important – countries need domestic diagnostic capacity which they are currently lacking, however, this local knowledge and engagement gap was identified as important to address to strengthen surveillance systems. An effective passive surveillance system requires trained professional but also aware farmers who can notice issues and comfortable reporting those to authorities.

Theme 1

Barriers to reporting, such as stigma, distrust, and poor awareness are well identified in literature (see for instance (Gates et al., 2021))., Those barriers are context-specific and as such, different context-specific solutions may be needed to address those barriers to unlock the potential of farmers to become active actors in surveillance systems. However, research already shows the potential benefits of raising awareness in farmers: for instance, community engagement has proven beneficial in the case of Timor-Leste, where training farmers enabled them to become better at reporting disease but also getting to know the extension staff (Millar et al., 2023).

Investing in One Health awareness at the local level could help through fostering farmers understanding of why biosecurity and reporting is important, while simultaneously building relationships and increasing trust with animal health officials. Animal health officials at the local level would also benefit from receiving One Health awareness training, and this could be conducted simultaneously, capacitating animal health officials who can then reached out to farmers.

One caveat is that reliable communication channels are not always in place. This can be due to social stigma, or this can be due to a lack of resources and remoteness. The materialisation of such activities may vary widely to account for those context-specific barriers. This is a constraint that needs to be considered when investing in awareness activities. Some national stakeholders are already thinking pragmatically about how to find solutions to enable two-ways digital communications, such as reflecting on the increased use of mobile phones in PNG or leveraging video messaging apps for diagnostics in Fiji.

Conclusion

The lack of One Health awareness and gaps in capacity identified by national stakeholders are important to address to improve passive surveillance in low-resource settings. While improving national diagnostic capacity is important, investing in capacitating farmers and local animal health actors could improve passive surveillance through enabling local actors to participate. However, this will require careful consideration of available communication channels and potential contextual barriers, which will need to be overcome. Those barriers can be structural such as remoteness, but also social and cultural, such as stigma, contributing to a lack of trust between animal health actors at all levels – from the government all the way to the farmers.

Keywords: Passive surveillance, One Health, Farmers, Asia-Pacific.

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Community Zoonotic Case Definitions in Rural Cambodia: Syndromic Knowledge, Reporting Barriers, and Design Considerations for a Community-Based Early Warning System

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Theme 1

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Summary

This paper presents findings from a qualitative study conducted in two provinces of Cambodia — Battambang and Stung Treng — aimed at documenting how rural communities perceive, identify, and respond to zoonotic disease signals. Using a Human-Centered Design (HCD) approach, the study maps the gap between technical case definitions and community-level knowledge, identifies the economic and social barriers that prevent early reporting, and proposes a risk threshold framework to guide the design of a functional One Health early warning system. The findings suggest that limited success of surveillance in this context is not primarily a technical problem, but a design problem — one that requires rethinking who the system is built for, and what it offers to the people closest to disease signals.

Introduction

The AfriCam project (Preventing and Monitoring Zoonotic Disease Emergence in Africa and Cambodia) is a multidisciplinary initiative investigating zoonotic risks at the intersection of hydrology, climate, and environment in Cambodia. Its broader objective is to strengthen existing surveillance programmes into an integrated One Health (OH) surveillance system capable of early detection (1). The project operates across two provinces with distinct socio-ecological profiles, and the work described here forms part of Component 3, focused on the implementation of surveillance and early detection strategies.

Cambodia sits at a particularly complex interface between human, animal, and environmental health. The country's rural landscape is shaped by smallholder agriculture, backyard poultry farming, free-ranging livestock, and a strong cultural tradition of consuming wild animals and bush meat. These conditions, combined with porous borders, climate-driven flooding events, and the heavy use of agricultural chemicals, create an environment where zoonotic spillover events are both plausible and difficult to detect early (2).

The two study provinces present contrasting but complementary profiles. Battambang is heavily oriented toward commercial livestock and rice production, with a relatively active veterinary presence and a community that has some historical memory of disease events, including a past H5N1 outbreak in a neighbouring village. Stung Treng is more remote, with smaller livestock holdings, a more passive volunteer surveillance system that has largely fallen inactive due to low local demand and insufficient government support, and a primary focus on wildlife conservation. Despite these differences, both provinces share a common challenge: formal surveillance structures exist, but early detection of zoonotic events is consistently delayed.

These delays are not primarily explained by a lack of protocols. Rapid Response Teams exist. Health centres operate weekly reporting systems. Village Animal Health Workers (VAHWs) are trained. The gap lies elsewhere — in how communities understand disease, in what reporting costs them economically, and in whether the system offers them anything in return. Addressing this gap requires starting from the community's own logic, not from the technical definition of zoonosis. Communities in both provinces have no specific Khmer term for zoonosis. Disease events that move between animals and humans are described narratively — as sicknesses that "jump" — without a conceptual category that would make them identifiable as something requiring specific action. Infectious outbreaks are frequently attributed to environmental causes — pesticide runoff, industrial pollution, unusual weather — rather than to pathogens. This environmental bias is not ignorance; it reflects lived experience, where chemical contamination and polluted waterways are visible, immediate, and recurring threats, while viral pathogens remain invisible and abstract (3).

Materials and Methods

Fieldwork was conducted between September and October 2025 across four villages in Ek Phnom district (Battambang) and Thala Borivat district (Stung Treng). Site selection followed criteria developed jointly with CIRAD and IRD, prioritising areas with high potential for disease emergence at the wildlife-livestock-human interface, high reliance on animal or forest products, and a range of economic activities and risk profiles to ensure both high-risk and lower-risk communities were represented.

The study used a Human-Centered Design (HCD) framework, which prioritises understanding the motivations, constraints, and decision-making processes of end users before proposing any intervention. This approach was chosen precisely because previous surveillance efforts in similar contexts had struggled to produce systems that communities actually used. Rather than starting from technical syndromic definitions and testing

Theme 1

community awareness of them, the study started from the community's own language, categories, and experience.

Thirty-six participants were recruited across three stakeholder tiers: local knowledge holders (small-scale farmers, village and commune chiefs, consumers, rangers), animal health actors (VAHWs, government veterinary staff, commercial farmers, animal feed suppliers), and human health professionals (health centre staff, Rapid Response Team members, private clinic workers). This diversity was deliberate — understanding the informal actors in the system, such as feed suppliers and private pharmacies, proved as important as understanding the formal ones.

Data were collected through in-depth interviews, focus group discussions, mini-workshops, and direct observations in markets, farms, homes, and community spaces (3). Card-sorting exercises using images of animal species were used to elicit responses about animal contact and disease recognition without requiring participants to engage with abstract terminology. Observations were conducted in parallel with interviews to identify the frequent disconnect between what people say they do and what they actually do when an animal falls ill. Data were analysed through affinity mapping and thematic clustering within digital collaboration tools.

Results

Economic barriers to reporting

The most consistent finding across both provinces is that livestock functions not only as a production asset but as a savings account. For families with no access to formal credit or insurance, animals represent an emergency fund — the thing you sell when a child is sick or a school fee is due. Household-level reporting of animal health event to authorities is therefore perceived as triggering immediate and total financial loss, through mandatory culling, farm lockdowns and market temporarily closure, with no compensation. This makes silence the economically rational response.

The consequence is a well-established informal pathway: at the first signs of illness, farmers slaughter and sell symptomatic animals to middlemen before authorities can intervene or consume sick or already dead animals. They treat poultry with human over-the-counter medicines — paracetamol, amoxicillin — purchased from local pharmacies, because involving a VAHW feels unnecessary and potentially dangerous. This informal treatment pathway is largely invisible to both animal and human health surveillance systems, and creates conditions where a sick animal can move through a market chain before anyone with formal training has seen it.

Mass mortality in poultry is perceived as normal. Farmers across both provinces described seasonal die-offs in April and during the September-October weather transition as expected events, linked to heat stress or rain, not to pathogens. Without a reference point that distinguishes this seasonal norm from an infectious outbreak, the threshold for seeking external help remains very high. In practice, VAHWs are rarely contacted until mortality is severe and already widespread.

Risk threshold framework

The study mapped community responses to disease signals into a four-level sensitivity framework (see Figure 1), separately for human and animal health, and validated across both provinces despite their different surveillance contexts.

At the low-sensitivity level, common signs such as runny noses, mild lethargy, or light respiratory sounds in poultry are treated with home remedies or human medicines purchased without prescription. No report is made, no concern is expressed, and the event is absorbed as background noise.

At the medium-sensitivity level, more specific signals appear — twisted necks in poultry, drooping wings, a handful of deaths, or early news of outbreaks in neighbouring areas — but the response remains private. Farmers may secretly slaughter, sell or consume sick animals, or bury carcasses without reporting. Social signals also appear at this level: community chatter at market stalls, and notably, the sight of researchers or officials in protective equipment collecting samples, which functions as a more powerful alarm trigger than any clinical sign.

High-sensitivity triggers are defined by specific mortality thresholds — ten to twenty birds per household dying simultaneously, or thirty to a hundred or more dying across a village within a short period — combined with social amplifiers such as viral content on TikTok and Facebook, warnings from village chiefs, or word-of-mouth about confirmed cases in nearby areas. At this level, consumers begin avoiding market poultry showing visible

Theme 1

signs — purple skin, bloody eyes, faecal residue — and some farmers begin contacting authorities, though many still first attempt secret slaughter.

Full outbreak-level response, including laboratory testing and government intervention, only occurs after mass mortality or confirmed human cases. By this point, the window for early detection has long passed.

For human health, the same escalation logic applies. H5N1 generates concern only when an outbreak is already confirmed nearby. During COVID-19, the most operationally useful signal documented was sudden anosmia — the loss of smell — which communities adopted as a reliable self-diagnostic marker in the complete absence of formal testing capacity. This is worth noting: communities developed their own functional case definition under pressure, and it worked.

Positive deviances

Several existing practices demonstrate that behaviour change related to reporting is possible under the right conditions, and offer concrete leverage points for system design.

Commercial farmers in both provinces conduct daily health checks, apply strict biosecurity, and self-research symptoms through YouTube and TikTok, not because they are better trained but because their economic model depends on early detection. They represent a practical model that neighbouring small-scale farmers respond to more readily than external officials.

Animal feed suppliers are perhaps the most underutilised resource in the current system. They provide vaccines, medicine, and feed on credit after a loss, functioning simultaneously as a bank and an informal veterinarian. Farmers trust them and visit them regularly, making them a natural surveillance node that currently operates entirely outside the formal reporting chain.

The Malaria Information System (MIS) demonstrates that digital reporting tools work in this context when they are simplified and institutionally supported. Village malaria workers use phones or tablets to record and report cases in real time — a model that has proven effective for an aging, volunteer-based workforce when given sufficient training and sustained government backing.

Village and commune chiefs emerged across both provinces as the most effective communicators for health measures during COVID-19. Villagers described them as "parents" — people whose instructions carry both authority and trust. Health messages and surveillance requests that came through chiefs were accepted; those that came through top-down mandates were more often ignored or resisted.

Discussion

The picture that emerges from this study is not of communities that are unwilling to participate in surveillance. It is of communities that have made rational calculations about what surveillance costs them and what it offers in return, and found the balance unfavourable. Addressing this requires more than simplifying case definitions or training more VAHWs. It requires redesigning the economic logic of reporting.

A sustainable EWS in this context needs at minimum three things that are currently absent. First, financial safety nets — some form of compensation or credit mechanism for families who report and lose animals to culling — to make reporting a viable option rather than a punishment. Second, accountability loops — systematic return of test results and follow-up information to the communities that provided samples — to demonstrate that the system works for them, not only for provincial or national health statistics. Third, formal integration of informal actors — feed suppliers, private pharmacies, commercial farmers — into surveillance networks, with appropriate training and clear reporting pathways.

The risk threshold framework documented here offers a starting point for co-designing syndromic case definitions that are grounded in local experience and expressed in local language. Simplified definitions such as "fever plus twisted neck plus more than ten dead birds in one day" are more actionable for a farmer or village chief than a clinical description of Newcastle Disease or H5N1. These community case definitions need to be validated and refined through co-construction workshops involving both communities and technical actors, and integrated into digital reporting tools that are adapted to the literacy and connectivity constraints of rural Cambodia (4, 5).

Theme 1

The broader lesson may be simple: surveillance systems that are designed around what health authorities need to know, without considering what communities need to be safe, will consistently underperform. Starting from community logic is not a concession — it is a precondition for a system that actually detects events early enough to matter.

Sensitivity level	Key signals	Social / environmental triggers	Community response
Low	Runny nose, mild rattling breath	Seasonal weather transition	Home remedies, no report
Medium	Twisted necks, drooping wings, scattered deaths	Community rumour, officials with PPE visible	Secret slaughter or sale, no formal alert
High	10–20 birds/household dying simultaneously	Viral social media, warning from the village chief	Avoidance behaviour, possible alert to the chief
Outbreak	Mass mortality, confirmed human cases	Lab confirmation, government notification	Market closure, testing, government intervention

Note: For human H5N1, the trigger escalation follows the same pattern. For COVID-19, sudden anosmia (loss of smell) was the primary community-level diagnostic signal used across both provinces in the absence of formal testing.

Table 1. Community risk threshold framework for zoonotic disease signals — poultry and human health (Battambang and Stung Treng, Cambodia, 2025)

Keywords: zoonosis, community surveillance, Human-Centered Design, early warning system, Cambodia.

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Strengthening Animal Rabies Outbreak Response through Community Engagement and One Health Approaches: Lessons from Local Contexts in Thailand

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Theme 1

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Summary

Rabies remains a persistent zoonotic threat in Thailand, requiring early detection and coordinated response to prevent human mortality. Despite significant progress toward elimination, challenges persist in achieving rapid detection and notification at the local level, particularly in high-risk areas like the northeast region, which is characterized by large free-roaming dog populations and inconsistent access to health services. This study examines lessons learned from local community engagement and One Health approaches implemented to strengthen rabies response in Thailand's upper northeastern region, with a focus on participatory and community-based surveillance and risk communication. We conducted a descriptive analysis of program experiences, surveillance processes, and community-based activities to better understand how frontline actors like community members, livestock volunteer, village health volunteers, animal and public health staff contributed to more timely and coordinated responses. Stakeholders shifted from primarily technical surveillance and vaccination approaches toward participatory models that engaged communities in rabies detection and reporting. Community members were trained to recognize rabies signs and used simplified reporting systems integrated into local structures, while risk communication through leaders and community activities improved awareness and timely reporting. In parallel, One Health coordination and municipal involvement strengthened collaboration between animal and human health sectors, enabling faster and more effective outbreak response. Lessons from local contexts in Thailand's upper northeastern region highlight how community engagement and One Health approaches serve as central pillars in strengthening rabies response. At the same time, strengthened coordination across human and animal health sectors under a One Health framework enables more integrated and efficient response actions. Together, these approaches illustrate how locally grounded, participatory strategies can significantly improve rabies response systems and accelerate progress toward rabies elimination in Thailand.

Methods

This study employed a descriptive qualitative analysis to examine community-based rabies surveillance and response in the upper northeastern region of Thailand, a recognized hotspot for emerging zoonotic diseases. The study focused on high-risk areas characterized by large populations of free-roaming dogs, recurrent animal rabies outbreaks, and limited access to veterinary services. The study investigated how participatory, community-driven strategies strengthen the timeliness and coordination of local responses while identifying systemic operational bottlenecks at the district and sub-district levels. Data were collected between October 2024 and March 2026 from program records, surveillance reports, coordination meetings, and field observations, supplemented by informal consultations with key stakeholders. Interventions included community capacity building, participatory surveillance with simplified reporting, risk communication activities, and strengthened One Health coordination. Data were analyzed using a descriptive approach, focusing on timeliness of detection and response, community participation, effectiveness of risk communication, and multi-sectoral coordination. Qualitative data were thematically analyzed to identify key patterns and lessons for improving rabies response.

Results

A total of 47 animal rabies outbreaks were reported across eight provinces in the upper Northeastern region of Thailand from October 2024 to September 2025. Rabies cases were detected predominantly in dogs (n=35), followed by beef cattle (n=7), jackal (n=2), cats (n=2), and buffalo (n=1). The distribution of outbreaks was highest in Mahasarakham and Mukdahan (n = 10 each), followed by Loei (n = 7), Kalasin, Khon Kaen, and Roi Et (n = 6 each), and lower numbers in Udon Thani and Nongkhai (n = 1 each). Pet dogs and cats are the primary interface driving rabies transmission dynamics in this region. Due to low vaccination coverage and unrestricted movement, free-roaming pets act as a critical bridge between wildlife reservoirs, livestock, and human populations. Livestock (cattle and buffalo) are mainly affected through spillover exposure following contact with infected animals, while wildlife (jackal) serves as a natural reservoir that can sustain and reintroduce infection into domestic animal populations. Across provinces, the timeliness of outbreak management varied by stage of the response cascade. Median detection time ranged from approximately 1 to 3 days, while notification was consistently rapid, occurring within one day in most provinces. In contrast, initial response time showed greater variability, ranging from approximately 2 to 5 days, with the longest delays observed in Loei (median 4.63 days, range 3–11 days).

Animal rabies outbreak management in the upper northeastern region of Thailand demonstrated a progressive shift toward more decentralized, community-supported systems, particularly under participatory surveillance and One Health coordination in a context where free-roaming dogs constitute the primary maintenance host and

Theme 1

principal rabies transmission risk at the human–animal interface. Outbreak detection increasingly originated at the community level, marking a transition from passive facility-based surveillance to active, community-driven case identification in a setting where rabies-positive free-roaming dogs remain the predominant source of exposure risk. Community members, head villagers, livestock volunteers, and village health volunteers played a central role in detecting suspected rabies cases through observation of abnormal animal behavior, unexplained animal deaths, and exposure incidents involving suspected rabid animals. The integration of simplified reporting mechanisms within local community structures facilitated earlier recognition and initiation of alert signals. Within the notification component, animal health authorities improved intersectoral information flow by sharing confirmed laboratory results from active and passive surveillance via the established One Health network at the provincial, district, and sub-district levels. In general, information was quickly distributed from community focal points to district livestock offices and relevant authorities via volunteer networks and local communication channels. This mechanism increased cross-sector situational awareness and allowed for more timely coordination of public health and veterinary response actions. In high-engagement areas, suspected cases were frequently reported shortly after observation, allowing investigation teams to be activated earlier. However, variability in notification timeliness persisted across settings, particularly in areas with poor communication networks and low community participation. Outbreak response was strengthened through improved multi-sectoral coordination under a One Health approach. Joint field investigations were conducted by animal health officers, public health personnel, and local administrative authorities, often supported by community volunteers who facilitated case location and contextual information (Figure 1). Response measures encompassed rapid risk assessment, epidemiological investigation, sample collection and laboratory confirmation, targeted vaccination of at-risk dog populations, movement restrictions where necessary, risk communication, community engagement, and coordinated intersectoral collaboration across relevant agencies. Digital communication approaches also contributed to earlier recognition of suspected rabies events by improving community awareness of clinical signs, exposure risks, and reporting channels, thereby increasing the likelihood of prompt identification and initial reporting at the community level (Figure 2). Compared to previous approaches, response actions were more integrated and timely, particularly in areas with established coordination mechanisms. Despite these improvements, operational bottlenecks were consistently identified across all stages. These included limited veterinary workforce capacity, logistical constraints affecting field deployment, delays in communication between sectors, and variability in community engagement. These constraints contributed to uneven performance in outbreak detection and response across locations.

Discussion

This study demonstrated a marked transition in animal rabies outbreak management in the upper Northeastern region of Thailand toward a more decentralized, community-engaged surveillance and response system. This transformation occurred in a high-risk epidemiological context where free-roaming dogs remain the dominant maintenance host and principal interface for rabies transmission between wildlife, livestock, and humans. The findings highlighted how strengthening community engagement and operationalizing One Health collaboration can improve early detection and response capacity at the local level.

The findings underscore that free-roaming dogs and cats function as the primary drivers of rabies transmission in the upper northeastern region, functioning as the critical epidemiological link across species and settings. Consistent with national surveillance patterns, dogs accounted for the vast majority of confirmed animal rabies cases, particularly among unvaccinated or semi-owned populations with unrestricted movement. The continued occurrence of spillover infections in cattle, buffalo, and cats indicated persistent gaps in achieving effective mass dog vaccination coverage and sustaining herd immunity at the recommended threshold. Moreover, the detection of rabies in wildlife reservoirs, such as jackals, reflected the presence of a complex transmission ecology that sustained rabies circulation at the wildlife–livestock–domestic animal interface. This study suggests that forest habitats and proximity to wildlife areas serve as critical risk factors for rabies remaining endemic in certain districts. Current control strategies have historically faced limitations due to a lack of environmental sector involvement and a primary focus on human health outcomes. Addressing this interface requires a more robust One Health surveillance system that actively integrates data from wildlife, livestock, and companion animal sectors to anticipate and prevent cross-species transmission events. Despite advancements in detection and notification, there is significant variation in outbreak response timeliness across different provinces in the northeastern region. While high-risk areas like Loei, highlight inconsistencies in local operational capacity. Furthermore, the lack of a real-time centralized data platform prevents synchronized actions between animal and human health sectors, often leading to siloed responses. Strengthening the speed and uniformity of field-level interventions is essential for achieving the national goal of zero human deaths by 2030. Consistent capacity building for frontline responders, such as livestock and public health volunteers, is vital to ensure that rapid response mechanisms are functional across all administrative levels.

Theme 1

The results highlight a definitive transition from passive, facility-based surveillance to proactive, community-driven models for early detection. Successful local initiatives, such as the Chiang Mai and Thungsong Models in other regions, demonstrate that empowering Local Administrative Organizations (LAOs) and community leaders to conduct independent disease surveillance creates a "bottom-up" approach that is essential in areas where free-roaming dogs remain the primary transmission risk. The application of the One Health framework has significantly strengthened notification mechanisms and information flow between the animal health, public health, and local administrative sectors. This integration is formalized through Memorandums of Understanding (MOUs) among multiple ministries, which facilitate the sharing of epidemiological data and laboratory results. Platforms such as Thai Rabies Net and the Rabies One Data system serve as digital conduits for information flow, allowing agencies to immediately notify relevant stakeholders of positive cases. This streamlined notification process enables faster activation of joint investigations and improves overall situational awareness at the district level.

While the speed of detection and notification has improved, the effectiveness of the initial response continues to be hindered by persistent operational bottlenecks. The study identifies significant variation in response timeliness across different provinces, often caused by limited veterinary workforce capacity, logistical constraints, and frequent staff turnover within local administrative units. These systemic challenges are exacerbated by the lack of a real-time centralized data platform, which can lead to fragmented or siloed response actions between sectors. To ensure a consistent and rapid response, it is critical to strengthen the capacity of Surveillance and Rapid Response Teams (SRRTs) and promote joint outbreak investigations under a One Health approach. Standardizing these response mechanisms is essential for Thailand to reach its goal of zero human deaths from rabies by 2030

However, despite these advances in community engagement and One Health coordination, several operational constraints continued to limit optimal performance of rabies outbreak response systems. These included limited veterinary workforce capacity, logistical challenges in field deployment, and high turnover among frontline personnel in local administrative units. In addition, uneven levels of community participation across districts affected the sensitivity and consistency of surveillance outputs. Strengthening Surveillance and Rapid Response Teams (SRRTs), standardizing joint investigation procedures, and investing in sustained capacity building at the community level were therefore essential to ensure consistent and effective implementation of rabies control measures.

Conclusion

This study highlights that strengthening animal rabies outbreak response in the upper Northeastern region of Thailand is increasingly achieved through the integration of community engagement and coordinated multi-sectoral collaboration consistent with One Health approaches. In a context where free-roaming dogs remain the primary rabies reservoir, community-based surveillance has become a critical entry point for earlier detection, more rapid notification, and improved linkage to response systems. The study provides key lessons from local contexts in Thailand, emphasizing that durable improvements in rabies control require not only technical interventions but also institutionalized community participation and resilient intersectoral coordination mechanisms.

Theme 1



Figure 1. Integrated community engagement across animal, public health, municipal, and community sectors within a One Health framework to strengthen rabies prevention and control

Keywords: animal rabies, outbreak, response, one health, Thailand.

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Community-based surveillance and community engagement for One Health disease prevention

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Theme 1

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Summary

Recent health crises have highlighted the fragility of health and governance systems in contexts exposed to strong environmental, climatic, and socio-economic pressures. Emerging diseases and pandemics have caused major human, economic, and environmental losses, reinforcing the consensus that prevention is more effective and less costly than crisis response. The One Health approach, as defined by the Quadripartite (WHO, WOAH, FAO, UNEP), provides an integrated framework linking human, animal, and ecosystem health and emphasises prevention through strengthened territorial resilience and cross-sector collaboration.

This presentation draws on evidence generated through Cirad and PREZODE initiative associated operational projects implemented in Africa and Southeast Asia, including AfriCam, BCOMING, EBOSURSY, Santé et Territoires, and ASEACA. Across multiple study sites in Guinea, Madagascar, Gabon, Vietnam, and other countries, researchers, public authorities, veterinary and health services, environmental actors, and community organisations have tested operational approaches for community-based surveillance and prevention.

Results demonstrate that communities are often the first to observe early warning signals such as unusual animal mortality, environmental degradation, or symptoms in humans. Community-based surveillance systems improve the speed, sensitivity, and quality of health alert management while strengthening trust between populations and institutions. Community agents act as critical intermediaries between local actors and technical services, facilitating information sharing, awareness-raising, mediation, and rapid response. Systems co-designed with communities and territorial stakeholders show stronger ownership, greater sustainability, and improved effectiveness in risk reduction.

Several operational lessons emerged consistently across countries. First, prevention is most effective when human, animal, and environmental sectors collaborate around shared local challenges. Second, governance mechanisms that clearly define roles and responsibilities across territorial and institutional levels improve coordination and responsiveness. Third, long-term investment in training, recognition, and support for community agents is essential for sustainability.

The presentation will discuss how these findings contribute to operationalising One Health prevention strategies and strengthening the science–policy–society interface. It will also highlight the relatively low cost of implementing community-based prevention systems compared with the economic burden of health crises. Finally, recommendations will be proposed for scaling up territorially anchored prevention systems through dedicated funding, continuous multidisciplinary training, participatory governance, and stronger integration between local and national levels.

Introduction

Recent epidemics have demonstrated the limitations of reactive health systems and the need to strengthen prevention capacities. While prevention is widely recognised as more cost-effective than crisis management, investments continue to focus primarily on emergency response. At the same time, the One Health framework has gained prominence as an integrated approach linking human, animal, and environmental health.

Communities living at the interface between people, animals, and ecosystems are often the first to detect signals associated with emerging health threats. However, despite their frontline role, local actors remain insufficiently integrated into formal prevention and surveillance systems. This presentation explores how community engagement can strengthen One Health prevention and surveillance strategies.

Methods

This presentation synthesises operational and research experiences conducted in partnerships in Africa and Southeast Asia. Case studies from Guinea, Madagascar, Gabon, Vietnam, Senegal, Cambodia, and other

Theme 1

countries were reviewed to identify key factors associated with effective community-based prevention and surveillance.

The analysis focused on:

- community-based surveillance mechanisms;
- interactions between communities and institutional actors;
- governance and coordination processes;
- training and support systems for community agents;
- integration of human, animal, and environmental health dimensions;
- operational sustainability and scalability.

Lessons learned were analysed qualitatively to identify recurrent operational determinants of successful prevention systems.

Results

Community agents as key actors in prevention

In several countries, community agents contribute to surveillance, awareness-raising, mediation, and alert systems. Their proximity to local populations enables rapid detection of unusual events and strengthens the connection between communities, researchers, and technical services. However, lack of formal recognition and limited financial support threaten the sustainability of these systems.

Territorial anchoring strengthens sustainability

Experiences in Madagascar demonstrated that prevention systems are more sustainable when integrated into territorial governance mechanisms and linked with local authorities and national One Health platforms. Co-design with local stakeholders improves ownership and continuity of actions.

Linking environmental management and health prevention

In Gabon, community organisations involved in forest resource management also contributed to zoonotic risk prevention and environmental surveillance. Integrating health prevention into natural resource management strengthened local engagement and facilitated early warning mechanisms.

Building science–policy–society dialogue

The Vietnamese One Health Partnership illustrates the importance of structured coordination between ministries, researchers, and technical actors. However, stronger integration of communities and territorial dialogue spaces remains necessary to ensure effective local implementation.

Cross-cutting operational lessons

Across all contexts, successful systems relied on:

- collaboration between human, animal, and environmental health sectors;
- clear governance and information-sharing mechanisms;
- recognition and support of community agents;
- participatory design approaches;
- long-term investment in training and local capacities.

These systems were shown to improve early detection, responsiveness, trust, and local ownership while remaining relatively low-cost compared with the consequences of health crises.

Discussion

The findings demonstrate that operationalising One Health prevention requires moving beyond top-down surveillance models toward territorially anchored and participatory systems. Prevention effectiveness depends not only on technical tools but also on governance, trust, community engagement, and sustainable financing.

The experiences presented show that community-based approaches can strengthen resilience, facilitate rapid detection of emerging risks, and support integration across sectors. They also highlight the importance of bridging local knowledge with institutional decision-making processes.

Theme 1

A major challenge remains the sustainability and scaling-up of these systems. Community agents frequently operate without formal status or stable resources, and prevention initiatives often depend on short-term projects. Embedding prevention within national One Health strategies therefore requires dedicated long-term funding, institutional recognition, and multidisciplinary training systems.

Conclusion

Preventing epidemics requires operationalising the One Health approach through stronger engagement of local communities. Experiences generated through PREZODE and associated projects demonstrate that community-based prevention systems are feasible, effective, and affordable.

The key challenge is no longer primarily technical but political and strategic: ensuring that prevention becomes a sustained public investment rather than a temporary response to crises. Strengthening dialogue between science, policy, and society, while supporting territorially anchored surveillance systems, will be essential to improving preparedness and resilience against future health threats.

Keywords: One Health, community surveillance, prevention, zoonotic diseases, PREZODE.

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Assessing One Health Surveillance Systems at the Human-Animal-Wildlife Interface in a Biodiversity Hotspot: Findings from Stung Treng Province, Cambodia

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Summary

Designing an effective One Health (OH) surveillance system requires, as a first step, a clear understanding of how existing systems actually work — not as they are described in official documents, but as they are experienced by the people who operate them. This paper presents the findings of a participatory assessment of health surveillance systems conducted in Stung Treng province, Cambodia, covering three sectors: human health, animal health, and wildlife health. Using a combination of semi-structured interviews and focus group discussions involving 203 participants from community to provincial level, the study mapped information flows across sectors, identified the barriers that prevent timely reporting, and documented stakeholder perceptions of the system's effectiveness. The main findings point to a deeply fragmented surveillance landscape, where human health infrastructure is relatively functional, animal health is partially operational but eroding, and wildlife health is almost entirely absent as a formal system. Across all three sectors, the dominant barrier is not technical but relational: a lack of trust in the system, driven by repeated experiences of slow or absent response after reporting. These findings now serve as a foundation for co-constructing a community-based OH surveillance pilot in the province.

Theme 1

Introduction

Cambodia sits at a particularly active interface between human populations and wildlife. The country has experienced significant zoonotic disease pressure over the past two decades — avian influenza, COVID-19, African Swine Fever, Lumpy Skin Disease — and its rural landscapes, particularly in remote provinces, combine multispecies livestock farming, active wildlife trade, and close proximity to forested areas with high biodiversity. In this context, early detection of zoonotic events depends on a surveillance system that can capture signals across multiple sectors simultaneously and transmit them upward in a timely and coordinated way.

Stung Treng province, in the northeast of the country bordering Laos, represents an especially relevant setting for this kind of assessment. It covers 11,092 km² of sparsely populated, biodiversity-rich terrain within the Mekong basin, including six protected areas, 21 community forests, large colonies of flying foxes and cave bats, and rivers teeming with aquatic species. Stung Treng is also notable scientifically: it is one of the sites where bat coronaviruses closely related to SARS-CoV-2 have been detected. Several previous surveillance efforts have been implemented here — including a wildlife health surveillance network and an 18-month community respiratory surveillance project funded by the French National Agency for Research (ANR) — making it a site with some institutional history in OH surveillance (1).

The work presented here is part of the BCOMING project (Biodiversity Conservation to Mitigate the risks of Emerging Infectious Diseases), funded under the European Union's Horizon Europe programme (grant No. 101059483). A central premise of the project is that co-designing a better surveillance system with communities and authorities requires first understanding the existing one in depth — its actors, its communication flows, and critically, the reasons why it does or does not function as intended (2).

Materials and Methods

The assessment was conducted in Stung Treng province, with fieldwork focused on the Thalaborivat district, where six community forests cover 16,606 hectares and one community covers 1338.54 hectares across five communes and eleven villages. Data collection took place between January and March 2024.

The methodology combined two participatory approaches (3). In the first phase, 11 semi-structured interviews (SSIs) were conducted with key informants representing a range of sectors and administrative levels: animal health (Provincial Animal Health and Production Office), wildlife and environment (Provincial Department of Environment, Forestry Administration at both provincial and district level), human health (Provincial Department of Health, one health centre), district authorities, commune authorities, community forestry representatives, and one conservation NGO (Angkor Centre for Conservation of Biodiversity). Each interview lasted approximately two hours. During interviews, participants were asked to draw the communication flow within and between sectors — reporting channels, response pathways, and actors involved — which produced three distinct flow diagrams for wildlife health, animal health, and human health. Participants also rated their satisfaction with the system using a five-point scale.

In the second phase, nine focus group discussion (FGD) workshops were conducted in March 2024, involving 192 participants distributed across three levels: seven workshops at community forestry sites, one at district and commune level, and one at provincial level. The FGDs were used to validate and enrich the information collected during interviews, identify cross-sectoral communication gaps, and generate participant-led recommendations for improvement. All sessions were audio-recorded with informed consent and transcribed for qualitative analysis using the Quirkoos tool. The communication flow diagrams were compiled using Whimsical software.

Results

Mapping the three sectors

The three communication flow diagrams revealed a clear and consistent gradient across sectors in terms of institutional development and operational functionality (Figure 1).

Human health has the most developed infrastructure, from community to national level. At the community level, Village Health Support Groups (VHSGs) and Village Malaria Workers (VMWs) work closely with health posts and health centres to detect and report cases. Digital tools are in active use: the malaria programme uses a dedicated mobile application, while the CamEMS and CamEwarn platforms serve for broader health monitoring

Theme 1

and zoonotic event reporting. Rapid Response Teams (RRTs) at operational district level are deployed within 48 hours of a reported event. Communication within the human health sector is generally functional and uses Telegram and phone calls routinely alongside formal reporting platforms.

Animal health sits at an intermediate level. The reporting chain nominally runs from Village Animal Health Workers (VAHWs) up to the Provincial Animal Health and Production Office and then to the General Directorate of Animal Health and Production (GDAHP) at national level. In practice, however, this chain is breaking down. Many VAHWs have stopped working — they are volunteers who receive no salary, must purchase medicines from their own pockets, and often see no useful response when they do escalate cases. The provincial animal health office has only four officers, who described being overwhelmed during outbreak events and unable to follow formal reporting procedures. Contracted farms and private service providers handle disease events internally, without notifying authorities. The CamEwarn platform, introduced to bridge human and animal health reporting, is underutilized: one provincial veterinarian reported having login credentials for the system but being unable to navigate it in practice.

Wildlife health is the most fragmented sector. A Wildlife Health Surveillance Network (WHSN) Telegram group exists at provincial level, with representatives from the animal health office, the Provincial Department of Environment (PDoE), wildlife rescue organisations, and conservation projects. But this group is known to few people and rarely active. Most community members — including forest rangers, hunters, and people who live inside or adjacent to protected areas — are unaware that any wildlife health reporting mechanism exists. When dead or sick wildlife is found, the default response is consumption, not reporting.

Barriers to surveillance performance

Ten challenges were identified through the combined SSI and FGD process. The two most frequently cited — raised in eight of nine FGDs — were delayed or reluctant disease reporting due to low trust in the system, and lack of data sharing and integration across sectors.

The trust problem is concrete and well-founded. Farmers describe reporting sick animals and waiting ten to fifteen days for any response, by which time the entire flock had already died. One participant said plainly: "I am afraid that when I report the case, they don't report to their upper level. That is why I don't want to report." Others described being told by village chiefs to slaughter and sell sick animals quickly rather than seek veterinary advice. The rational response to these experiences is to stop reporting — and that is what many communities have done. The same dynamic appears in wildlife health: villagers who fell ill after consuming wildlife meat sought care at private clinics but did not report, partly from fear of legal consequences and partly because they expected no useful response from authorities.

The absence of feedback mechanisms reinforces this cycle. Participants who had contributed to surveillance activities — collecting tick and blood samples, submitting reports — described never receiving results or follow-up. A provincial veterinarian recounted asking for results from a sampling campaign and simply not receiving them. Without feedback, the system loses credibility, and people who might otherwise be willing to participate disengage.

Intersectoral data sharing is a separate but related problem. Within the human health sector, communication is relatively good. But between human health and animal health, information exchange is almost absent at the provincial level. Staff expressed concern that sharing data with another sector without authorisation from their superiors could result in disciplinary consequences. The result is that each sector operates with information the others would need in order to detect and respond to a potential zoonotic event.

Cultural and economic barriers compound the structural ones. When dead wildlife is found in fresh condition, consuming it is a food security strategy, not reckless behaviour — in contexts of genuine poverty, this makes sense. Selling sick poultry at a discount before the authorities intervene is economically rational when there is no compensation for mandatory culling. Training on zoonotic diseases alone is unlikely to be sufficient to change these behaviours.

What stakeholders want

Despite the frustrations documented above, all stakeholder groups expressed strong willingness to participate in a better-designed system. This came through clearly in the FGDs — many participants described the workshop itself as the first time they had seen how different actors were connected, and several expressed genuine enthusiasm for implementing a shared communication structure. The most consistent recommendation across groups was the establishment of a formal Provincial One Health Coordination Group, led by a deputy provincial

Theme 1

governor, with representatives from all three sectors. A provincial-level Telegram platform for inter-sectoral alert sharing was widely supported, as was the designation of clear focal points for wildlife health at commune level. Participants also emphasised that any new system must include a mandatory feedback loop — test results and follow-up information returned to communities after a report is filed.

Discussion

The picture that emerges from Stung Treng is of a surveillance system that is structurally present but functionally inadequate — not because the actors lack motivation, but because the system as currently designed does not offer them anything in return for the effort and risk of reporting. Rebuilding this requires addressing trust before addressing technology.

Some elements are already in place and should be built upon rather than replaced. The Malaria Information System demonstrates that digital reporting works in this context when properly supported, simplified, and linked to a visible response. The COVID-19 experience showed that rapid, coordinated, multi-level communication is possible when there is perceived urgency and institutional commitment. Conservation NGOs already maintain informal wildlife health networks that could be formalised. These are real entry points, not just aspirational starting points.

The BCOMING project is now using these findings to facilitate a co-construction process with provincial authorities, community forestry groups, and health actors — designing a community-based OH surveillance pilot that takes the economic and relational barriers seriously, not as side constraints but as central design problems (4, 5). The assessment itself appears to have had some catalytic effect: several participants described the communication flow workshops as the first time they had discussed these issues across sectors, and the demand for a provincial OH coordination structure grew directly out of the FGD process.

Dimension	Human health	Animal health	Wildlife health
Key community actors	VHSG, VMW, health posts	VAHW, village chiefs	Rangers, hunters, NGO staff
Reporting tools in use	Telegram, CamEMS, CamEwarn, malaria app	Telegram, phone, CamEwarn (limited)	SMART patrol app (partial), Telegram (WHSN)
Frequency of cross-level reporting	Regular	Irregular	Rare to absent
Cross-sectoral information sharing	Rare	Rare	Absent
Main barrier	Preference for private clinics; fear of reporting illegal events	Low trust; economic loss; VAHW dropout	No awareness of reporting mechanism; consumption of carcasses
Response time (when it occurs)	Within 48h (RRT)	10–15 days (reported cases)	Within 2 days (if NGO involved)
Stakeholder motivation	High	Moderate, declining	High in principle, no formal outlet

Note: Data derived from 11 semi-structured interviews and 9 focus group discussions involving 192 participants, conducted January–March 2024, Thalaborivat district, Stung Treng province, Cambodia.

Figure 1. Comparative overview of health surveillance communication flows across three sectors in Stung Treng province, Cambodia (2024)

Keywords: Stakeholder mapping, zoonotic disease, early warning system, community-based surveillance, Cambodia.

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Drivers of underreporting and strategies for improvement of surveillance of Q fever in Italy: the case study of Emilia Romagna region

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Q fever is a globally endemic zoonosis. Domestic ruminants are the main reservoirs, often showing subclinical signs. In humans, it can cause fever, pregnancy loss, and occasionally pneumonia or neurological complications. In Europe, it is a Category E disease under the Animal Health Law, requiring mandatory surveillance. In Italy, surveillance mainly targets abortions, though case definition differs from EU standards. Between 2010 and 2025, epidemiological investigations in Italy reported a pooled herd prevalence of 43.2% (range: 35–59%) and a within-herd prevalence of 15% (range: 3–37.8%), using both PCR and ELISA. However, no Q fever outbreaks have been notified to WOAH's WAHIS, whereas the Italian Animal Disease Information System (SIMAN) reported an average of 5.4 cases per year between 2015 and 2025. Serological surveys in humans showed an average prevalence of 33.7% (range: 8.6–62.9%), yet only 22 cases were reported on the Italian infectious disease surveillance platform PREMAL (2001-2025). The available data point to a potential underreporting of Q fever in Italy.

This study aims to investigate the factors contributing to the potential underreporting of Q fever in Italy across veterinary and public health domains (V&PH). In Emilia Romagna (Italy), interviews and questionnaires were administered to 20 veterinarians working in Local Health Authorities (LHAs), ruminant' farms, and Zooprophylactic Institutes (IZS), and to 62 human health professionals, including general practitioners, LHAs infectious disease specialists, and officials from the Ministry of Health. Among veterinarians, 90% self-reported low-to-medium knowledge of Q fever. Farm veterinarians correctly identified the main clinical signs in animals, and 60% reported having suspected Q fever on farms within the past two years. Their assessment of the zoonotic risk was split: 60% rated it as medium- high, and 40% as low. All were aware of mandatory surveillance. Sixty percent routinely sampled abortions; others did so only during abortion storms or after consulting LHAs for guidance. LHAs and IZSs veterinarians reported that suspected cases are sent to official laboratories, with confirmed cases notified in SIMAN and reported internationally. In public health, 41.5% of doctors reported no knowledge of Q fever, only 50% considered zoonotic risk during anamnesis, and 36% were unaware of mandatory notifications requirements. Limited understanding of diagnostic and notification protocols emerged. Across V&PH, key barriers included poor disease awareness, non-specific symptoms, unclear notification protocols, fear of LHA-imposed restrictions (for farmers), and under-diagnosis of animal abortions.

This study in Emilia Romagna region shows that, in public health, notification is hindered by poor disease awareness, insufficient attention on zoonoses, and an inadequate knowledge of reporting procedures. In animal health, although more than half of interviewed veterinarians are aware of Q fever, of its zoonotic risk, and acknowledge mandatory surveillance, abortion is the principal target of Q fever monitoring and the coverage is not ideal. The paucity of data on Q fever circulation are insufficient to promote effective risk management strategies. These findings call for continuous professional training of V&PH professionals and the integration of standardized diagnostic and notification protocols, with a clear case definition, in national legislation.

Keywords: Q fever, Surveillance, Italy, Under-reporting.

Theme 1

Case story presentations

Spot It in Animals, Stop It in Humans: Cambodia's Avian Flu Defense

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Context

Highly Pathogenic Avian Influenza (HPAI) A/H5N1 (Gs/GD/96-lineage) has been circulating in Cambodia since its first introduction in 2004 [1], with 84 officially reported poultry outbreaks and 93 human cases recorded as of early 2026 [2, 3]. The cumulative case fatality rate stands at approximately 55.9% [2]. After eight years without human detections between 2014 and 2022, viral activity surged significantly between 2023 and 2025, resulting in 34 human cases and 10 deaths [2, 4]. This upward trend continued into early 2026, with two notable human cases confirmed in Banteay Meanchey on 15 March and Oddar Meanchey on 29 March, both linked to backyard poultry exposures [3, 5].

To address complex zoonotic threats such as avian influenza, the Royal Government of Cambodia established the One Health Inter-Ministerial Coordinating Committee(OH-IMCC) in 2016 [6]. This body provides a robust institutional framework and high-level leadership, unifying the Ministry of Health (MOH), the Ministry of Agriculture, Forestry and Fisheries (MAFF), and the Ministry of Environment (MOE) under a single strategic mandate [7]. By streamlining multisectoral communication and resource sharing, this framework has successfully operationalized One Health in Cambodia. This is evidenced by the deployment of joint investigation teams capable of launching synchronized, rapid responses on the ground within 24 hours of notification, fundamentally shifting the national approach from reactive to proactive disease management [3, 5].

By streamlining multisectoral communication and resource sharing, this framework has successfully operationalized One Health in Cambodia. A key milestone in this operationalization was the formal joint endorsement of the One Health Rapid Response Team (OH-RRT) Standard Operating Procedures by the three ministries, providing a unified technical protocol for field interventions [8]. This is evidenced by the deployment of joint investigation teams capable of launching synchronized, rapid responses on the ground within 24 hours of notification, fundamentally shifting the national approach from reactive to proactive disease management [3, 5].

Case study

When first signals were received in March 2026 from Banteay Meanchey province first and later on from Oddor Meanchey province, coordinated outbreak response teams were established and deployed to the field for epidemiological investigation and outbreak containment.

Banteay Meanchey province – Preah Netr Preah district

Following reports of domestic poultry mortality in Rumpeak village, Chnuor Mean Chey commune, in early March 2026, a multisectoral investigation was launched. On March 11, the National Animal Health and Production Research Institute (NAHPRI), in collaboration with the Provincial Office of Animal Health and Production (OAHP), conducted field surveillance and collected six diagnostic samples from symptomatic chickens. Simultaneously, environmental assessments were performed at the nearby Rohal Kes bird sanctuary to monitor wild bird health. On March 13, RT-PCR testing at NAHPRI confirmed that 100% of the collected poultry samples were positive for A/H5N1.

In response to the animal outbreak, the Ministry of Health (MOH) initiated human clinical surveillance, identifying a 45-year-old female resident with respiratory symptoms and a history of direct contact with infected birds. A human sample was collected and confirmed positive for A/H5N1 by the National Institute of Public Health (NIPH) on March 14. Integrated intervention results between March 13–18 included the culling of 32 infected poultry and the implementation of rigorous biosecurity measures across two high-risk households. Public health teams conducted contact tracing, distributed Oseltamivir (Tamiflu) to exposed individuals, and provided the

Theme 1

primary case with hospital-based isolation and specialized medical care. No further human case was detected within the community following these synchronized containment efforts.

Oddar Meanchey province – Banteay Ampil district

Following reports of high mortality in domestic poultry (65 chickens and 45 ducks) in Tumnup Thmey village starting March 22, 2026, joint investigation teams comprising animal and human health sectors were deployed. The National Animal Health and Production Research Institute (NAHPRI) and the Provincial Office of Animal Health and Production (OAHP) conducted diagnostic sampling on March 25, with five samples testing positive for A/H5N1 via RT-PCR on March 26. Expanded active surveillance on April 1 identified a second affected household with 61 sick and dead birds, which also yielded H5N1-positive results.

In a coordinated effort, the Ministry of Health (MOH) and agricultural officials identified a 3-year-old male with a history of direct exposure to the infected backyard flocks. The case was confirmed positive for A/H5N1 by the National Institute of Public Health (NIPH) on March 29 and the Institut Pasteur du Cambodge (IPC) on March 30. Genetic sequencing using Oxford Nanopore GridION technology identified the virus as a reassortant Clade 2.3.2.1e, consistent with genotypes circulating in Cambodian live bird markets since 2023 [9] .

Integrated response measures executed between March 30 and April 3 included the culling of 107 poultry and the disinfection of 34 households and 2.2 km of village thoroughfares. Public health interventions included hospital-based isolation and Oseltamivir treatment for the pediatric case, contact tracing with prophylactic antiviral distribution, and multisectoral risk communication reaching over 340 community members, including students and teachers. No secondary human cases were identified, confirming the success of the synchronized One Health containment strategy.

Discussion

Historically, in many regions with endemic viral circulation, human H5N1 cases have acted as "sentinels" for the presence of viruses in animals and in the environment. In these scenarios, the detection of the virus in poultry often follows or coincides with the identification of a human infection rather than preceding it [10 -12].

While One Health is globally recognized as the pragmatic approach to adopt, its application at the local or community level is yet rarely demonstrated. It is essential to transform the concept of One Health into concrete actions with field-based examples and models that actively apply the One Health principles. Implementing initiatives at the local or community level is critical for achieving genuine, long-term benefits for individuals and populations.

The 2026 H5N1 responses in Banteay Meanchey and Oddar Meanchey underscore the effective operationalization of Cambodia's One Health strategy. Prompt sharing of information across animal and human health sectors was instrumental for establishing joint investigation teams immediately upon poultry alerts, leading to Cambodia successfully shifting from reactive to proactive surveillance. This systematic One Health approach enabled the detection of H5N1 in two individuals who were asymptomatic at the time of screening. Early confirmation allowed for the immediate administration of adequate treatment, significantly increasing the probability of clinical success compared to traditional detection triggered only after severe symptom onset.

The operationalization of field-level One Health strategies has proven life-saving by linking animal outbreak investigations directly to pre-emptive human case-finding. Had these cases not been identified through active community-level surveillance, medical intervention would likely have been delayed until the onset of debilitating symptoms—a stage where treatment efficacy can be significantly compromised. By deploying this coordinated multisectoral response, the Royal Government of Cambodia has moved beyond passive reporting toward a model of early intervention that prevents fatalities and halts community transmission at the source.

The next challenge for Cambodia may lie in the nationwide scaling of this model to ensure a consistent response to every signal across all provinces. Nevertheless, this success provides a blueprint for effective disease control and demonstrates that optimized One Health operationalization is achievable and sustainable within low- and middle-income country (LMIC) contexts.

Ultimately, these efforts serve as a critical defense not only for the Cambodian people but for global health security. As a nation on the frontline of zoonotic spillover, Cambodia's ability to identify and contain subclinical infections at the animal-human interface is essential for preventing the emergence of viruses with pandemic potential. This integrated framework demonstrates how a national commitment to One Health can proactively

Theme 1

mitigate the global risk of a human-to-human transmissible avian influenza outbreak, acting as a vital shield against the next pandemic.

Conclusion

The 2026 H5N1 outbreaks responses in Cambodia successfully implemented a proactive One Health model, shifting from reactive, sentinel-based detection to proactive, community-level surveillance that identified subclinical cases early. This operationalization of localized, multisectoral surveillance proved to be a life-saving, sustainable approach to managing zoonotic threats and enhancing global health security in low- and middle-income country contexts.



Figure 1 - Maps of Preah Netr Preah district, Banteay Meanchey province and Bantay Ampil district, Oddar Meanchey province in Cambodia where 2026 poultry outbreaks and human cases were detected

Keywords: Community, One Health, Joint outbreak investigation, Early detection, Cambodia.

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Theme 1

Impact of an integrated diagnostic network on strengthening passive surveillance in Mato Grosso, Brazil

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Passive surveillance is a fundamental component of animal health systems, playing a key role in the early detection of diseases of sanitary and economic importance. However, responses to suspected animal diseases are often limited to ruling out officially controlled diseases, with limited capacity to address the broader needs of livestock producers. In this context, the Instituto de Defesa Agropecuária do Estado de Mato Grosso (INDEA-MT), Brazil, implemented an Integrated Diagnostic Network for livestock producers as an institutional strategy that brings together the Official Veterinary Service, academic and research institutions (Universidade Federal de Mato Grosso – UFMT), and the production sector (Fundo Emergencial de Saúde Animal de Mato Grosso – FESA-MT). This approach aims to expand diagnostic capacity, improve service resolutiveness, and strengthen passive surveillance. An evaluation of the Integrated Diagnostic Network was conducted through a structured questionnaire applied to livestock producers assisted by the official veterinary service. The study included producers who reported suspected diseases and received differential diagnoses in 2024 and 2025. A total of 45 valid responses were obtained, representing approximately 85% of eligible producers across different regions of the state. Indicators assessed included the contribution of diagnosis to decision-making, reduction of production losses, perception of service quality, confidence in the service, and response time. Quantitative and qualitative analyses were performed to assess the impact of the intervention. The results demonstrated a high impact of diagnostic support on herd health management. A total of 93.4% of producers reported that the diagnosis helped or greatly helped decision-making regarding animal management or treatment. Similarly, 91.1% reported a reduction in economic losses, and an equivalent proportion indicated decreased herd losses, including mortality, reduced productivity, and disease progression. The importance of diagnostic information was highlighted by 86.7% of respondents, who considered it very or extremely important for production management. Service evaluation showed high satisfaction levels, with 97.8% of producers rating the service as satisfactory or very satisfactory. All respondents (100%) reported confidence and technical reliability in the service, as well as willingness to seek assistance again in the event of new disease suspicions. The Net Promoter Score (NPS) reached 93.3, indicating an internationally recognized level of excellence. In terms of operational efficiency, 84.4% of producers rated response time as fast or very fast. Qualitative findings reinforced the perception of service resolutiveness, highlighting reduced uncertainty, improved decision-making confidence, and practical application of technical recommendations in herd management. The Integrated Diagnostic Network improved the resolutiveness of the official veterinary service and strengthened passive surveillance by enhancing the system's capacity to detect and respond to animal health events. Increased producer confidence and perceived usefulness of the service contribute directly to greater engagement and voluntary reporting of disease suspicions, thereby increasing surveillance sensitivity. This approach represents a shift from a system focused on ruling out officially controlled diseases to a problem-solving model that addresses producers' needs. The integration of diagnostic support with field activities enhances the effectiveness of surveillance systems and supports early detection of diseases of sanitary and economic importance.

Keywords: Passive surveillance, Diagnostic network, Animal health services, Farmer engagement, Surveillance system evaluation.

Theme 1

Strengthening One Health Surveillance Coordination in Lao PDR: Findings from a Multi-Sectoral Mapping Study and National Workshop

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Summary

Lao PDR faces significant zoonotic disease risks at the human-animal-wildlife interface, yet surveillance across the human, animal, wildlife, and environmental sectors remains largely fragmented and poorly coordinated. This case story documents three complementary activities carried out in 2025 under the Sustainable Wildlife Management (SWM) Programme: a national One Health (OH) surveillance systems mapping study, an assessment of the wildlife health surveillance network using the OASIS evaluation framework, and a national multi-stakeholder workshop held in Vientiane on 16 June 2025. The workshop brought together 30 participants from three government ministries and eight non-governmental organisations. Through participatory methods including a cross-sectoral SWOT analysis, the process generated shared findings, validated recommendations, and built a degree of inter-sectoral ownership that desk-based studies alone cannot produce. The results point to four priority directions: formalising multi-sectoral coordination structures, developing a national wildlife surveillance strategy, strengthening human resources at decentralised levels, and redesigning community engagement around trust and incentives rather than compliance.

Context

Lao PDR is a landlocked country in Southeast Asia with a very rich biodiversity, and it is widely considered a high-risk area for zoonotic disease emergence. The reasons for this are well known: large and diverse wildlife populations, frequent contact between humans and animals, an active wildlife trade, and borders that are difficult to monitor with several neighbouring countries. Beyond this, the health infrastructure remains limited, veterinary services are understaffed, and the consumption of wildlife is deeply embedded in local culture and livelihoods. All of this creates conditions where a spillover event could happen and go undetected for some time.

Despite this situation, the surveillance systems that exist across the human, animal, wildlife, and environmental sectors have been working largely independently from each other. Although Lao PDR already possesses many of the foundations required for a stronger OH surveillance system: motivated actors, existing collaborations, regional networks, and increasing political recognition of OH approaches, there is very little formalised exchange of data between surveillance systems as well as vertically between national, provincial, district, and community levels. Mechanisms for joint investigation or coordinated response are almost absent and highly dependent on personal relationships rather than institutionalized ones.

The Sustainable Wildlife Management (SWM) Programme (1), funded by the European Union and implemented in several countries in Africa, Latin America and Asia, works to promote the sustainable use of wildlife while protecting biodiversity and reducing health risks at the interface between humans, animals and the environment. In Lao PDR, assessments carried out within the SWM Programme had already shown that surveillance systems needed strengthening, and that better coordination between sectors, along with a One Health (OH) approach, was necessary to improve detection and prevention of zoonotic diseases. To respond to this, three activities were designed and carried out in 2025 by CIRAD and the National University of Laos (NUoL), with the support of FAO and WCS:

(i) a national mapping study of OH surveillance systems, based on desk review and stakeholder interviews;
(ii) an assessment of the wildlife health surveillance network, using the OASIS (Operational Assessment of Surveillance and Investigation Systems) framework; and

Theme 1

(iii) a national workshop, held on 16 June 2025 at LaôTel Hotel in Vientiane, and entitled "Strengthening One Health Surveillance Coordination in Lao PDR."

This case story is mostly focused on the workshop and what came out of it, though the mapping study and the wildlife surveillance assessment provide important context for the findings.

Methods

The workshop was organised together by CIRAD, NUoL, FAO, WCS, and Lao government partners. Thirty participants attended, coming from a range of sectors and institutions. On the government side, 15 officials represented three ministries: the Ministry of Health (MOH), the Ministry of Agriculture and Fisheries (MAF), and the Ministry of Natural Resources and Environment (MoNRE). The other 15 participants came from eight non-governmental organisations: FAO, WCS, the World Health Organization (WHO), the Lao-Oxford-Mahosot Hospital-Wellcome Trust Research Unit (LOMWRU), Institut Pasteur du Laos (IPL), WWF, the Lao Conservation Trust for Wildlife (LCTW), and CIRAD.

The day was organised around participatory methods. In the morning, the three studies were presented in plenary, covering the OH surveillance systems mapping, the wildlife surveillance network assessment (2), and the OASIS evaluation findings (3). After each presentation, participants were invited to discuss, correct or add to what had been shown — not just to listen.

In the afternoon, the group worked through a Strengths, Weaknesses, Opportunities and Threats (SWOT) analysis. Four mixed groups of around eight people each rotated through four thematic tables, spending about 15 minutes at each one with a facilitator. The mixing of participants across sectors was intentional, to avoid the exercise becoming a series of separate sectoral conversations. At the last station, all groups were asked the same question: what new mechanism, structure or coordination process could make OH surveillance more integrative and collaborative in Lao PDR (4)? The workshop closed with reflections from three designated observers — a representative from the Department of Livestock and Fisheries (MAF), a senior researcher from CIRAD, and a representative from WCS.

Outcome / Impact

Validation of surveillance system maps

When the mapping study was presented, participants broadly recognised what was shown and confirmed it as accurate, while also bringing corrections and additions — particularly regarding the human health sector, where some information in the original maps needed updating. The discussions made clear that wildlife disease surveillance in Lao PDR is still relatively new, having been started around 2015, and that it sits outside the official government surveillance system. This was not a surprise to most participants, but putting it on paper and discussing it openly was useful. Several participants from the Department of Livestock and Fisheries noted that before expanding the wildlife surveillance network, a proper national strategy would need to be developed first — without that, any expansion would risk being disconnected and unsustainable.

SWOT analysis

The SWOT exercise produced a lot of material, reflecting perspectives from different sectors that do not often sit in the same room (figure 1). On the strengths side, participants pointed to a number of things that already exist and could be built on: partnerships between WCS and provincial agricultural offices, a field epidemiology training programme within the MOH, the presence of motivated individuals in key institutions, and a growing political interest in OH approaches. Regional networks such as SEAOHUN and LAOHUN were also mentioned as existing assets that are underused.

Weaknesses were discussed openly and with some candour. The most recurring issues were unclear reporting pathways between sectors, slow and largely paper-based reporting processes, the absence of a national information system for animal health data — covering both domestic animals and wildlife — and a very limited number of people with wildlife veterinary training. One comment in particular captured the fragility of the system well: the entire wildlife health surveillance network in the country depends heavily on a single expert, and this cannot continue. Poor data sharing between ministries, and the absence of any OH coordination at the local level, were also raised repeatedly.

On the opportunities side, participants pointed to the potential of digital reporting tools including smartphone-based platforms, growing international interest in pandemic preparedness funding, and the possibility of

Theme 1

adapting tools already in use in one sector for use in another. The political momentum around OH, both nationally and regionally, was seen as a window that should be used rather than waited on.

Threats discussed included political instability and changes in leadership that can disrupt ongoing programmes, the particular sensitivity of wild meat consumption as an entry point for surveillance — hunters and farmers will not report if they fear punishment — cross-border wildlife trade, and the effects of climate change on ecosystems and wildlife movement. Social media was also mentioned, notably its role in facilitating illegal wildlife trade through platforms like YouTube and Facebook.

Observer reflections

The three observers offered complementary perspectives that helped to close the day. There was broad agreement that genuine progress has been made in Lao PDR — the level of collaboration between NGOs, research institutes and government is real, and the number of people now talking to each other about OH has grown. But the structural problems have not gone away: bureaucratic reporting delays, insufficient and unstable budgets, and the absence of any formal national coordination mechanism continue to reduce what the system can achieve.

The CIRAD observer raised a point worth keeping in mind: the risks of zoonotic disease transmission do not only happen in forests or protected areas. They also happen at market level, at points of wild meat trade and consumption. Surveillance systems that do not reach these spaces will miss important signals. He also returned to the question of community trust — without it, no reporting system will work as intended, regardless of its technical design.

The WCS observer pointed to the long-standing cooperation between the Faculty of Agriculture and partner organisations, and noted that the experience in community engagement and conservation already accumulated by these institutions is an asset that should be more formally integrated into any future OH surveillance framework. The recommendation was that a main coordinating institution be identified for OH implementation, rather than continuing with arrangements that rely on goodwill and personal relationships.

What participants agreed on

Despite the diversity of people in the room, the four groups came to very similar conclusions when asked about new coordination mechanisms. A formal National One Health Surveillance Committee came up in all four responses. This committee would need a mandate, a budget, representation from all relevant sectors, and links to provincial and district levels. Alongside it, participants envisioned a central OH operational hub — a dedicated space where data from human, animal, wildlife and environmental surveillance could be brought together and acted upon. Training of young people at the community level, short and practical rather than academic, was mentioned as a way to build something that would last beyond the life of any single project.

Relevance for Others

A few things from this experience seem worth sharing for others working in similar contexts.

The combination of desk-based mapping and participatory workshop is more than a methodological preference — it changes what comes out. A mapping study produced on its own, however thorough, remains an external document. When it is presented back to the people it describes, and when those people can push back, add to it, and correct it in real time, the result is something different: a shared reference that participants feel some ownership over. This is not a small thing, particularly in contexts where inter-sectoral trust is still being built.

The SWOT format worked well precisely because it was mixed. Putting a government official from the health ministry in the same group as someone from WCS and a researcher from NUoL, and asking them to fill in the same table together, creates conversations that would not happen otherwise. The rotation also helped — no one institution dominated any one theme.

The question of community engagement came up repeatedly, and not as an abstract principle. In a country where wild meat consumption is common and legally ambiguous, any surveillance system that relies on communities voluntarily reporting observations will fail if those communities do not trust what happens after they report. This is a design problem, not a communication problem. It requires thinking carefully about what communities get in return for their participation, and what guarantees they have about how information will be used.

Theme 1

Finally, this work was stronger for being part of a broader programme. The SWM Programme's work on value chains, wild meat consumption and community livelihoods gave the OH surveillance work a context it would not have had otherwise. Surveillance systems that are designed and implemented in isolation from the economic and social drivers of zoonotic risk will always be working against the grain.

Recommendations

What came out of the workshop, and from the observer reflections, points in a few clear directions.

The most urgent need is a formal multi-sectoral and multi-level coordination structure. A National One Health Surveillance Committee, with real authority, a dedicated budget, and representation from health, agriculture, environment and wildlife sectors, would provide the institutional home that currently does not exist. Without something like this, the progress made through projects and partnerships will remain fragile and difficult to sustain after funding ends.

Wildlife surveillance in particular needs its own policy framework. The current situation — in which wildlife disease surveillance exists but has no formal status within the government system, no standardised protocols, and no agreed referral pathways — is not workable at scale. A national strategy developed through a properly inclusive process, defining priority diseases and species and clarifying who is responsible for what, would be an important step.

Human resource constraints need to be addressed directly. Training needs to reach provincial and district levels, not stay concentrated at the centre. A mapping of existing human resources, as several participants suggested, would give a clearer starting point. And investment in university-level OH education — including practical field training — is one of the few things that will produce durable results over time.

On community engagement, the approach needs to change (5). Expecting communities to report wildlife health observations when the main consequence they can foresee is legal trouble is not a realistic surveillance strategy. Approaches that combine health services, conservation incentives and livelihood alternatives with reporting have a much better chance of generating useful data, and of building the kind of trust that makes the whole system more resilient.

	Helpful	Harmful
Internal	**Strengths:** Existing WCS–provincial partnerships; FETPV field epidemiology programme (MOH); motivated individuals in key institutions; growing political recognition of OH; SEAOHUN and LAOHUN regional networks	**Weaknesses:** Unclear cross-sectoral reporting pathways; paper-based reporting; no national animal/wildlife health information system; single wildlife health expert nationally; no local-level OH coordination
External	**Opportunities:** Digital reporting tools; international pandemic preparedness funding; adaptable tools across sectors; political momentum for OH at national and regional level	**Threats:** Leadership turnover disrupting programme continuity; fear of legal consequences limiting community reporting; cross-border wildlife trade; climate change effects on wildlife movement; social media facilitating illegal trade

Figure 1. SWOT synthesis from the national One Health surveillance coordination workshop, Vientiane, Lao PDR, June 2025. Generated through participatory group rotation across four thematic stations, 30 participants from government and non-governmental sectors.

Keywords: One Health, surveillance, zoonotic diseases, cross-sectoral coordination, wildlife health.

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Short oral presentations

Roles of community animal health workers in surveillance and early warning – a regional overview in South East Asia

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Community Animal Health Workers (CAHWs) play an important role in animal disease surveillance and early warning systems across Southeast Asia, particularly in rural areas where access to formal veterinary services is limited. This regional overview synthesizes findings from Cambodia, Lao PDR, the Philippines, and Viet Nam, drawing on a structured literature review complemented by bilateral consultations with country stakeholders.

The study employed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) framework. A comprehensive literature search using broad keywords was conducted to capture relevant publications on CAHWs in the four countries. Titles and abstracts were screened for relevance, with eligible articles managed and grouped by country in EndNote. Full texts were reviewed, and reference lists were manually searched to identify additional sources. The selection process was documented using a PRISMA flowchart. Bilateral meetings with FAO ECTAD country teams were conducted to incorporate practical, country-specific perspectives on CAHW deployment.
Across countries, CAHWs contribute to surveillance through routine observation, reporting of suspected cases, participation in vaccination campaigns, and promotion of biosecurity practices. However, their roles and level of integration into national surveillance systems vary considerably. Viet Nam and the Philippines demonstrate stronger institutional integration, with CAHWs formally linked to government systems. In contrast, in Cambodia and Lao PDR, CAHWs primarily operate as private, fee-based providers, with more ad hoc engagement in government-led surveillance activities.

Several cross-cutting challenges affect the effectiveness of CAHWs in early warning systems, including inconsistent training, limited coordination with veterinary authorities, weak systems to track active workers, high turnover, and reliance on external funding. At the same time, CAHWs remain a critical interface between communities and formal surveillance systems, highlighting their potential to strengthen early warning if appropriately supported.

Further national-level analyses are recommended to refine these findings and inform context-specific strategies for strengthening CAHW systems.

Keywords: Community Animal Health Workers, surveillance, early warning, PRISMA, Southeast Asia.

Engagement of key stakeholders for the development of a participatory surveillance system of equine pregnancy and perinatal loss in Northern Italy

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Theme 1

Equine pregnancy and perinatal losses (EPPL) have a significant impact on the equine industry, including international trade, animal welfare, and public health [1]. In Italy, data on the etiology and risk factors of EPPL are limited [2], with no effective up-to-date reporting system in contrast with other EU countries [3]. This study introduces EQUIPER, a community-based participatory surveillance system of EPPL in Italy, for breeders (B) and veterinarians (V). EQUIPER aims to monitor and make accessible to stakeholders data on incidence and risk factors of EPPL. EQUIPER services will actively support stakeholders to manage EPPL, through continuous educational programs, laboratory diagnostic support and integrating epidemiological data with machine learning predictive tools made accessible through a user-friendly dashboard. To engage stakeholders, the EQUIPER multidisciplinary team organized a voluntary EPPL training day in University of Bologna. During this event, a knowledge and practice survey on EPPL was conducted targeting breeders and veterinarians present during the training through two anonymous on-line multiple-choice questionnaires via Microsoft forms: one tailored for B (34 questions) and one for V (31 questions). Questionnaires were structured in 5 sections: (1) intention to participate to a surveillance system; (2) general information, demographic data, professional experience; (3) knowledge of EPPL; (4) practices adopted to prevent EPPL; (5) experiences and management of EPPL in the last 3 years. The knowledge domain categories were assigned to participants as follows: “very knowledgeable” (>75% correct answers), “knowledgeable” (>50%) and “not knowledgeable” (<50%). Statistical analyses were conducted using R. All participants completed the questionnaire real time (23 V and 37 B). Most respondents (96% V and 84% B) would like to actively participate in EQUIPER, however 16% B and 4% V expressed the need for more information to decide and none disagreed. Regarding EQUIPER services, about half of V (55%) expressed the need for economical and logistic facilitation to dispatch samples to laboratory, while B (51%) expressed the need for regular training courses about EPPL. Participants acknowledged the need for an app/web dashboard (37% B and 34% V) to access data on EPPL and for educational activities on the epidemiology of infectious diseases (34% V and 8% B). Very knowledgeable (16% B and 8% V), knowledgeable (32% B and 56% V) and not knowledgeable (51% B and 34% V) stakeholders were identified. Although aware of the principal causes of abortion, knowledge gap included also the capacity to identify signs of high-risk pregnancy and abortion, a particularly important gap for passive surveillance components. Abortions, placentitis, and dystocia are reported as main problems in mares over the past 3 years, with less than one-third of respondents having a management plan for these issues. This study lays the groundwork for the development and implementation of EQUIPER, a participatory surveillance system for EPPL in Italy. B and V expressed clear interest in EQUIPER services which are recognized as highly relevant by stakeholders. However, considering their crucial role as sentinels of EPPL, targeted continuing education programs are needed with programs including risk factors for EPPL and related prevention strategies.

Keywords: breeders, veterinarians, surveillance, abortion, horses.

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Can participatory co-design improve the operability of risk-based community surveillance for zoonoses in transforming landscapes? A Philippines case-study

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INTRODUCTION:

Theme 1

Climate change and land-use change are transforming ecological and socio-economic systems, increasing interactions between humans, domestic animals, and wildlife, and raising the risk of zoonotic disease emergence. In the Philippines, these dynamics are exacerbated by high biodiversity, rapid environmental change, and uneven surveillance capacity, particularly in remote and resource-limited areas. While the One Health approach promotes integrated and intersectoral responses, its operationalization remains inconsistent. Community-based surveillance offers a promising, adaptive approach to early warning, yet often lacks sensitivity and structure. Integrating risk-based approaches into community-based systems may improve their efficiency, timeliness, and operability by focusing resources on high-risk areas. This research aims to examine how participatory co-design can support the integration of risk-based approaches into community-based early warning surveillance systems for zoonotic diseases in the Philippines.

MATERIALS AND METHODS:

This methodological PhD project combines qualitative and quantitative approaches across four main activities. First, a situational analysis and scoping review will assess existing surveillance systems and the integration of risk-based approaches into early warning systems. Second, spatial risk mapping will be conducted using multi-criteria decision analysis (MCDA), integrating environmental, socio-economic, and epidemiological data, as well as local knowledge and gender perspectives, to identify high-risk areas for zoonotic disease emergence. Third, a stakeholder analysis using interviews, focus groups, and participatory methods will inform the co-design of a localized, risk-based, community-based surveillance system through iterative workshops involving actors from human, animal, and environmental health sectors. The proposed system will be modeled and prospectively evaluated using scenario tree analysis to estimate its sensitivity. Finally, insights from all activities will be synthesized into a transferable operational framework, validated through participatory processes and supported by policy engagement activities.

RESULTS:

This study will generate a scoping review on the integration of risk-based approaches into early warning systems, a spatial risk mapping methodology adapted to data-scarce contexts, and a co-designed pilot surveillance system illustrating how risk-based strategies can enhance operability and adaptability. The main output will be a practical framework outlining key principles, tools, and performance indicators for integrating risk-based approaches into community-based surveillance systems.

DISCUSSION:

By emphasizing participatory co-construction, local knowledge, and gender considerations, this research seeks to strengthen intersectoral collaboration and improve the acceptability, sustainability, and effectiveness of early warning systems. Aligning surveillance design with context-specific risk dynamics is expected to support more timely and cost-effective detection of zoonotic disease emergence in the Philippines.

Keywords: One Health, Intersectorality, Early-warning surveillance, Emerging infectious diseases, Climate change.

One Health field site: Advancing intersectoral engagement and implementation at the grassroots level in Southeast Asia

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Theme 1

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Introduction

In Vietnam and Southeast Asia, rapid agricultural and climate changes, along with close human-animal interactions, drive emerging and re-emerging zoonotic diseases, food safety risks, and antimicrobial resistance (AMR). Gaps in preparedness and responses, surveillance, interventions, and coordinated action continue to threaten public health, livestock, and ecosystems. Active implementation of One Health (OH) at grassroots and community levels is essential to support a holistic approach to addressing these challenges. This presentation demonstrates case stories about how engagement activities and OH implementation towards disease prevention and surveillance at community levels in Vietnam and Lao PDR.

Materials and Methods

The OH field site has initiated since 2018, when local authorities, research institutes and universities from human and animal health sectors signed a collaboration agreement to improve OH research, training and implementation in Thai Nguyen province. The OH field site had official established in Phu Binh district, Thai Nguyen in 2022.

Diverse activities such as AMR/AMU prevention, food safety interventions, and rabies and HPAI vaccination campaigns were implemented. The model integrates training, student field practice, and local programs while supporting emergency responses, including post-flood and typhoon recovery, farm disinfection, and community sanitation.

Building on its success, the OH field site approach has been scaled to Vientiane in 2024 and Luang Prabang, Lao PDR, in 2025.

Results

Over 300 local authority staff, university lecturers and students in both countries have equipped and understood and implemented activities using OH approach in the communities. More than 1,000 Livestock value chain actors (farmers, butchers, retailers), and over 5,000 community members have benefited from OH field site activities on disease and AMR prevention, food safety interventions, etc. One Health field sites have gained better recognition by local authorities and created a platform to facilitate different activities at the commune. In addition, the OH field site is as a study site to support research and training the next generation of OH workforce, including students, researchers, and technical staff.

Conclusions

The OH field site is relevant to Vietnam and regions as it addressed directly health challenges in the communities. It serves as a hub to share and strengthen collective efforts and investment in grass-root levels for better impact on policy and OH intervention. The OH field site could have a high potential to scale and link to relevant partnerships (local authorities, universities, unions, associations), projects and development programs across communities and countries.

Acknowledgements

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Keywords: Intersectional collaboration, Zoonoses, Food safety, AMR, One Health.

Livestock Identification and Registration System (LIRS) as an integrated tool for a community rabies vaccination program, A pilot project from Vietnam

Theme 1

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This study presents an evaluation of the Livestock Identification and Registration System (LIRS) as an integrated tool for a community rabies vaccination program in two communes of Tây Ninh province and communes of Dong Thap province, Vietnam, in 2025. The study aimed to assess the factors influencing the acceptance of maintenance fees and to gather feedback from pet owners after a four-month trial period.

The initial phase of the trial, conducted in April 2025 in Tay Ninh with 1280 dogs and in Dec 2025 in Dong Thap with 600 tags. The trial has successfully identified 70.9% and 42.8%of the total pet population and 93.6 and 74.8 % of vaccinated animals using LIRS in Tay Ninh and Dong Thap, respectively. A significant finding was that 81.21% of households (in Tay Ninh) agreed to pay an annual fee of 24,000 VND per pet to maintain access to the system. The level of education was found to be a key factor influencing this willingness to pay, with a higher educational background correlating with a greater understanding of benefits and therefore acceptance of the fee. However, a follow-up survey in Tay Ninh province after four months revealed significant challenges with the durability of the physical tags. Only 15.62% of pets retained both the collar and the QR code tag, while a substantial number lost either the tag or both items due to pets' physical activity (51.16%) or irritation from the collar (21.46%). The free ranging dogs behavior with new collars explained the lost, where first time wearing collars might cause the sensitivity to collar irritation due to irregular use.

In conclusion, the LIRS system pilot shows great potential for digitalizing pet management and supporting rabies control efforts. To ensure its long-term viability, recommendations include improving the durability of the collars and QR codes (piloting new tags materials and technology), enhancing community outreach, and fully integrating LIRS into annual vaccination campaigns. This approach could provide a sustainable model for rabies control, advancing Vietnam's goal of eliminating rabies in humans by 2030.

Poster presentations

Investigation of Recurrent Canine Rabies and Community KAP Survey in a Rural District of Maha Sarakham Province, Thailand (Sep 2024 – 14 Feb 2025)

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Summary

This study investigates recurrent canine rabies transmission in Chuen Chom District, Thailand, by integrating epidemiological investigation with a community-based Knowledge, Attitudes, and Practices (KAP) assessment. The most recent case involved a vaccinated but insufficiently immunized, free-roaming male dog, likely exposed during the breeding season when increased movement elevates contact rates. Similar cases have recurred annually within the same seasonal window, indicating persistent transmission dynamics in the area. Findings highlight critical gaps in rabies control. Although reported vaccination coverage in owned dogs exceeded operational targets, the absence of booster doses, exclusion of free-roaming and unrestrained animals, and inaccurate population data result in suboptimal herd immunity and likely overestimation of coverage.

Theme 1

Surveillance is further weakened by delayed or absent reporting of suspected cases, limiting timely outbreak detection and response. The KAP analysis revealed moderate knowledge but persistent misconceptions, with knowledge declining with age and lower levels observed in outbreak-affected communities. Despite generally positive attitudes, a weak relationship between attitudes and practices indicates that awareness does not consistently translate into appropriate preventive behaviors. High levels of free-roaming and low sterilization rates further reinforce transmission risk. Overall, the persistence of rabies in this setting is driven by the interaction of epidemiological risk, behavioral gaps, and operational limitations. These findings underscore the need for integrated control strategies that ensure adequate herd immunity, strengthen surveillance and reporting systems, and deliver targeted, context-specific community engagement, supported by improved coordination between local authorities and health sectors.

Methods

A cross-sectional study was conducted between September 2024 and 14 February 2025 in Chuen Chom District, Maha Sarakham Province, Thailand, integrating an epidemiological investigation with a community-based KAP survey. The study focused on the most recently affected village while also assessing district-wide prevention and control measures. Data were obtained from rabies surveillance systems, local administrative organizations (LAOs), the Department of Livestock Development (DLD), and field investigations, including active case finding through forward and backward tracing, household and stakeholder interviews, and environmental assessments. A total of 392 respondents were recruited through convenience sampling across affected and non-affected villages using structured questionnaires covering demographic characteristics, knowledge, attitudes, and practices. Data were analyzed using descriptive statistics, Spearman's correlation to assess relationships among KAP components, and stepwise multiple linear regression to identify associated factors.

Results

1. Epidemiological Investigation and Active Case Finding

Between 2023 and January 2025, eight confirmed canine rabies cases were reported in Chuen Chom District, involving both owned and stray dogs. Among owned dogs, half had been vaccinated, but all had received only a single dose without boosters. All cases exhibited aggressive behavior, with additional neurological signs observed in some animals. Most cases occurred in intact, free-roaming male dogs, and all infected animals had bitten other animals, with several cases involving human exposure.

The most recent case occurred in Village 9, Subdistrict K, involving a 17-month-old, free-roaming owned dog with a history of single-dose vaccination. The case was likely associated with increased dog movement during the breeding season, leading to exposure through contact with other dogs. Rapid response measures were implemented, including case notification within one day and initiation of control measures within two days. Forward tracing identified multiple animal and human exposures, and ring vaccination and quarantine were conducted within a 1–1.5 km radius. No additional confirmed cases were identified in the same village, although two suspected cases were detected in a nearby subdistrict without epidemiological linkage. A substantial discrepancy was identified between reported and actual animal population data. Field surveys indicated approximately 41% higher numbers than volunteer-reported data, resulting in overestimation of vaccination coverage. Vaccination activities were limited to owned and physically restrainable animals, contributing to suboptimal herd immunity.

2. Assessment of Rabies Prevention Measures

Rabies prevention and control activities varied across subdistricts. While all areas conducted biannual animal population surveys, only one subdistrict included stray animals, indicating limited surveillance scope in most areas. Vaccination strategies differed, including house-to-house delivery, fixed-point services, and owner-based vaccine collection. Across all areas, vaccination targeted primarily owned animals, leaving a proportion unvaccinated due to handling challenges. Reported vaccination coverage ranged from 71% to 86%; however, these estimates were likely inflated due to underreporting of animal populations. Booster vaccination was inconsistently implemented. Gaps were also observed in cold chain management and training, with some areas lacking adequate infrastructure and technical support. No subdistrict implemented alternative vaccination approaches for hard-to-reach animals. Community education activities, particularly in schools, were not integrated into rabies prevention programs.

3. Community Knowledge, Attitudes, and Practices (KAP)

Theme 1

The KAP survey included 392 respondents from 16 villages, with the majority representing non-affected areas. Most respondents were older adults and engaged in agriculture. Among participants, 64% were pet owners, with a high proportion allowing free-roaming animals and only 25% reporting sterilization. Vaccination practices among pet owners were inconsistent. Although 66% reported annual vaccination, a considerable proportion had irregular or no vaccination, primarily due to inability to restrain animals, misconceptions regarding appropriate vaccination age, and limited awareness. Most vaccinations were administered by local volunteers. Knowledge assessment revealed moderate overall scores, with several critical misconceptions. A substantial proportion of respondents believed that rabies occurs only in summer, that vaccination is limited to adult animals, and that rabies is treatable after symptom onset. Attitudes toward rabies prevention were generally positive, with most respondents agreeing on the importance of vaccination and seeking medical care following animal bites. However, these attitudes were not consistently reflected in practices. Among respondents who had encountered suspected rabid animals, 40% reported taking no action, while only 38% notified authorities. Feeding of stray animals was still reported by a notable proportion of respondents. Although most individuals who experienced animal bites sought medical care, many did not perform appropriate wound management prior to visiting healthcare facilities. Statistical analysis demonstrated significant positive correlations between knowledge and attitude ($r = 0.33$, $p < 0.001$) and between knowledge and practice ($r = 0.21$, $p < 0.001$). In contrast, the relationship between attitude and practice was weak and not statistically significant. Regression analysis indicated that knowledge was negatively associated with increasing age and residence in outbreak-affected areas, while males had higher knowledge scores. Practices were generally suboptimal and were significantly poorer in resource-limited subdistricts.

Discussion

The confirmed rabies case in this investigation involved an intact, free-roaming adult male dog with insufficient vaccine-induced immunity, detected during the year-end breeding season. This profile is consistent with well-established risk factors for canine rabies transmission. Intact male dogs are hormonally driven to roam extensively in search of mates, substantially increasing their contact rates with other animals (1). Furthermore, the estrous cycle in female dogs—which occurs most commonly during the winter and post-rainy season—triggers heightened roaming and aggression in males, compounding exposure risk (2). Free-roaming behavior has been widely recognized as a primary driver of rabies contact rates in endemic settings (3). The district-level survey conducted in this study found that 78% of dogs were free-roaming and 75% were unsterilized, conditions that collectively sustain elevated transmission potential. These findings reinforce that the biological and behavioral characteristics of unrestrained male dogs render them disproportionately likely to encounter and propagate the rabies virus within rural communities.

The recurrence of rabies cases during the same seasonal period across consecutive years points to persistent, unresolved gaps in surveillance and case notification. Outbreak recurrence is consistent with transmission dynamics in which unvaccinated, free-roaming, or stray dogs traveling along main roads serve as vehicles for virus dispersal (4). Studies of rural dog movement in conservation areas have shown that free-roaming dogs preferentially use trails and roads for travel rather than forest habitat, facilitating geographic spread of infection along predictable corridors (5). A particularly concerning finding from the community survey was that 40% of respondents reported that they did not respond to or report animals suspected of having rabies. This degree of underreporting substantially impedes timely outbreak response and contact tracing, allowing potential chains of transmission to continue undetected. Unnotified rabies cases represent a critical blind spot in surveillance systems, making it difficult to estimate true disease burden or to deploy targeted interventions before secondary spread occurs.

Animal rabies prevention efforts by LAOs were found to be inadequate in several respects. Dog population surveys were inaccurate, largely due to limited manpower; only two LAOs had an operational plan for stray dog enumeration, relying heavily on Village Health Volunteers (VHVs) without formal coordination structures. This mirrors challenges documented in Africa, where limited accessibility and poor knowledge of dog population sizes are key barriers to effective rabies control (6). Inaccurate population data directly undermines the ability to calculate and achieve target vaccination coverage thresholds. The vaccination campaign itself also exhibited critical deficiencies. Despite reported coverage of nearly 80% among owned pets, the absence of booster vaccination likely erodes herd immunity over time, as rabies-specific antibody titers in dogs can fall below protective levels within 180 days of initial vaccination (7). Annual single-dose campaigns targeting only owned and restrained animals leave large segments of the dog population—particularly stray and free-roaming dogs—entirely unprotected. Alternative delivery strategies, such as vaccine-loaded darts or oral rabies vaccine, could extend coverage to unrestrained populations. Additionally, emphasis on dog population management through

Theme 1

sterilization programs may reduce population turnover and size, making vaccination coverage more tractable and sustainable over time (8).

The KAP survey revealed important community-level gaps that directly affect rabies prevention. Knowledge scores were inversely associated with age, a troubling finding given that elderly individuals who remain at home are at heightened risk of dog bite exposure (9). Declining knowledge with age, combined with greater vulnerability, creates an underserved subgroup requiring targeted educational outreach. Several common misconceptions were identified: many respondents believed that rabies occurs only during summer, that vaccination is only necessary for adult animals, and that the disease is treatable once clinical signs appear. These misconceptions carry concrete public health consequences. Seasonal misperceptions lead to reduced vigilance and lower vaccination uptake outside the summer period. The belief that rabies is curable after symptom onset is particularly dangerous, as it may delay or preclude timely post-exposure prophylaxis (PEP), which is the only effective intervention once exposure has occurred. Perhaps most strikingly, villages with a prior history of rabies outbreaks demonstrated significantly lower knowledge scores and less favorable attitudes toward rabies prevention than unaffected communities. This counterintuitive finding suggests that prior exposure to an outbreak does not automatically translate into improved awareness or behavioral change, possibly reflecting inadequate follow-up education, limited community engagement, or the normalization of risk over time. This pattern underscores the need for sustained, targeted, and localized educational interventions rather than one-time awareness campaigns.

Taken together, the findings from this investigation highlight a convergence of epidemiological, operational, and behavioral factors that sustain canine rabies transmission in this rural district. The persistence of rabies despite existing vaccination programs is consistent with the global evidence that vaccination coverage alone is insufficient when structural barriers prevent adequate herd immunity from being achieved and maintained. Meeting the internationally recommended threshold of 70% population-level immunity requires not only high nominal coverage but also inclusion of stray and free-roaming dogs, regular booster doses, and accurate population estimates (8). The strong association between community KAP deficits and village-level outbreak history further demonstrates that technical veterinary interventions must be complemented by robust public health communication strategies. A One Health framework—integrating animal health, public health, and community engagement—offers the most coherent approach to breaking the cycle of recurrent rabies outbreaks. This investigation provides an evidence base for redesigning local rabies prevention programs by addressing the identified gaps in surveillance, vaccination delivery, dog population management, and community education in a coordinated and sustained manner.

Conclusion

The recurrent rabies case in this study reflects ongoing transmission driven by free-roaming, unsterilized dogs with insufficient immunity, particularly during the breeding season. Control efforts remain limited by underreporting, inaccurate population data, and vaccination strategies that exclude unrestrained animals and lack booster doses, resulting in suboptimal herd immunity. KAP findings further reveal gaps between knowledge, attitudes, and practices, with lower awareness in previously affected communities, indicating that experience alone does not ensure improved prevention. Overall, rabies persistence arises from the interaction of epidemiological risk, behavioral gaps, and systemic constraints. Strengthening control efforts requires an integrated approach that improves surveillance, expands inclusive vaccination, and enhances targeted community engagement, while ensuring that interventions are adapted to local context and implementation realities within a One Health framework.

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Keywords: Canine rabies, Investigation, KAP survey, Maha Sarakham, Epidemiology.

Theme 1

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Evaluating Risk Awareness and Behaviours to Enhance Avian Influenza Communication Strategies in Cambodia

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Context

Highly pathogenic avian influenza (HPAI) H5N1 remains a major impact for animal, human health and economy in Cambodia. Poultry production and trade networks, including extensive cross-border movements of live birds and poultry products, facilitate the introduction and spread of both highly pathogenic and low pathogenic avian influenza virus (AIV) strains. Persistent circulation of these viruses increases the risk of reassortment events that may result in strains with enhanced zoonotic or pandemic potential.

In Cambodia, women play critical roles in poultry production, slaughter, and processing, often in smallholder settings. These roles, combined with limited access to protective equipment and information, place women—and children in close contact with poultry—at elevated risk of infection with zoonotic AIV. National laboratories have confirmed multiple human infections with AIV in recent years, with children under sixteen disproportionately affected. It is therefore essential that women and children are specifically included in communication messages and materials that promote protective practices and reduce infection risks.

Methodology

Existing community engagement messages and materials currently used in Cambodia have not been updated for over 15 years. To ensure materials are evidence-based, audience-relevant, and aligned with current FAO guidance and One Health principles, a consultative workshop was organized, bringing together representatives of key national stakeholders, with the purpose to validate findings from the review of existing communication materials, co-develop new messages and visuals, and prioritize channels for dissemination to high-risk populations, particularly women and children.

In a second phase, the project supported the development of a comprehensive, evidence-based Social and Behaviour Change (SBC) strategy and materials suite to address Highly Pathogenic Avian Influenza (HPAI). By

Theme 1

establishing a streamlined coordination mechanism between government authorities and development partners, the initiative facilitated rigorous feedback cycles for graphic and audiovisual production, ensuring technical accuracy and behavioural resonance.

Results

The strategy was informed by a systems-lens desk review and primary data collection, defining priority behaviours and audience segments linked to animal and human health outcomes. Central to the process was a stakeholder validation workshop and target audience focus group discussions (FGDs), which refined messaging architecture and creative principles based on real-world comprehension and acceptability.

A finalized, operationally-ready risk-communication strategy was developed and a suite of validated, digital- and print-ready materials designed for immediate rollout in outbreak contexts.

Conclusion

The development of this evidence-based SBC strategy and updated materials suite marks a critical transition from outdated communication models to a modern, One Health-aligned approach in Cambodia. By integrating gender-sensitive messaging and rigorous stakeholder validation, the project ensures that risk communication is not only technically accurate but also culturally and behaviourally resonant for high-risk groups, particularly women and children. These operationally-ready tools provide the necessary framework for rapid, effective mobilization during HPAI outbreaks, ultimately strengthening national health security and reducing the risk of zoonotic transmission.



Figure 1. Avian Influenza Risk Awareness in a Cambodian school

Keywords: Avian Influenza, Risk awareness, Behaviour change, Gender, At-risk practices.

Theme 2

Theme 2: Science - society - policy dialogue for effective surveillance

Oral presentations

A participatory progressive framework to guide development of national animal disease surveillance and early warning capacities in Asia

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Summary

Animal disease surveillance systems in Asia remain constrained by a number of factors. These include: limited sustainable resources to implement field activities other than from external partners, lack of formalised surveillance protocols and plans covering all prioritised diseases, and few analyses conducted on surveillance data to inform decision-makers. These general gaps represent an opportunity to generate guiding principles and build countries' capacities using a systematic approach. This abstract presents the development of a progressive framework designed to support co-development of surveillance and early warning capacities through structured, inclusive dialogue processes with stakeholders from veterinary services and development partners.

FAO convened a regional consultation held in Bangkok in December 2025. There were 45 participant stakeholders from nine countries, including government representatives, international organizations, and technical partners. Using participatory methodologies, participants jointly developed a stepwise framework structured across five surveillance domains.

The resulting framework defines progressive capacity levels and milestones that allow countries to clearly identify steps to take to build their surveillance and early warning capacities adapted to their specific situation. Applying this framework at a sub-regional level will facilitate collaborative approaches to build capacities between countries, development partners and economic communities such as the Association of Southeast Asian Nations (ASEAN).

Introduction

Animal and zoonotic diseases continue to challenge food security, livelihoods, and public health systems across Asia. The region's diverse livestock production systems, complex value chains, and high levels of animal movement contribute to the emergence and spread of transboundary animal diseases and zoonoses. In response, countries have made significant efforts to strengthen surveillance and early warning systems.

Despite these investments, surveillance systems remain uneven in their performance and sustainability. Persistent challenges include limited use of surveillance data to inform decisions, few operational surveillance protocols covering all countries' prioritised diseases, and resources that are often dependent on external projects, along donors' priorities.

Improving surveillance effectiveness requires moving beyond traditional, top-down approaches toward collaborative and participatory models, where strategies are co-developed through dialogue between national stakeholders and development partners. Such approaches can enhance ownership, ensure alignment with local contexts, and improve the translation of evidence into action.

Countries in Asia and the Pacific, as well as regional partners such as ASEAN have requested guidance to support the development of their animal disease surveillance capacities by identifying specific actions they may take based on their national contexts.

To address this gap, a regional consultation was convened to develop a progressive framework for strengthening animal disease surveillance and early warning systems in Asia. A central objective of the workshop was to

Theme 2

identify guiding principles and develop a foundation for a progressive pathway to build surveillance and early warning capacities for countries in Asia and the Pacific.

Materials and Methods

A regional consultation was conducted in Bangkok, Thailand, from 2 to 4 December 2025, bringing together 45 participants from nine Asian countries, as well as representatives from international organizations, regional bodies, and development partners. Participants included epidemiologists, laboratory specialists, policymakers, and programme implementers.

A participatory approach was adopted to facilitate multi-actor dialogue to develop a progressive pathway to surveillance and early warning capacities that reflect countries' needs. During the workshop, participants provided their inputs through participatory exercises which ensured consensus and shared ownership.

The framework was developed through a four-step process.

- Five core tracks of surveillance systems were identified, with additional sub-tracks further refining the pathway.
- Participants co-developed endpoint statements for each sub-track, representing an ideal, developed capacities for each of these components of a surveillance/early warning system.
- Through participatory ranking exercises, participants developed the baseline and intermediate capacities from the endpoint statements. This step ensured that the pathway reflected a logical progression from beginning to end.
- Finally, participants defined capacity level milestones as indicators for transition between levels.

Previous regional consultations and existing surveillance assessments informed the process. This ensured alignment with established tools while introducing a stronger focus on stakeholder engagement.

Results

The consultation resulted in a draft progressive framework structured around five core tracks and associated sub-tracks, consisting of baseline and mid-point capacities leading to endpoints representing fully realised capacities (Table 1). Between each step in the progressive framework, milestones provide guidance on moving from one capacity level to the next.

The draft progressive framework was circulated amongst participants to validate the outputs of the workshop. Continuing work is planned through 2026 to further refine as the Progressive Framework for Surveillance and Early Warning Capacity-Building In Asia and the Pacific through a technical working group. This group will identify measurable indicators and link the framework with existing surveillance system evaluation methodologies such as the Food and Agriculture Organization of the United Nations' Surveillance Evaluation Tool (SET).

The consultation workshop demonstrated that co-development processes can lead to greater alignment of priorities between implementers of surveillance and development partners, while guiding countries to reach a common objective for better surveillance and early warning in Asia and the Pacific.

Discussion

The progressive framework developed through this consultation provides a practical model for building national surveillance and early warning systems while maintaining collaborative approaches at the regional level.

A key contribution of this work is to demonstrate that co-development processes can be systematically integrated into surveillance framework design. This approach enhances the relevance and feasibility of surveillance strategies that are, as they are informed by the perspectives and experiences of all stakeholders involved who thus feel ownership of the product.

Limitations include the reliance on expert consultation rather than empirical implementation. Further work is needed to test the framework in practice and evaluate its impact on surveillance outcomes.

Theme 2

Conclusions

The progressive framework developed through this consultation provides a structured pathway to build surveillance and early warning capacities at national level, while maintaining a collaborative approach at the sub-regional level. It allows countries to follow steps towards fully realised capacities while adapting their development processes to their specific contexts.

By institutionalizing dialogue processes and promoting co-development of strategies, the framework enhances the alignment between development partner and national priorities, and operational realities. It offers a scalable model for improving surveillance system performance and supporting effective responses to animal and zoonotic disease threats.

Track 1 – Planning, design and evaluation	
Sub-track 1.1 Institutional organisation	Formalized legal frameworks and strategies with clearly defined objectives and institutional roles – developed with input from local, community, private-sector and multisectoral stakeholders - guide surveillance planning and implementation. Governance structures ensure planning reflects local priorities and embrace technological innovation in the design and implementation of surveillance activities.
Sub-track 1.2 Risk assessment	Capacity assessments and performance reviews are systematically carried out by a trained national animal-health workforce, with recommendations routinely used to improve surveillance effectiveness, functionality, and sensitivity, to plan and prioritize corrective actions, and to guide resource prioritization and mobilization.
Sub-track 1.3 Evaluation	Trained workforce assess risks (likelihood and impacts) of disease incursion and spread - including through joint risk assessments - in routine and emergency situations. Findings systematically guide evidence-based surveillance planning, prevention and control strategies, and risk communication to safeguard farmers, the public, and support safe trade.
Track 2 – Implementation of surveillance	
Sub-track 2.1 Surveillance methods	Animal health trends are regularly and consistently monitored, including (all) priority and emerging diseases, through the cost-effective, harmonized application of validated surveillance methods, ensuring sensitivity and timeliness across all administrative levels enabling evidence-based decision making.
Sub-track 2.2 Surveillance workforce	Surveillance activities are delivered by sufficient, fully competent and equipped workforce, including public and private sectors across all sectors and all administrative levels in both routine and emergency situations.
Track 3 – Laboratory	
Sub-track 3.1 Diagnostics	A fully integrated, interoperable, documented and quality-assured laboratory network provides timely, accurate, and well-interpreted diagnostic results and data that consistently inform relevant stakeholders and national surveillance decisions.
Sub-track 3.2 Laboratory data and networks	High quality, and effective sample referral system and diagnosis are sustainably provided nationwide through an accredited laboratory system applying validated techniques for all prioritised and emerging diseases.
Track 4 – Information systems	
Sub-track 4.1 Epidemiology data collection	Complete, accurate, standardized, verifiable and timely data from all types of surveillance is consistently collected and collated, across all administrative levels for monitoring and reporting of all priority and emerging diseases.
Sub-track 4.2 Data management and utilisation	Accurate surveillance and risk information is communicated in an appropriate, transparent, user-friendly and timely manner tailored to all relevant stakeholders at all levels (and internationally), both routinely and during emergencies.
Track 5 – Information sharing and advocacy	
Sub-track 5.1 Communications	Accurate surveillance and risk information is communicated in an appropriate, transparent, user-friendly and timely manner tailored to all relevant stakeholders at all levels (and internationally), both routinely and during emergencies.
Sub-track 5.2 Intersectoral collaboration	A formalized, documented, sustainable and effective "multi-sectoral" mechanism coordinates high-level policy, routine and transparent information exchange with all relevant stakeholders, and harmonized and joint planning and responses.

Table 1. Endpoints developed for each sub-track of the progressive pathway for surveillance and early warning capacities in Asia and the Pacific

Keywords: Surveillance, Early warning, Progressive pathway, Partnerships.

One Health Strategy 2019: A Review of Nepal's Multisectoral Health Framework

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ABSTRACT

The One Health paradigm integrates human, animal, and environmental health to address complex, interlinked threats such as zoonotic diseases, antimicrobial resistance (AMR), food safety hazards, and climate-sensitive health risks. Nepal, characterized by high biodiversity, intensive human–livestock–wildlife interfaces, open

Theme 2

borders, and rapid socio-ecological change, faces elevated vulnerability to emerging and re-emerging zoonoses. In response, the Government of Nepal adopted the One Health Strategy 2076 (2019 AD), South Asia's first formal multisectoral framework to operationalize coordinated surveillance, joint risk assessment, preparedness, and response across the Ministry of Health and Population, Ministry of Agriculture and Livestock Development, and Ministry of Forests and Environment. This review critically examines the legal, institutional, and operational dimensions of Nepal's One Health Strategy within the country's federal governance architecture established by the 2015 Constitution. The analysis synthesizes early implementation gains establishment of federal coordination mechanisms, incremental interoperability, and donor-supported AMR surveillance alongside persistent constraints including fragmented legal mandates, uneven provincial uptake, fiscal limitations, and incomplete digital interoperability. The paper argues that Nepal's One Health Strategy provides a credible policy architecture for spillover prevention and pandemic preparedness, but its transformative potential depends on legal enshrinement.
Keywords: One Health; zoonoses; antimicrobial resistance; multisectoral governance; Nepal

INTRODUCTION

The One Health paradigm (human, animal and ecosystem health) has become a global change agent. About 3 out of 4 emerging infectious diseases are zoonotic in origin, which originates from animal reservoirs and spillfeeds to humans primarily at the interface where the environment is disturbed by human activities (World Health Organization, 2017; Food and Agriculture Organization of the United Nations, 2019). The One Health paradigm is at the core of the emergence and propagation of large-scale threats, such as avian influenza (H5N1), rabies, Ebola, Nipah virus and antimicrobial resistance (AMR). Globalization, including more intensive agriculture and trade in wildlife, rapid urbanization, deforestation and climate change has exponentially increased the risks. The One Health approach was formally agreed by the Quadripartite Alliance (World Health Organization (WHO) FAO, United Nations Environment Programme (UNEP) and World Organisation for Animal Health (WOAH) One Health Joint Plan of Action (2022–2026) and calls for surveillance, risk assessment and governance in a multisectoral platform to address zoonotic spillovers and their prevention in a proactive manner (World Health Organization et al., 2022). It highlighted the need for integrated surveillance systems, data-sharing, genomic sequencing, and ecosystem restoration initiatives to prevent spillovers in a cost-effective manner. The One Health approach maximizes scarce resources by breaking down institutional silos in public health, veterinary medicine, agriculture, and the environment to develop resilience of inter-connected systems that support SDG 3 [Good Health and Well-Being], 13 [Climate Action], and 15 [Life on Land]) and the emerging pandemics. However, substantial barriers still exist that threaten efficient implementation of One Health. National policies remain fragmented, inequity in capacity between the Global North and South is still pervasive, and wildlife trade remains insufficiently regulated.

Nepal's One Health Strategy 2019

Nepal's One Health Strategy 2019 is the first multisectoral strategic framework in South Asia that intentionally links one health domains to alleviate emerging threats of zoonosis. It operationalizes the global One Health concept by integrating surveillance, joint risk assessment, capacity building, preparedness and advocacy to address one health challenges (Government of Nepal, 2019). It emerged in the context of recurrent zoonotic outbreaks including highly pathogenic avian influenza (H5N1) first detected in poultry in 2009 and periodic recurrences; endemic of rabies with 6–32 human deaths reported annually; and antimicrobial resistance (AMR) in smallholder livestock systems. It was formalized through inter-ministerial coordination between Ministry of Health and Population (MoHP), Ministry of Agriculture and Livestock Development (MoALD), and Ministry of Forests and Environment (MoFE) and approved by the Council of Ministers in December 2019. The One Health Strategy 2019 operationalizes national commitments by harmonizing with international commitments and standards, such as the Quadripartite Alliance One Health Joint Plan of Action (2022–2026) and Nepal's commitments to the International Health Regulations (IHR 2005), thereby facilitating multisectoral governance, multisectoral surveillance, and multisectoral response to zoonotic and emerging diseases. Importantly, the One Health Strategy 2019 operates within the constraints and opportunities of the federal architecture prescribed by the Constitution of Nepal, which establishes a three-tier governance system and devolves concurrent powers in areas, such as health services, agriculture and livestock development, and the environmental domain, to the province and local governments. Decentralisation, which includes subnational distribution of activities, aims to increase local responsiveness and agility, community ownership and contextual adaptability to zoonotic inputs, but risks mandates (de)multiplexing, fiscal disproportionality, (de)balancing capacities by tier, with potential detrimental effects to multisectoral coordination and One Health consistency.

Theme 2

Core Components and Objectives

One Health Strategy 2019 formally approved by the Council of Ministers, articulates a cohesive multisectoral architecture to integrate human, animal, and environmental health amid escalating zoonotic pressures. Its stated vision - "Achieve optimal health outcomes through effective management of shared risks across human, animal, and environmental domains" and associated holistic ontology support cross-sector work to promote systemic resilience in Nepalese settings. The strategy's vision aligns with global Quadripartite imperatives but contradicts the coordination-principles of the Bar-on Report, which favors sovereignty to preemptively recognize and mobilize consilience rather than demonetize and respond post hoc. The overall One Health Strategy goal operationalizes the overall vision by acting as an umbrella for One Health activities - "To promote One Health activities through coordinated surveillance, prevention, and resource optimization for priority threats: emerging and reemergence zoonoses and novel sectoral spillovers".

The implementation framework is structured around four interlocking objectives that cascade coherently across the federal tiers of governance.

Build networks of stakeholders for coordination.

This component implies polycentric governance: a Federal One Health Steering Committee (Ministers of MoHP, MoALD and MoFE) to arbitrate politics; Technical Coordination Committees (Directors and Epidemiologists) to operationalize; and devolved provincial/local analogues for execution. Networks include non-state actors, e.g. Nepal One Health Institute and NGOs, and define data-sharing protocols and joint outbreak declaration. In practice, this will precipitate federal fragmentation post-2015 Constitution, with concurrent powers (Article 57) that could lead to mandate overlaps; biannual meetings ensure alignment; and focal points embedded within ministries.

Build robust early warning systems

This objective, focused on sentinel surveillance, calls for community-based event monitoring and digital platforms for real-time risk mapping of priority pathogens (rabies, H5N1, Japanese encephalitis). It also calls for laboratory networking, genomic sequencing hubs and cross-border alerts. Consistent with IHR (2005) and JEE metrics, it aims at 80% timeliness of detection, building on pre-2019 gaps exposed by H5N1 delays; rapid response teams (RRTs) at the provincial level operationalize alerts, reducing over weeks response lags to days.

Upscaling Multisectoral Capacities

Human capital, infrastructure and curricula in IAAS/TU medical programs strengthens capacities. Gender-equitable training targets women smallholders, while Codex-aligned food safety modules focus on wet markets. This tackles rural-urban disequilibria via urban-rural twinning and donor-leveraged scholarships.

Engaging at community levels

Bottom-up resilience is driven by behavior change: targeted IEC campaigns help ethnic smallholders understand zoonoses, and embed One Health in Farmers' Field Schools; political advocacy raises budget lines; evidence-based storytelling to counter misinformation/disinformation.

There are five strategic pillars that enable the implementation of the One Health Strategy in Nepal: coordination; surveillance/labs (human-animal); capacity building; preparedness; and communication. These pillars act as a matrix that works across sectors to produce outputs with measurable impact, including 45% of key performance indicators achieved by 2023 as shown in the MoHP/MoALD joint audits. The coordination pillar is represented by high-level steering committees made up of federal ministers and technical working groups to provide policy coherence across the ministries of health, agriculture, and forest, with cascades through provincial and municipal levels through bylaws that allow for local control of the planning process while respecting Nepal's 2015 constitutional devolution (Article 57). The surveillance and laboratory pillar operationalizes the data fusion of animal and human health platforms with networked diagnostics at national laboratories to provide risk stratification and support for priority pathogens. The capacity pillar brings targeted upskilling, epidemiology trainings, genomic sequencing modules, and food safety curricula, with multisectoral human resource development as a priority and gender-sensitive approaches to address time gaps. The preparedness pillar is represented with simulation drills and prepositioning of resources. The communication pillar is represented by community health networks that mobilize advocacy to instigate behavioral change and the adoption of biosecurity practices. Finally, the federal adaptability of the Strategy, through provincial customization, makes Nepal a South Asian exemplar of localized One Health praxis in the face of resource constraints. Yet, this potential hinges on legal enshrinement via a dedicated One Health Act to impose binding inter-ministerial

Theme 2

obligations, alongside fiscal ringfencing (e.g., 2% ringfenced allocations from health/agriculture budgets) and digital interoperability mandates to surmount enduring silos, data asymmetries, and donor dependency, thereby transforming aspirational architecture into resilient, equity-infused public health infrastructure aligned with SDGs 3, 13, and 15 (United Nations, 2015).

Priority Areas and Risks Addressed

One Health Strategy 2076 (2019) delineates priority areas centered on new, re-emerging, zoonotic, and novel diseases, operationalizing multisectoral efforts that span wildlife conservation, food safety, and environmental management to preempt shared health threats at human-animal-ecosystem interfaces. The Strategy's multisectoral lens integrates these risks through delineated action domains: zoonotic disease prioritization mandates joint surveillance for 12 high-burden pathogens, leveraging wildlife interfaces in 20+ protected areas; food safety aligns with Codex Alimentarius via multisectoral inspections of informal markets; AMR stewardship promotes antibiotic formularies and resistance mapping across veterinary/public health labs; and environmental health incorporates climate risk modeling for vector-borne escalations, linking to National Adaptation Plans.

Strategic alignment with international norms amplifies efficacy: full concordance with International Health Regulations (IHR 2005) core capacities ensures 24/7 event reporting via unified platforms, while Joint External Evaluations (JEE) benchmarking elevated from 40% in 2017 to projected 60% by 2026 bolsters national committees' roles in prevention, detection, and response (World Health Organization, 2022). National One Health committees operationalize JEE indicators (e.g., zoonotic surveillance scoring), fostering real-time data fusion from EWARS (human events) and AHMIS (animal health), with wildlife inputs from Department of National Parks (Ministry of Health and Population, 2023).

This framework not only mitigates immediate burdens—estimated at NPR 5 billion annually in rabies/AMR costs—but preempts pandemics, as COVID-19's wet-market echoes underscored, positioning Nepal's federalized approach as a scalable model for LMICs navigating biodiversity-agriculture-health nexuses.

Implementation Progress (2019–2026)

Nepal's One Health Strategy 2019 AD has laid a foundational multisectoral framework for addressing interconnected zoonotic, AMR, and environmental health threats, yet its implementation reflects a mix of progress and persistent structural challenges. It established key governance mechanisms, including federal steering and technical committees involving the Ministry of Health and Population (MoHP), Ministry of Agriculture and Livestock Development (MoALD), and Ministry of Forests and Environment (MoFE). At the provincial level, advancements in federal health transition such as health policies enacted in Gandaki and Lumbini provinces have supported broader domestication efforts, but dedicated provincial One Health bylaws remain limited, with most activities guided by federal directives rather than distinct subnational legislation. Official capacity building continues under entities like the Epidemiology and Disease Control Division (EDCD) and Central Veterinary Laboratory (CVL), rather than a centralized "Nepal One Health Institute."

Surveillance enhancements show incremental gains, with the 2025 National SOP for the Early Warning and Reporting System (EWARS) prioritizing interoperability and digital integration. However, full real-time interfacing with the Animal Health Management Information System (AHMIS) for zoonotic alerts is still in pilot or testing phase. Performance metrics indicate moderate attainment; mid-term reviews of the Nepal Health Sector Strategic Plan (NHSSP 2023–2030) suggest alignment with around 55% indicator progress in related areas, while the 2022 Joint External Evaluation (JEE) highlighted lower scores (typically 20–40% in response and workforce categories). The Universal Health Coverage (UHC) service coverage index stood at approximately 58 in 2023, progressing toward SDG targets of 65+ by 2030, though the pace remains gradual amid systemic constraints.

Disease-specific efforts underscore both achievements and gaps. Rabies control mass dog vaccination have advanced community awareness and response, yet national incidence reductions are not yet substantiated by surveillance data, complicated by vaccine supply issues and fluctuating cases. AMR containment benefits from Fleming Fund-supported surveillance in poultry and livestock, with protocols for active monitoring in broilers and other populations, alongside training for farmers and veterinarians on biosecurity and rational use.

CONCLUSION

Nepal's One Health Strategy 2076 (2019 AD) marks a pivotal shift toward institutionalizing multisectoral governance for zoonotic diseases, antimicrobial resistance (AMR), food safety, and climate-sensitive health risks within a federal system. Early implementation demonstrates the feasibility of coordinated action in resource-

Theme 2

constrained settings, reflected in the establishment of federal steering and technical committees. To translate policy intent into durable practice, Nepal should prioritize four enabling reforms: (i) enactment of a dedicated One Health Act to clarify mandates, accountability, and inter-ministerial obligations; (ii) predictable, ring-fenced financing across health, agriculture, and environment budgets; (iii) interoperable digital platforms linking human, animal, and wildlife surveillance in real time; and (iv) sustained investment in subnational laboratories, workforce development, and community-based surveillance.

Keywords: One health, Zoonoses, Policy, Nepal.

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Case story presentations

An Exploratory Assessment of Targeted Surveillance for Bovine Spongiform Encephalopathy in Great Britain

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Context

Overview of Bovine Spongiform Encephalopathy Surveillance

Transmissible Spongiform Encephalopathies (TSEs) are a group of neurodegenerative zoonotic diseases. Bovine Spongiform Encephalopathy (BSE) affects bovines and is categorised into two distinct forms: Atypical (H-BSE or L-BSE) which is sporadically occurring, and Classical (cBSE) which is a food-borne prion disease transmissible by the prion protein (1). The first confirmed case of cBSE in Great Britain (GB) was identified in 1986, and the first case epidemiologically linked to contaminated feed was confirmed in 1988. This marked the beginning of the BSE epidemic in cattle and had substantial social, economic and biosecurity impacts within the GB cattle industry. BSE posed a significant global risk for countries that had imported cattle and cattle products from GB, due to the long incubation period of BSE. In response to the outbreak, strict regulations were implemented. The 'Ruminant Feed Ban' was introduced in July 1988, followed by the 'Reinforced Feed Ban' in August 1996, which banned all use of mammalian protein in animal feed. Cattle born after the reinforced feed ban (BARB) became essential for surveillance by providing evidence on the effectiveness of regulations.

Development of GB BSE Surveillance

Regulations introduced to comply with EU Laws (EC999/2001) (now UK regulations) served as the foundation of the BSE Surveillance System in GB. Surveillance aimed to identify and remove BSE-infected cattle, to prevent infected tissues from entering the food chain and to rebuild global confidence in GB beef trade. The Department

Theme 2

of Environment, Food and Rural Affairs (DEFRA) and the Animal and Plant Health Agency (APHA), implemented surveillance and restrictions in GB which operated through two streams of statutory surveillance:

- Passive – introduced in 1986; requires any cattle displaying clinical signs suspicious of BSE to be reported by stakeholders to APHA for investigation.
- Active – introduced in 2001; current testing requires all eligible fallen stock cattle over 48 months that were born in UK and EU (except for Bulgaria and Romania); and cattle over 24 months born in Bulgaria, Romania, and non-EU states. All cattle from abattoirs over 48 months that are subject to emergency slaughter or sick at ante-mortem must be tested. Fallen stock cattle are reported by keepers to sampling sites, who are responsible for organising the collection, sampling and disposal of the carcase. Brainstem samples are submitted for BSE testing at designated testing laboratories using IDEXX HerdChek BSE-Scrapie. Key information is captured by sampling sites on submission forms, either by hand or populated using specialist software, including farm details, animal information (eartag, cable tie reference, date of birth, date of death, reason for death and clinical signs observed) and sample details. An annual average of 103,284 cattle were tested through Active Surveillance (2020-2025) (2).

Since the introduction of regulations, the incidence of BSE has significantly reduced in GB, from a peak of over 36,000 cases in 1992 to just over 1,000 cases in 2002, decreasing to only single sporadic cases of cBSE in 2018, 2021 and 2024. A total of 181,142 BSE cases have been confirmed, of which 179,183 were detected through Passive Surveillance and 1,959 through Active Surveillance. Following the Reinforced Feed Ban, only 179 cBSE and 10 Atypical BSE BARB cases were detected demonstrating the effectiveness of control measures (2).

Alignment with World Organisation of Animal Health Standards

Since joining the Office International des Epizooties (OIE) in 1924, now known as the World Organisation for Animal Health (WOAH), GB have striven to align surveillance practices with regular recommendations provided by WOAH. The GB BSE surveillance programme has promoted ongoing awareness and training programmes to stakeholders to ensure long-term statutory compliance and collaboration. Stakeholders include those involved in the management, rearing and production of cattle including: breeders, owners and keepers, veterinarians, transporters, slaughterhouses, abattoirs, disposal sites, software providers, unions and clubs. The robust surveillance system enabled GB to achieve WOAH BSE-Risk status of Negligible in 2025. This was awarded following consideration of eight years of surveillance data that highlighted GB had met strict criteria, including effective feed controls, suitable surveillance provisions, full investigation of BARB BSE positive cases, and comprehensive risk assessment (3).

In 2023, WOAH published new recommendations for BSE surveillance under Article 11.4.20 (3). Recommendations encourage a shift from high-volume, prescriptive testing (GB's current Active Surveillance strategy) towards a more flexible, risk-based approach. This aims to target animals that are epidemiologically justified, that are more likely to be infected. This is based on presence of known clinical signs associated with BSE which include: aggression or apprehension; hyperaesthesia (increased sensitivity to touch, light or sound); and ataxia (changes in posture and movement) (4). WOAH have classified four targeted groups:

A. Bovines displaying progressive BSE-like clinical signs.
B. Bovines displaying neurological or behavioural signs at slaughterhouses or abattoirs.
C. Bovines unable to rise or walk without assistance with appropriate clinical history that rules out other causes of recumbency.
D. Bovines found dead with appropriate clinical history that rules out other common causes of death.

Existing Surveillance

Cattle in Group A are currently captured through BSE Passive Surveillance in GB, which provides a rich clinical history through investigation of the animal and associated holdings (both natal and rearing). Therefore, continued engagement with stakeholders to promote awareness of BSE-like signs is essential to ensure all suspect cases are reported.

Cattle in Group B are captured through BSE Active Surveillance in GB slaughterhouses and abattoirs during ante-mortem inspection, which would not be slaughtered for human consumption. However, no data are currently collected on clinical signs in existing data capture methods.

Cattle in Groups C and D are partly captured in the current BSE Active Surveillance programme in GB as submissions to veterinary investigation centres and postmortem providers, however this was not originally consolidated for reporting purposes. For all fallen stock submissions, limited data are collected on clinical history, which limits the ability to distinguish between BSE-like reasons for death and other reasons for death.

Theme 2

Therefore, this case study explores the required work to address the gap of clinical history for fallen stock cattle. This will be necessary if GB adopt the move towards risk-based surveillance, to meet the new WOAH recommendations.

Feasibility Work and Outcomes for New WOAH Recommendations

Cattle Fallen Stock Postmortem Data

Keepers organise postmortem examinations of fallen stock cattle, which is shared to provide clinically validated data including observed signs and final diagnosis. It was identified these data could be used to address Groups C or D of the above WOAH reporting requirements. Analysis initially extracted data from the TSE Surveillance System database (TSESS) to identify eligible animals tested, which was cross-referenced against laboratory systems to identify relevant submissions containing postmortem information. Data were cleaned, consolidated and categorised into Group C or D (of the WOAH reporting groups above) if relevant clinical history was provided, using PowerBI and SQL. Missing data points were identified, such as corresponding references across both systems, however this was resolved and clarified with the postmortem facilities, and the importance of inclusion was conveyed.

This new data processing and reporting approach successfully utilised existing data capture infrastructure, enabling the routine inclusion of clinical signs data from postmortem submissions in the annual reporting to WOAH.

Cattle Fallen Stock BSE Clinical Signs Data Capture

In March 2025, additional questions were introduced to the GB cattle fallen stock submission forms, to record the presence of BSE-like clinical signs. These were defined from clinical signs provided by WOAH and terminology adapted for stakeholders with a non-veterinary background, including: Changes in behaviour (Apprehension); sensitive to touch and sound (Hyperaesthesia); uncoordinated (Ataxia); and other neurological signs (4). As these are reported by the keeper and recorded by the sampling sites, a tick-box option (Yes, No or Not Known) was implemented for consistency and accuracy. This aligned with the WOAH recommendation to provide clinical history for fallen stock and offers a possibility to use new fields to introduce targeted surveillance of high-risk groups.

From July 2025, the new cattle fallen stock submission form containing BSE clinical signs data capture was circulated for mandatory completion amongst stakeholders. Where no information was provided on the submission forms, clinical signs were completed as 'Not Known' during data entry by the testing laboratory. During uptake and compliance monitoring, a high return of 'Not Known' responses were identified (94%) due to behavioural and operational barriers. These included the absence of keepers during the carcass collection processes, non-statutory requirement to provide additional information, uncertainty of responsibility to provide data (keeper or sampling sites) and the default completion of unanswered clinical sign fields as 'Not Known'. To address this, the ownership and importance of completing the new clinical history fields was communicated to stakeholders by engaging through articles, conferences, training and meetings. Communications highlighted incentives for keepers to participate regarding improvement for GB trade and animal health reporting. Further work is being actioned by the testing laboratory to no longer record missing data as 'Not Known', to better identify sites where forms are not being completed.

This engagement resulted in a three-fold increase in response rates providing a definitive 'Yes' or 'No' response, opposed to 'Not Known', increasing from 6% in July 2025 to 19% in December 2025. This indicates that sampling sites are increasingly asking keepers about the presence of clinical signs. Overall, the BSE clinical signs data provided were useful to support the WOAH annual reporting requirements and exploratory work into risk-based surveillance. However, continued collaboration is required to improve data quality and completion rates.

Cattle Fallen Stock Reason for Death Encoding

Currently, the reason for death of fallen stock cattle is captured on the cattle submission forms as a free-text field, which often provides clinical signs observed at the time of death. These data are provided by the keeper and captured during notification and collection of the carcasses by sampling sites. To further support WOAH reporting of clinical signs, historical reason for death data were extracted from TSESS from a total of 893,362 cattle fallen stock between 2016 and 2023. Following data cleaning, text mining and manual coding in RStudio Software, 156 broad groups of reasons for death were initially identified. These groups were combined into 11 categories based on: the clinical syndrome, the body system affected, or the aetiology (Table 1). Categories that

Theme 2

included BSE-like clinical signs, and categories that included syndromes with non-specific signs that could be associated with BSE, were identified.

To determine whether the 11 newly defined reason for death categories distinguish between BSE-like syndromes and non-BSE-like syndromes, data on the reason for death of 56 cBSE and Atypical BARB BSE cases, diagnosed between 2000 and 2023, were extracted from TSESS. It identified that over 70% of BSE cases would have been categorised as Recumbent/downer cow, Other, or Unknown. Based on this analysis, further categories may be required to distinguish frequently reported reasons for death in 'Other'.

Reason for Death analysis was successful in identifying and defining 11 categories, with classification into BSE-like clinical signs. The reduction of categories from 156 broad groups was essential to integrate data capture fields with current cattle fallen stock forms, for potential future use in targeted surveillance. Further R scripts are being developed to classify real-time submission data into the new categories to support preparation of annual reports to WOAH for Groups C and D. This will enable additional data to be reported to align with WOAH recommendations, prior to surveillance strategy amendments. The outcome of this work highlighted the importance of having a high-quality dataset to conduct retrospective analysis, to successfully provide evidence for potential future practices.

Relevance and Recommendations for Wider Groups

Acknowledgement of the amendment to WOAH recommendations and response strategies are key for countries working towards negligible risk status. By aligning BSE surveillance with WOAH, the global approach ensures collective research and control measures for animal diseases. The benefits of negligible risk status include financial incentives such as expanded geographical trade opportunities, reduction of operational processes for stakeholders, and enhanced global confidence in biosecurity. Adherence to WOAH guidelines has enabled 53 countries to achieve BSE Negligible Risk Status (5), demonstrating robust surveillance systems can be implemented on varying scales, dependent on bovine populations, disease threat or economy, to aid animal health surveillance.

Existing GB surveillance data used for exploratory analyses assessed and evidenced the potential impact of changes required to align with WOAH recommendations. Whilst this work is preliminary, early engagement has been key to ensure surveillance infrastructure is suitable and stakeholders are consulted to identify and address potential barriers. Strong engagement with stakeholders is recommended through a range of methods, including meetings and phone calls, articles promoting awareness and guidance documentation. Engagement has promoted trust, credibility and highlights a shared commitment with the cattle industry to maintain GB's negligible risk status.

Future Work

Further work is continuing to refine the reason for death categories required based on analysis outputs. In addition, work to quantify the total cattle fallen stock records to the categories using RStudio software is underway, to rapidly analyse live data and support discussions regarding risk-targeting surveillance. Prior to the public implementation of the categorisation framework, a limited number of sampling sites will be involved in a pilot study to assess operational feasibility, ensure categories are intuitive and consistently applied, and identify any practical issues prior to wider implementation.

During discussions with stakeholders, a move towards paperless systems was identified, therefore digital data solutions are being developed aiming to reduce administrative burden, improve accuracy and increase timeliness of reporting. Initial consultations with private livestock software providers have identified requirements, timelines and suitable approaches to ensure all changes are successfully implemented. Potential impacts on stakeholders and management strategies will need to be discussed ahead of implementation.

This exploratory work has successfully outlined current projects underway to align with WOAH recommendations, including the collation and reporting of postmortem data, and addition of clinical signs questions to submission forms. Further engagement with stakeholders is required to promote awareness of the clinical presentation of BSE-like clinical signs, to ensure stakeholders can accurately and consistently identify and report BSE suspects. Analytical work to identify potential changes to shift towards a risk-based surveillance system include categorisation of reason for death, with the aim to encode categories to ensure accurate and efficient data capture. However, prior to amendment of surveillance, European Food Safety Authority (EFSA) work will be reviewed, and risk assessments conducted to assess potential implications of proposed changes to ensure animal health security for GB and their trading partners. All suggestions will be evidenced and shared

Theme 2

with DEFRA, to factually support any proposed changes. If changes are implemented, continued stakeholder engagement with enable the promotion of new processes, and annual monitoring will be instated to ensure GB's surveillance system remains robust.

To conclude, Active Surveillance, rather than targeted surveillance, will continue until GB are confident with proposed approaches to risk-based surveillance. Early findings indicate the importance of a robust surveillance system to analyse and provide strong evidence for proposed changes to surveillance strategies. Collaboration and early communication with stakeholders will be essential to ensure data-driven evidence is complemented by industry insights, to support the continued success of BSE surveillance within GB.

Code	Code Name	Likely to include cattle with BSE-like clinical signs
1	Neurological and behavioural Disorders	Yes
2	Gastrointestinal & Poisoning	No
3	Respiratory and cardiovascular disorders	No
4	Recumbent/ Downer cow	Yes
5	Reproductive system issues	No
6	Milk Fever/ nutritional metabolic disorders	Yes
7	Found dead/ sudden death	No
8	Generalised infectious diseases	No
9	**Other,** including euthanasia, old age, accident, trauma, Musculoskeletal issues	No
10	APHA Bovine Tuberculosis reactor/ welfare	No
11	Unknown	Yes

Table 1. Proposed categories for reasons for death.

Keywords: Bovine Spongiform Encephalopathy (BSE), World Organisation of Animal Health (WOAH), Targeted Surveillance, Risk-based Surveillance.

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Theme 2

Short oral presentations

Leveraging surveillance data to map sources and spread of *Salmonella Enteritidis* in four European countries

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The trend for *Salmonella* infections in the EU has been increasing since 2020. The most common serovar causing human infections is *Salmonella Enteritidis* (*S. Enteritidis*), which accounted for over 50% of recorded infections in 2024, according to the European Union One Health 2024 Zoonoses Report. The primary source of these infections is poultry. The focus of this project is therefore bacterial isolates from this sector. Multi-country outbreaks of *S. Enteritidis* ST11 occur frequently and it is difficult to resolve these outbreaks because the genetic variation detected using cgMLST is low. This project aims to improve the available methods by enhancing genomic resolution and advancing source tracing. The goal is to better understand the spread of *S. Enteritidis* throughout the EU and identify opportunities for intervention. This will be achieved using existing data from the surveillance systems in both food, animal, and human sector in Belgium, Denmark, Sweden, and the Netherlands. These surveillance data have been supplemented with additional sequences from the last 10 years, accompanied by epidemiological information linking them to the poultry industry. A preliminary SNP analysis has already been conducted. This confirmed that strains found across Europe are highly similar, with phylogenetic clusters containing isolates from different countries as well as spanning multiple years. Further analysis will investigate the presence of plasmids, resistance and virulence genes of interest to determine whether these provide additional discriminatory power. In addition, novel bioinformatics approaches, such as analysis of the flanking regions of genes of interest, will be performed. We expect these methods to improve our understanding of evolutionary mechanisms and help identify transmission routes. Ultimately, we aim to perform phylodynamic analysis to trace the spread of *S. Enteritidis* in the region over the past 10 years, reconstructing transmission pathways and identifying potential introduction events. We hope that our findings will contribute to the development of effective intervention strategies and support the resolution of international foodborne outbreaks.

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Poster presentations

Mekong One Health Innovation Program (MOHIP): Connecting North and South to Improve Health Security through One Health Approach

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The Mekong region faces many interconnected health challenges such as climate change and extreme weather, vector-borne and communicable diseases, food, water, and environmental pollution, emerging and zoonotic diseases, pandemic preparedness and cross-border health threats, health system resiliency and equity. These challenges are exacerbated by rapid urbanization, expanding human-wildlife interactions, and the need for integrated health policies. Funded by the US Department of State and administered by Michigan State University (MSU), the Mekong One Health Innovation Program (MOHIP) sought to strengthen regional health security through collaboration by experts across North and South and help prevent, detect, and respond to complex health challenges at the human-animal-environment interface. Through a collaborative network of universities, MOHIP sought to inform and educate people on One Health approach; facilitate interdisciplinary research employing OH approach; generate evidence for policy and practice; and expand collaboration and networking through webinars and symposia. The program empowered over 200 professionals and students through a

Theme 2

course on One Health and over 1,123 people through OH-focused webinars (MSU GHI, 2026, 2026b; Mekong-U.S. Partnership, n.d.).

In research, six collaborative research initiatives were undertaken across Thailand, Vietnam, and Lao PDR.

Thailand

i) The border area zoonotic exposure study mapped infectious risks among stateless border populations, revealing that pig and chicken management is deeply intertwined with cultural practices (Yeemard et al., 2026). The findings led to a cross-border educational exchange, training medical students and faculty from the US. It recommends that robust cross-border animal surveillance is crucial to prevent global spillovers of zoonotic pathogens.
ii) The *Streptococcus suis* prevalence study examined the transmission pathways of *S. suis* between swine, humans, and environments.

Vietnam

iii) The Mekong basin antibiotic and resistome surveillance project tracked antibiotic contamination, coliform bacteria, and the environmental resistome across Thailand and Vietnam.
iv) The microplastic-mediated AMR initiative examined the synergistic link between microplastic pollution and accelerated antimicrobial resistance in aquatic environments. The resulting models inform policymakers regarding national antibiotic-resistant bacteria action plans and bolster scientific methodologies for managing domestic aquatic ecosystems.

Lao PDR

v) The project on Brucellosis surveillance in Vientiane established a baseline epidemiology data on Brucellosis, a zoonoses affecting livestock and humans. By building interagency response systems, it reduces spillover risks, enhances livestock trade safety, and elevates health security.
vi) The *Schistosoma mekongi* study in Khong district mapped the prevalence and local perceptions of *S. mekongi*. It provides veterinarians and public health professionals with critical data to control *S. mekongi* and protecting people traveling to endemic areas.

These multi-sectoral research projects provide important operational baseline for managing cross-border biosecurity threats. Collectively these research, education and outreach projects focused on mitigating critical regional threats by tracking the interconnectedness of human, animal, and environmental health. The MOHIP's accomplishments provide a sustainable foundation for continued regional collaboration and offer a model for advancing One Health capacity, innovation, and resilience beyond Lower Mekong.

Keywords: One Health, health security, multisectoral collaboration, cross border surveillance, Lower Mekong.

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Theme 3

Theme 3: Evaluation and impact assessment of surveillance systems

Oral presentations

Attributes and frameworks for surveillance evaluation in veterinary public health: a scoping review

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Summary

Evaluating disease surveillance is essential to ensure that systems generate valuable information efficiently. This scoping review provides a global overview of the attributes and frameworks used to assess veterinary public health surveillance systems over the past 15 years. A literature search conducted on PubMed and Scopus (2010–2025) identified 125 eligible studies. The surveillance systems were implemented worldwide, reflecting region-specific priorities in species and diseases under surveillance. We identified and analysed 67 evaluation attributes covering both commonly used and underutilized measures of system performance. Eighteen evaluation frameworks were documented; however, their applications remain limited, particularly in the animal health domain. Surveillance evaluation emerges as a globally relevant topic across human, animal, and One Health (OH) domains. These findings offer practical guidance for selecting attributes and designing future assessments.

Introduction

In veterinary public health, surveillance is defined as the systematic, continuous or repeated, measurement, collection, collation, analysis, interpretation, and timely dissemination of animal health data from defined populations (1). Regular evaluation ensures surveillance systems remain effective and informative for decision-making (2). Surveillance evaluation attributes were reviewed in 2009 during a workshop at the International Symposium on Veterinary Epidemiology and Economics (3) and further discussed with key experts at the 2011 ICAHS workshop (1). Subsequent reviews in 2012 and 2015 examined evaluation attributes, methods, frameworks (2), and approaches (4), providing recommendations that guided the development of new evaluation frameworks. To our knowledge, since 2015 there have been no further attempts to comprehensively describe surveillance evaluation attributes and methodological frameworks in place to assess surveillance in veterinary public health at a global level. This review aims to address this gap by examining evaluations conducted over the past 15 years, focusing on attributes and frameworks while investigating their application in real-world settings.

Methods

This study aims to identify the attributes and evaluation frameworks used to assess the performance of surveillance systems targeting animal infectious diseases and zoonotic diseases. This review followed the methodological guidance for scoping reviews developed by the Joanna Briggs Institute and the PRISMA extension for Scoping Reviews. PubMed and Scopus were searched using strategies adapted from Drewe et al. (2) and Graziosi et al. (5), limited to English-language publications from 2010 to 2025. Studies were considered eligible if they evaluated surveillance system performance using defined evaluation attributes or presented a framework incorporating such attributes. Evaluations focusing on animal infectious diseases or zoonoses were included. Systems related to aquaculture, entomological surveillance without animal/human involvement, environmental pathogen circulation, or antimicrobial resistance were excluded. Eligibility was determined through abstract screening and full-text reading. If a study evaluated multiple systems, data were collected separately for each system.

Theme 3

Results

Literature search

A total of 554 records were retrieved from PubMed and Scopus. After duplicate removal, 452 abstracts were screened, 118 full texts assessed, and 69 studies deemed eligible. Manual reference screening added 56 publications, resulting in the inclusion of 125 papers: 116 reporting evaluations of 157 surveillance systems, and nine describing evaluation frameworks.

Characteristics of the included surveillance systems

The identified surveillance systems were implemented across Europe (40.8%), Africa (19.1%), North America (15.3%), Asia (14%), Oceania (3.8%) and South America (2.5%). A small proportion spanned multiple continents (1.3%) or represented simulation studies without a defined location (3.2%). The number of surveillance evaluations published annually ranged from 4 to 23 (mean 10.4), with fluctuating trends until 2021, followed by a decline. Approximately one-third of surveillance systems targeted humans (34.4%), and 12.1% targeted both humans and animals. Among systems focusing on animals, 7.6% targeted multiple animal species, while cattle and poultry were the most frequent individual targets. Articles on human health surveillance mostly focused on Africa, Asia, and North America, whereas veterinary public health systems were mainly reported in Europe. The most common scenario involved surveillance systems targeting multiple diseases. The individual diseases most frequently reported included avian influenza, bovine tuberculosis, rabies, zoonotic influenza and African swine fever, among others.

Attributes and methods applied to evaluate surveillance systems

A total of 67 evaluation attributes were identified and grouped into five classes: organization, implementation, performance, impact, and OH approach. The number of attributes assessed per evaluation ranged from one to 24: 30.6% used one attribute, 21.7% used two, 19.7% used three to five, 24.2% used six to 10, and 3.8% used more than 10. Sensitivity and timeliness were the most frequently assessed attributes.

Sensitivity (52.2% of the evaluations) was predominantly applied in the evaluation of animal health surveillance and across various contexts, including operational surveillance systems, systems developed and tested through simulation modelling, and epidemic intelligence frameworks. It was used to assess early detection capability, to demonstrate freedom from infection and to evaluate cost-effectiveness, combined with cost. Timeliness (47.1%) measured time to detect outbreaks or cases, the ability to identify health events within preset time limits, delays from detection to notification, delays from detection to specimen submission, or on time receipt of reports. Its use was more common in human health surveillance. Other commonly used attributes include simplicity, usefulness, flexibility, acceptability, representativeness, data quality, cost and completeness. Cost (19.1%) was mainly assessed in animal or combined animal-human surveillance, typically estimating direct and indirect expenses. Cost-effectiveness analyses occurred only in animal health.

A wide range of methods were used to assess the attributes. Qualitative approaches, including key informant interviews and participatory methods primarily assessed implementation attributes. Quantitative methods, incorporating a range of mathematical and economic models, were employed to assess mainly performance and impact attributes.

Frameworks for surveillance evaluation

In total, 60 (38.2%) evaluations used frameworks specifically designed for surveillance evaluation. The most frequently applied framework was the “CDC's Updated Guidelines for Evaluating Public health Surveillance Systems” (2001), primarily used in human health surveillance, particularly in Africa and Asia. Other CDC frameworks included the 1998 guidelines and the “Framework for Evaluating Public Health Surveillance System for Early Detection of Outbreaks”, which complements the Updated Guidelines by emphasizing early detection. The WHO “Early Warning Alert and Response Network in Emergencies (EWARN) evaluation protocol”, based on CDC's guidelines, was used to assess EWARN systems in Africa and Asia, designed for emergencies. Similarly, the WHO “Guidelines for Evaluating a National Surveillance System” and the “National Technical Guidelines for Integrated Disease Surveillance and Response (IDSR)” were applied alongside CDC guidelines to assess IDSR systems and surveillance in refugee settlements. The “Communicable disease surveillance and response systems – Guide to monitoring and evaluating”, was used to assess a pilot surveillance app in Africa. These public health surveillance evaluation frameworks provide structured guidance and share common components, including defining the health event and evaluation scope, describing the system and objectives, assessing performance attributes, engaging stakeholders, and summarizing findings with recommendations.

Theme 3

Seven studies employed frameworks specifically developed for animal and veterinary public health surveillance, with OASIS being the most common. Other frameworks included the RISKSUR EVA tool, SERVAL, and Grosbois et al.'s rationale (6). Additional frameworks targeted specific contexts, such as syndromic surveillance systems (7) and hazard-specific livestock surveillance (8). Four studies applied OH oriented frameworks, primarily the "Network for the Evaluation of One Health (NEOH)". Rivers et al. (9) proposed a model for output-based surveillance of zoonotic threats, while Babo Martins et al. (10) developed a conceptual framework to quantify the economic value of OH integration. Among non-empirical studies, additional frameworks were identified, including SurF, supporting biosecurity and animal health surveillance evaluations, and OH-EpiCap, assessing OH surveillance capacity.

Discussion

This review provides a comprehensive overview of attributes and frameworks applied to surveillance systems evaluations between 2010-2025, highlighting how performance is assessed and where methodological gaps remain. Surveillance evaluations were unevenly distributed across regions and domains, reflecting differences in surveillance objectives and socio-economic contexts. Many systems targeted multiple diseases or syndromes, consistent with integrated surveillance approaches, while others primarily focused on zoonoses due to their regulatory and public health relevance.

Sensitivity and timeliness were the most frequently assessed attributes, consistent with previous findings (2), confirming their central role in determining surveillance capacity to detect health events and respond promptly. Sensitivity was more commonly evaluated in veterinary public health, where surveillance often supports regulatory objectives such as disease freedom. In contrast, human health surveillance placed greater emphasis on timeliness, simplicity and usefulness, reflecting operational priorities. Economic attributes were rarely assessed, despite their importance, particularly in animal health decision-making. Sociological attributes, especially acceptability, are key to system performance (4) but were also inconsistently evaluated, suggesting that stakeholders' perspectives are not yet systematically included in evaluations.

A wide range of qualitative and quantitative methods were observed. Observed patterns were largely consistent with the nature of the attributes. Combining qualitative and quantitative approaches remains relatively uncommon but offers added value by allowing comparison between perceived and measured system performance.

Evaluation frameworks ranged from general-purpose tools to specialised approaches. The CDC's Updated Guidelines remained the most widely applied, particularly in public health, highlighting their continued influence. Frameworks developed within the veterinary domain, though flexible across species and diseases, were applied less consistently, possibly due to lower awareness, perceived complexity, or insufficient training and dissemination rather than lack of relevance. The most common attributes in evaluation frameworks mirrored those used in studies, suggesting a shared core set (i.e. sensitivity, timeliness, simplicity, flexibility, representativeness, acceptability, and data quality) widely relevant across surveillance contexts. Differences across frameworks mainly concerned how evaluation components were defined and grouped, particularly data-related elements. Several attributes, such as risk-based criteria definition, training and communication were rarely applied. This likely reflects feasibility constraints rather than limited relevance. While some attributes, such as communication, may be broadly applicable (as in SERVAL, which treats communication as a primary attribute across all surveillance objectives), others are more contexts-dependent and should be selected according to evaluation objectives and decision-making needs.

Overall, these findings confirm that surveillance evaluation is globally relevant and highlight opportunities to broaden attribute selection and strengthen methodological integration.

Keywords: Surveillance systems, Surveillance evaluation, Evaluation attributes, Surveillance evaluation frameworks.

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Epidemiology and Surveillance of Rabies in Animals in Sa Kaeo Province, Thailand, 2016–2025

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Summary

Rabies remains an important zoonotic disease and public health concern in Thailand, particularly in areas with persistent animal reservoirs and cross-border movement [1–3]. This study aimed to describe the epidemiological characteristics of rabies in animals and evaluate the performance of the surveillance system in Sa Kaeo Province during 2016–2025. A cross-sectional analysis of 757 submitted samples identified 70 positive cases (9.25%), with dogs accounting for the majority (88.57%). Samples submitted through clinical surveillance showed substantially higher positivity rates than those submitted for rabies-free area certification. Multivariate analysis demonstrated that clinical surveillance submission (adjusted OR = 57.32; 95% CI: 23.46–173), owned animal status (adjusted OR = 6.94; 95% CI: 4.04–11.86), and residence in border districts (adjusted OR = 2.24; 95% CI: 1.06–4.81) were significantly associated with rabies detection. These findings highlight the critical role of the surveillance system in identifying cases and high-risk areas, while also reflecting the limitations of passive, symptom-based surveillance systems [4–7].

Methods

Study Design and Data Source

A cross-sectional study was conducted using data from the national rabies surveillance database (thairabies.net) between 2016 and 2025. The dataset included information on sample submissions, diagnostic results, animal species, ownership status, vaccination history, geographic location, and purpose of submission.

Rabies Surveillance System

Rabies surveillance in Sa Kaeo Province, a border province adjacent to Cambodia, is conducted under the national animal rabies surveillance program coordinated by the Department of Livestock Development (DLD), Thailand. The system primarily relies on passive, symptom-based surveillance, supplemented by targeted sample submissions for rabies-free area certification and outbreak investigations.

Suspected rabies cases are identified by field veterinarians, livestock officers, or local authorities based on clinical signs, history of animal bites, or abnormal behavior. Carcasses or brain samples from suspected animals are submitted to designated regional laboratories for diagnostic confirmation. Laboratory results are recorded in the national surveillance database.

Theme 3

Theme 3

The surveillance system includes two main categories of sample submission: (1) clinical surveillance from animals showing signs compatible with rabies, and (2) surveillance for rabies-free area certification. Epidemiological information is collected for each sample to monitor trends and identify high-risk areas.

Data Analysis

Descriptive statistics were used to summarize epidemiological characteristics. Risk factors associated with rabies detection were assessed using univariate and multivariate logistic regression analyses. Spatial distribution was analyzed using R software.

Results

Between 2016 and 2025, a total of 757 animal samples were submitted for rabies diagnosis in Sa Kaeo Province, of which 70 tested positive, resulting in an overall positivity rate of 9.25%. Among the positive samples, dogs accounted for most cases (62/70; 88.57%). By species, dogs had the highest number of submitted samples (374 samples), with a positivity rate of 16.58%. Cattle and foxes showed high positivity proportions (80% and 100%, respectively), although the number of samples in these groups was limited. No positive cases were detected among cats or other species. Regarding the purpose of sample submission, samples submitted for clinical surveillance showed a substantially higher positivity rate than those submitted for rabies-free area certification (41.14% vs. 0.83%). When classified by ownership status, owned animals had a higher positivity rate than stray or unknown-status animals (30.93% vs. 6.06%). Animals with a recorded vaccination history had a positivity rate of 18.60%, whereas those without or with unknown vaccination history had a positivity rate of 8.68%. Seasonal analysis showed similar positivity rates across summer, rainy, and winter seasons, with no substantial differences observed. However, animals in border districts had a higher positivity rate than those in non-border districts (14.33% vs. 5.78%). Temporal and spatial analyses indicated that rabies cases were detected throughout the study period, with clustering observed in certain districts, particularly along the international border. In univariate logistic regression analysis, factors significantly associated with rabies detection included clinical surveillance submission (OR = 83.03, 95% CI: 35.83–241.95), owned animal status (OR = 6.94, 95% CI: 4.04–11.86), vaccination history (OR = 2.40, 95% CI: 1.01–5.17), and residence in border districts (OR = 2.73, 95% CI: 1.65–4.59). In multivariate logistic regression analysis, three factors remained significantly associated with rabies detection: clinical surveillance submission (adjusted OR = 57.32, 95% CI: 23.46–173), owned animal status (adjusted OR = 6.94, 95% CI: 4.04–11.86), and residence in border districts (adjusted OR = 2.24, 95% CI: 1.06–4.81).

Discussion

The continuous detection of rabies cases throughout the study period indicates ongoing virus circulation in the animal population, consistent with global and regional reports that dog-mediated rabies remains endemic in many parts of Asia [1–3]. Dogs were the primary reservoir in this study, in line with established epidemiological evidence identifying domestic dogs as the main source of transmission to humans and other animals in endemic regions [2,3]. Clinical surveillance submissions showed markedly higher positivity rates than samples submitted for rabies-free area certification. This finding reflects the characteristics of passive, symptom-based surveillance systems, which primarily capture animals showing clinical signs or involved in exposure incidents. Such systems are known to have high sensitivity for detecting suspected cases but may not represent the true disease prevalence in the population [4]. The higher detection rate among owned animals should be interpreted with caution, as it likely reflects surveillance bias rather than a true increase in infection risk. Owned animals are more likely to be observed and submitted for laboratory testing when abnormal behaviour occurs, whereas infected stray animals may die unnoticed outside the surveillance system. Similar limitations of passive rabies surveillance have been reported in previous studies and international guidelines [4,5]. Animals residing in border districts showed significantly higher detection rates, highlighting the epidemiological importance of transboundary areas. Border regions often experience frequent movement of animals across administrative or national boundaries, increasing the risk of disease introduction and spread [6,7]. These findings support the need to strengthen surveillance and vaccination programs in border areas as part of integrated One Health strategies [5,7]. Overall, the findings demonstrate both the strengths and limitations of the current surveillance system. Passive surveillance is effective for detecting clinically suspected cases and guiding immediate control measures, but it is prone to selection and detection biases and may not accurately reflect the true epidemiological situation [4]. Strengthening active surveillance, particularly among stray and wildlife populations and in border districts, would improve the representativeness and effectiveness of the rabies surveillance system and support national and global elimination goals [1,7].

Conclusion

Theme 3

Rabies continues to circulate in the animal population of Sa Kaeo Province. Clinical surveillance, ownership status, and border location were key factors associated with detection. Strengthening both passive and active surveillance systems, particularly in border areas, is essential for sustainable rabies control and elimination.

Keywords: Epidemiology, Rabies, Surveillance, Thailand, Transboundary.

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Case story presentations

Strengths and gaps of animal disease surveillance systems in Asia and the Pacific: lessons from the application of FAO's Surveillance Evaluation Tool (SET)

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Context

Animal diseases, including endemic, transboundary, and zoonotic animal diseases, continue to have significant impacts on livelihoods, food security, and public health across Asia and the Pacific. Their economic consequences can be substantial, affecting production systems, trade, household incomes, and public health. Effective animal disease surveillance systems are therefore a cornerstone of protecting both animal and human populations, enabling early detection, timely response, and the design of evidence-based disease control programmes.

Despite their importance, veterinary surveillance systems are often underfunded compared to public health systems. This imbalance creates persistent challenges in implementing comprehensive and sustainable surveillance activities, particularly at subnational and field levels. In this context, strengthening surveillance capacities requires not only technical solutions but also evidence-based prioritization of resources and coordinated action across multiple stakeholders.

Several evaluation frameworks are available to assess surveillance systems, each with different scopes and objectives. The World Health Organization (WHO)'s Joint External Evaluation (JEE) focuses primarily on public health capacities, with some components addressing intersectoral coordination for surveillance. The Performance of Veterinary Services (PVS) Pathway, developed by the World Organisation for Animal Health (WOAH), assesses veterinary services more broadly, including selected elements related to surveillance. Lastly, the Food and Agriculture Organization of the United Nations (FAO)'s Surveillance Evaluation Tool (SET), is specifically dedicated to animal disease surveillance systems and comprises 96 indicators covering institutional organization, laboratory capacity, surveillance activities, workforce, data management, communication, and evaluation. SET was developed based on the Outil d'Analyse des Systèmes de Surveillance (OASIS) by French Agency for Food, Environmental and Occupational Health & Safety (ANSES).

SET missions follow a structured and participatory process. The preparatory phase involves assembling an evaluation team, engaging national focal points, and reviewing relevant documentation such as surveillance plans, standard operating procedures, and regulatory frameworks. The implementation phase consists of an

Theme 3

approximately 10-day in-country mission during which a wide range of stakeholders are interviewed, including representatives from veterinary services, field officers, community animal health workers, laboratory personnel, private sector actors, and stakeholders from public and environmental health sectors. This multi-actor engagement is central to understanding the operational realities of surveillance systems. Based on interviews and document review, the evaluation team scores the system across the 96 indicators and develops tailored recommendations in close coordination with national authorities. The post-mission phase culminates in a final report shared with the Chief Veterinary Officer, and, where authorized, published for broader dissemination.

Between 2019 and 2025, SET was implemented in six countries in Asia (Indonesia, Viet Nam, Cambodia, Lao PDR, Pakistan, and the Philippines) under a variety of projects aimed at strengthening national surveillance capacities. The regional application of the tool has provided a unique opportunity to identify common strengths and gaps across diverse country contexts, while also fostering dialogue among stakeholders and partners.

Outcome / impact

The use of SET in Asia and the Pacific has highlighted both shared strengths and recurring areas for improvement across animal disease surveillance systems in the region (Figure 1). These findings provide a practical evidence base for guiding national and regional capacity-building efforts.

Common strengths identified include:

- Institutional organization: Information-sharing between sectors occurs in many countries, often through informal mechanisms, particularly when addressing One Health issues.
- Laboratory networks: Diagnostic capacities are in place for priority diseases, especially within central veterinary laboratories.
- Surveillance activities: Active surveillance programmes are conducted, notably for high-impact diseases such as highly pathogenic avian influenza (HPAI) and African swine fever (ASF).
- Surveillance workforce: Opportunities exist for field epidemiology training, including programmes such as the Fiels Epidemiology Training Programme for Veterinarians (FEPTV), the Indonesian Pelvi programme, and the Applied Veterinary Epidemiology Training (AVET).
- Data management: Electronic reporting tools have been developed and piloted in several countries across the region.
- Communications: Informal communication networks, often using messaging applications such as WhatsApp or Telegram, are widely used and effective for rapid information exchange.
- Evaluation: Multiple external evaluations (e.g. SET, PVS, JEE) have been conducted, contributing to increased awareness of system strengths and weaknesses.

At the same time, several systemic gaps were consistently identified:

- Institutional organization: Surveillance activities are frequently dependent on project-based funding, largely supported by external partners. Sustainable domestic funding streams remain limited, and resources for essential field activities (such as travel, training, and operational supplies) are often insufficient.
- Laboratory networks: Maintaining laboratory operations is challenged by constraints in reagent supply, limited implementation of quality assurance systems, and a lack of laboratory information management systems (LIMS) in many settings.
- Surveillance activities: Key elements such as clearly defined surveillance objectives, standardized case definitions, and formalized procedures (including standard operating procedures and surveillance plans) are often lacking. Risk assessments are not routinely conducted and therefore do not consistently inform surveillance design.
- Surveillance workforce: Training opportunities are not systematically structured, and there is limited formal onboarding or refresher training for personnel involved in surveillance at different levels of the system. Many training activities remain linked to external projects rather than embedded within a comprehensive national workforce development strategy.
- Data management: Regular analysis of surveillance data is limited, and results are not consistently used to inform decision-making. Feedback of epidemiological analyses to field actors is often insufficient, with analyses typically conducted on an ad hoc basis in response to specific requests or emergencies rather than as part of routine processes.
- Communications: External communication strategies targeting the public and key surveillance partners are often underdeveloped.
- Evaluation: Few systems have established key performance indicators or internal monitoring and evaluation mechanisms to support continuous self-assessment and improvement.

Theme 3

Beyond identifying strengths and gaps, SET has demonstrated tangible impacts at country level. In Indonesia, recommendations from the evaluation guided the development of coordinated zoonotic disease surveillance guidelines, the implementation of training activities at national and subnational levels, and the joint prioritization of zoonotic diseases across sectors. The integration of surveillance data was further strengthened through the use of the SIZE platform to facilitate information sharing between sectors. In Pakistan, findings from the evaluation contributed to a government commitment of approximately 4 billion Pakistani rupees to invest in strengthening the national animal disease surveillance system. More broadly, SET outputs have supported countries by providing an evidence base for designing surveillance-related projects, facilitating coordination among development partners, and informing national policies and strategies to advocate for resource allocation.

However, some limitations affect the general overview of surveillance system capacities in Asia and the Pacific. External evaluations provide only a snapshot in time and may not fully capture evolving system capacities. Differences in methodologies across evaluation frameworks can lead to variations in findings, and not all evaluation reports are publicly available, limiting the completeness of regional analyses. Additionally, the diversity of country contexts means that regional generalizations may not fully reflect specific national situations.

Relevance for others

This case highlights the value of structured surveillance evaluations as practical tools to support evidence-based decision-making and multi-actor engagement. For countries, such evaluations help identify strengths and gaps while enabling prioritization of capacity-building efforts based on concrete evidence. The participatory nature of SET, involving stakeholders from multiple sectors and administrative levels, also facilitates dialogue and shared understanding of surveillance challenges and opportunities.

For development partners and regional organizations, the aggregation of evaluation findings provides a strategic overview of common priorities, enabling better alignment of interventions with country needs and promoting more efficient use of resources. This is particularly important in contexts where multiple partners are engaged in surveillance capacity development.

Recommendations

This regional overview of gaps and strengths in Asia and the Pacific represents a first step to developing coordinated strategies to build surveillance systems capacities in the region. In order to continue to maximise the impacts of such evaluations to partner countries, several recommendations can be made:

- Continue conducting surveillance system evaluations across the region to fill existing gaps in the regional overview and strengthen the evidence base
- Ensure stronger linkage between evaluation outputs and the design and implementation of surveillance-related projects and initiatives
- Advocate for increased and sustained government investment in animal disease surveillance systems
- Promote coordinated approaches to surveillance capacity-building, enabling governments and development partners to work towards shared strategic roadmaps rather than parallel initiatives
- Strengthen linkages with existing frameworks and regional mechanisms, such as One Health platforms and regional organizations such as the Association of Southeast Asian Nations (ASEAN), to support harmonized and scalable approaches to surveillance capacity building
- Conduct comparative evaluations every 3–5 years to monitor progress at national and regional levels
- Expand the use of impact assessments to better understand and demonstrate the benefits of surveillance system evaluations

Theme 3

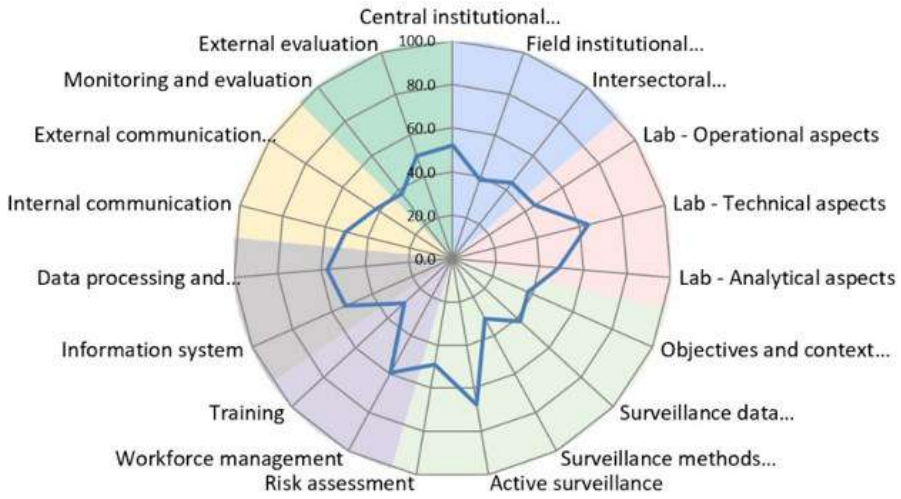


Figure 1. Comparative gaps and strengths of animal disease surveillance in Asia and the Pacific based on FAO's Surveillance Evaluation Tool (SET)

Keywords: Surveillance evaluation, Evidence-based capacity-building, Translating evidence into policy.

Short oral presentations

Evaluation of the poultry scanning surveillance system in England and Wales

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Summary:

In this study, we evaluated the poultry scanning surveillance system in England and Wales following the Surveillance Evaluation Framework (SurF) (Muellner et al. 2018). Our evaluation objectives included: i) Evaluate surveillance performance, ii) Assess the coverage and representativeness, and iii) Identify operational strengths and weaknesses. The surveillance system design presented beneficial characteristics supporting attributes like multiple utility and historical data. On the other hand, some of the main findings resulting from this evaluation included the lack of standardised surveillance objectives, the quality of data affected by data completeness, selection bias and unknown representativeness.

Introduction:

The poultry scanning surveillance system, delivered by the Animal and Plant Health Agency (APHA) in England and Wales, aims for the early detection of new and re-emerging disease threats (NRTs) in poultry species. This is a passive surveillance system which covers a wide range of non-regulated diseases. The case inclusion is voluntarily initiated by veterinary practitioners. The systematic implementation of evaluations is essential to ensure that surveillance systems remain fit for purpose (Drewe et al. 2012b; Stark and Häsler 2015; Muellner et al. 2018). To date, there has not been a comprehensive systematic evaluation of the poultry scanning surveillance system, and it is unknown to what extent the voluntary nature of submissions might impact representativeness. The APHA recognises the uncertainty in the collected animal health-related data, which includes the unknown representativeness of the target population (APHA 2025). Additionally, the voluntary participation can lead to under-reported disease levels (Geddes et al. 2021), and this can be particularly important in passive surveillance systems (Gates et al. 2021; Phiri et al. 2024). Collectively, these aspects emphasise the need to evaluate the poultry scanning surveillance system.

Materials and Methods:

Theme 3

In this study, the poultry scanning surveillance system was evaluated following the Surveillance Evaluation Framework (Muellner et al. 2018). 21 attributes were selected through expert consultation, and 14 of them were assessed through expert consultation, document review and analysis of surveillance data.

Results:

The findings resulting from this surveillance evaluation provided three main outcomes: i) Description of the system, objectives, structure, users, target population, design and processes; ii) The strengths and weaknesses of qualitative attributes; and iii) The assessment of quantitative attributes.

Discussion:

This has been the first surveillance evaluation implemented in the poultry scanning surveillance system for England and Wales. The application of this method has the potential to be systematically applied and transferable to this and similar surveillance systems. The findings could support surveillance users by identifying areas requiring improvement within the system, as well as providing support to decision makers in prioritising resource allocation. The selected evaluation framework allows evaluators to adapt the process to the available resources. However, the inherent flexibility and lack of standardisation in the evaluation design, data collection and interpretation have the potential of introducing bias in the process. To address the constraints in the evaluation process, adopting a structured, transparent and logical approach is essential to ensure credibility of the results (Drewe et al. 2012a; Muellner et al. 2018).

Keywords: Surveillance, Evaluation, Voluntary, Passive, Poultry.

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Theme 3

Optimal control for animal health surveillance and intervention strategies applied to ASF and HPAI

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Introduction

Designing effective control strategies for transboundary animal diseases requires balancing epidemiological impact with practical, economic, and operational constraints not only at official veterinary services considering producers perspective and impacts. Optimal control approaches offer a structured way to compare alternative interventions, especially when decision makers must weigh multiple, sometimes competing objectives in a systematic way. In the context of animal health, these methods can support the design of surveillance systems, and evaluate the feasibility of intervention portfolios under diverse outbreak conditions and the always difficult resource allocation. Here, we present a set of modelling case studies illustrating how optimisation frameworks can be used to explore control options for high priority livestock diseases in Europe.

Methods

We re-used and developed mechanistic models for two contrasting systems: African swine fever (ASF) in wild boar populations in Germany and Highly Pathogenic Avian Influenza (HPAI) in poultry systems in France. Each model was coupled with an economic evaluation component that quantified both intervention expenditures and outbreak consequences. For HPAI, we assessed combinations of vaccination coverage, and the rates of culling, and preventive depopulation. For ASF, we examined strategies targeting minimizing the outbreak duration and detection efficiency, incorporating hunters' detection rate and carcass removal capacity. Wild boar density estimates were refined using national surveillance data as priors to calibrate the Enetwild wildlife density model. A global–local hybrid optimization algorithm was used to explore feasible strategy combinations across a wide range of cost assumptions and operational constrains evaluating the sensitivity to parameter changes.

Results

Preliminary results show that across both pathogens, optimisation revealed that the most effective strategies depended strongly on the assumed economic environment and epidemiological context. For HPAI, increasing vaccination costs shifted the optimal balance toward greater reliance on culling, whereas lower culling costs favoured broader vaccination coverage. For ASF, intermediate ratios between carcass removal effort and detection pressure produced the shortest outbreaks, highlighting the importance of coordinated surveillance and removal activities. Sensitivity analyses showed that small changes in unit costs or operational limits could substantially alter the recommended strategy.

Discussion

Our findings demonstrate that optimization can clarify how economic and epidemiological factors jointly shape the performance of disease-control strategies. Also, the central importance of a well-defined objective-function to evaluate disease-control/intervention strategies, as different formulations can lead to markedly different recommendations. Explicitly incorporating economic costs into animal health models ensures that proposed interventions remain realistic and feasible, aligning epidemiological impact with practical resource constraints. Our results show that no single intervention is universally optimal; instead, systematic exploration across objectives and scenarios is essential to identify strategies that perform robustly under varying epidemiological and economic conditions when designing control policies for animal infectious diseases. Our next step will be to incorporate social impacts commonly faced by producers usually not included in the overall cost of outbreak management.

Theme 3

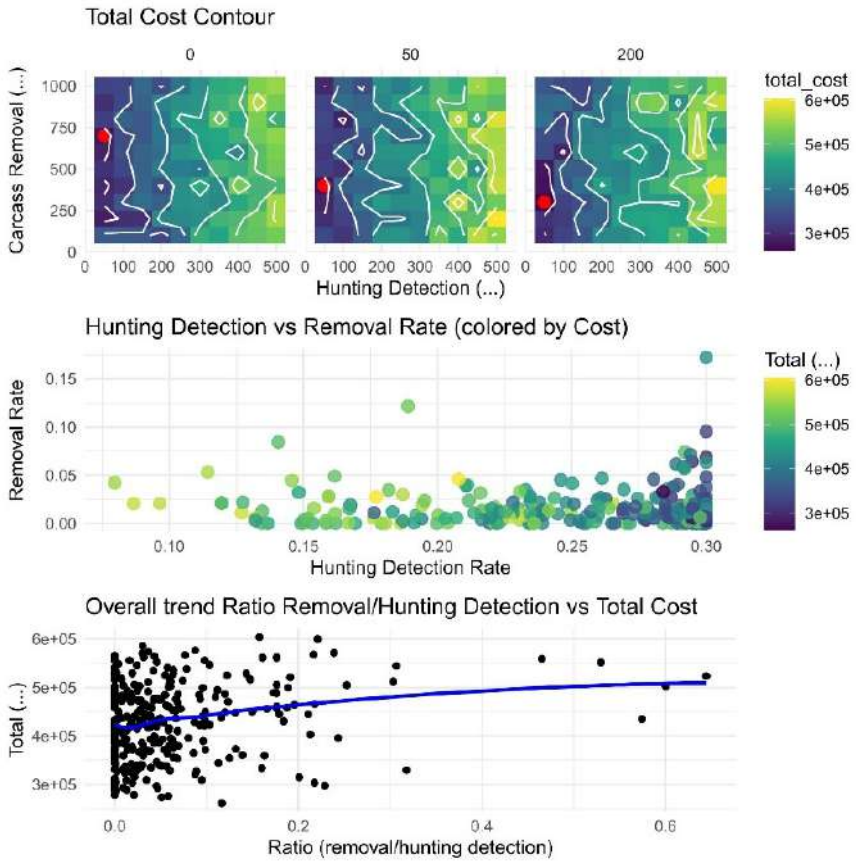


Figure 1. Optimization results ASF: Hunting detection vs removal and outbreak duration time penalty

Keywords: ASF, HPAI, optimisation, modeling, decision-making.

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Theme 3

Quantitative evaluation of the sensitivity of a wildlife health surveillance network for the detection of highly pathogenic avian influenza H5N1 in Cambodia

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Summary

Early detection of highly pathogenic avian influenza (HPAI) H5N1 in wild bird populations requires surveillance networks that are not only operational but demonstrably sensitive. This study presents a quantitative evaluation of the Wildlife Health Surveillance Network (WHSN) in Cambodia, using a scenario tree approach applied to seven protected areas over the period October 2024 to March 2025. Node probabilities were estimated from network data and expert elicitation, with uncertainty propagated through Monte Carlo simulations. At a design prevalence of 0.1%, site-level sensitivity ranged from 0.005 at Prek Toal to 0.388 at Rohal Kes, and global sensitivity reached 0.869 at a design prevalence of 0.1%. Standardized regression and a Tornado diagram identified sampling as the dominant driver of system performance (β = 0.896), followed by discovery (β = 0.374) and notification (β = 0.081), while training coverage showed no direct effect. These results provide a practical basis for targeted reinforcement of the network, with priority given to sampling logistics, patrol coverage, and notification feedback loops.

Introduction

Wildlife plays a central role in the emergence and spread of zoonotic diseases. HPAI H5N1, in particular, has circulated in Southeast Asia for over two decades, with wild waterbirds — especially *Anseriformes* and *Ciconiiformes* — serving as reservoir hosts capable of disseminating the virus across long distances, often without visible clinical signs (1). Cambodia is a recognised biodiversity hotspot in the region, and the intensification of interactions between wildlife, domestic animals, and human populations — driven by deforestation, agricultural expansion, and wildlife trade — has increased the risk of spillover events with both animal health and public health consequences. Between February 2023 and August 2024, Cambodia reported 16 confirmed human H5N1 infections, and in 2021, a mass mortality event affected more than 2,000 wild birds in the southeast of the country, underlining the ongoing and active circulation of the virus.

To address this risk, the Wildlife Conservation Society (WCS) established in 2014 the Wildlife Health Surveillance Network (WHSN) in Cambodia, a passive surveillance system targeting mortality and morbidity events in wild birds across protected areas. The network relies on field actors — rangers, community forestry agents, conservation staff — trained to detect, report, and sample unusual events, following a Standard Operating Procedure (SOP) defined in 2023. In parallel, the BCOMING project (Biodiversity Conservation to Mitigate the Risks of Emerging Infectious Diseases), funded by the European Union, has been supporting the reinforcement of this network by integrating quantitative assessment approaches and connecting surveillance objectives to broader biodiversity conservation goals (2).

Despite the existence of the WHSN and its integration into national health surveillance frameworks, the actual sensitivity of the network for detecting HPAI H5N1 had not been formally quantified. In a context of limited resources and competing priorities, understanding where the system fails — and why — is a prerequisite for targeted and cost-effective improvement. This study applies the scenario tree method to estimate the sensitivity of the WHSN across seven protected areas and to identify the operational nodes that most constrain detection performance.

Theme 3

Materials and Methods

Study sites and target population

Seven wetland sites frequented by wild waterbirds were selected for inclusion: Boeung Snae (BS), Anlong Pring (AP), Boeung Prek Lpeou (BPL), Ang Trapeang Thmo (ATT), Rohal Kes (RK), Toul Prum (TP), and Prek Toal (PT). These sites differ considerably in terms of avian diversity and density, surface area, geographic location, proximity to poultry farms, and the number and training status of field agents. The target population consisted of wild birds present at each site, classified into six taxonomic categories based on their order: *Ciconiiformes*, *Anseriformes*, *Pelecaniformes*, *Charadriiformes*, Raptors, and other species. Each category was assigned a relative infection risk derived from published literature and from WCS bird count data, reflecting differences in susceptibility to H5N1 and observed mortality rates across studies conducted in Asia and elsewhere.

Data sources and period of study

Data covered the period October 2024 to March 2025. Two main sources were used. First, the WHSN database provided information on species detected, collection dates and sites, carcass condition, sampling status, and the number of trained and untrained agents per site. Bird counts by protected area were provided by WCS. Second, a structured questionnaire was administered to key actors in the network: officers from provincial animal health offices estimated infection risk by site and by bird category, while field agents from the provincial environment departments provided information on detection and notification probabilities, as these are the steps they carry out directly on the ground. Questionnaires were translated into Khmer via KoBoToolbox, and responses were collected remotely by telephone or Telegram before being translated into English, exported into Excel, and analysed in R.

Scenario tree construction and parameter estimation

The scenario tree method decomposes the surveillance process into successive nodes, each associated with a probability or proportion, to estimate the overall probability that the system detects at least one infected animal if the pathogen is present at a given prevalence (3). Nodes were defined in chronological order and structured into three categories: category nodes (protected area, bird species group, agent training status), an infection node, and detection nodes (discovery, notification, sampling, PCR confirmation) (4).

The infection node was built by combining an ecological risk score for each site — based on proximity of poultry farms within a 5 km radius, history of avian influenza outbreaks, and presence of wetland habitats — with a biological risk component weighted by the proportion of each bird category present at the site. Expert elicitation responses were modelled using PERT distributions to account for parameter uncertainty. PCR test sensitivity was fixed at 0.95 based on laboratory data.

Monte Carlo simulations were then run to propagate uncertainty through the tree and estimate site-level and global sensitivity for four design prevalence values: 0.03%, 0.04%, 0.05%, and 0.1%.

Sensitivity analysis

To identify which nodes most influenced system performance, a standardized multiple regression was conducted using the node probabilities as predictors and site-level sensitivity as the outcome. A Tornado diagram was also constructed by varying each parameter independently between its 10th and 90th percentiles and measuring the resulting range of predicted global sensitivity, which provided a visual and quantitative measure of each node's influence.

Results

Node parameter estimates

Parameter estimates varied substantially across sites. The proportion of trained agents ranged from 26% at Boeung Snae to 100% at Anlong Pring. Discovery probabilities ranged from 0.075 at Prek Toal to 0.577 at Rohal Kes, and notification probabilities from 0.344 to 0.680. The sampling probability was uniform across sites at 0.807, derived directly from the WHSN database.

Site-level sensitivity

At a design prevalence of 0.1%, site-level sensitivity showed strong variation. The lowest values were observed at Prek Toal (0.005; 95% CI: 0.002–0.010), Boeung Prek Lpeou (0.033; 0.018–0.058), and Boeung Snae (0.054; 0.033–0.084). Higher sensitivities were estimated at Toul Prum (0.231; 0.147–0.333), Ang Trapeang Thmo

Theme 3

(0.268; 0.175–0.379), Anlong Pring (0.278; 0.169–0.417), and particularly Rohal Kes (0.388; 0.237–0.555). These differences reflect the combined effect of local infection risk, patrol coverage, and detection chain performance rather than any single factor.

Global sensitivity

Global sensitivity — the probability that the system detects at least one case across all sites — increased with design prevalence: 0.456 (95% CI: 0.253–0.479) at D = 0.03%, 0.556 (0.322–0.581) at 0.04%, 0.638 (0.385–0.663) at 0.05%, and 0.869 (0.622–0.886) at 0.1%. This reflects the mechanical relationship between prevalence and detection probability: as more animals are potentially infected, the chance of encountering at least one becomes greater.

Sensitivity analysis

The standardized regression identified sampling as the dominant driver of system sensitivity ($\beta = 0.896$, $p < 2\times10^{-16}$), followed by discovery ($\beta = 0.374$, $p < 2\times10^{-16}$) and notification ($\beta = 0.081$, $p < 2\times10^{-16}$). Training coverage had no direct effect ($\beta = 0.0003$, $p = 0.891$), though this likely reflects the fact that training acts indirectly through its influence on discovery and notification rather than as an independent predictor. The model explained 95.5% of variance in sensitivity (adjusted $R^2 = 0.9545$).

The Tornado diagram confirmed this hierarchy. Around a median global sensitivity of 0.770, sampling produced the widest range of predicted values (0.680 to 0.862; range 0.182), followed by discovery (0.735 to 0.806; range 0.071), notification (0.762 to 0.778; range 0.015), and training (range 0.00006).

Notification barriers

Among the 66 field agents who responded to the questionnaire, all (100%) identified not knowing who to contact as a barrier to reporting, and an equal proportion felt that notification was not part of their formal responsibilities. Almost all (99%) cited the absence of feedback following previous reports as a discouraging factor. Despite these declared obstacles, 92% stated that none of these factors would actually prevent them from reporting a sick or dead bird — suggesting that motivation is present, but the structural conditions for notification are not.

Discussion

The scenario tree approach proved well suited to this context. It allows explicit modelling of each step of the surveillance chain, integrates expert knowledge where formal data are absent, and propagates uncertainty through PERT distributions rather than relying on point estimates. It is also more appropriate than capture-recapture methods here, as the latter require independent data sources and a sufficient volume of confirmed cases with independent detection pathways — conditions that are rarely met in wildlife surveillance (5).

The most immediate operational implication of our results is the priority of the sampling node. Even where discovery and notification function reasonably well, the proportion of reported cases that are actually sampled and sent to the laboratory remains the strongest determinant of whether the system can confirm an event. This suggests that improvements to sampling logistics — kit availability, cold chain, transport to Institut Pasteur du Cambodge for PCR confirmation — would have a greater impact on sensitivity than expanding training coverage in its current form.

Discovery is the second priority, and the results suggest that patrol coverage and the ability of field agents to recognise mortality events are the relevant dimensions. Standardised alert signs and simplified field guides, rather than comprehensive training programmes, may be more effective at this stage. The low discovery probability at Prek Toal is a particular concern given the site's large area and density of waterbirds.

On notification, the questionnaire results are instructive. Field agents are not reluctant to report — the vast majority say they would report regardless of barriers. The problem is structural: unclear roles, no designated contact, and no feedback loop after reporting. These are fixable problems that do not require significant new resources.

Training coverage, as measured, had no direct effect. This probably reflects the fact that training was captured as a binary proportion of staff who had received any training, rather than a measure of operational competence. Transitioning to competency-based indicators, with standardised practical assessments, would likely reveal a different and more actionable picture.

Theme 3

Finally, our results differ from a previous 2022 evaluation of the same network, which covered fewer sites and did not incorporate expert elicitation. Both methodological differences and possible changes in surveillance effort between the two periods may explain these discrepancies.

Keywords: avian influenza, wildlife surveillance, scenario tree, sensitivity, Cambodia.

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Poster presentations

Risk-based active surveillance in rural establishments: design, implementation and sensitivity assessment in Mato Grosso, Brazil

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Introduction

Maintaining animal health status and international sanitary certification requires surveillance systems capable of early detection of diseases of economic and sanitary importance. Mato Grosso, one of the world's largest livestock-producing regions, had a herd of 31,629,397 cattle, 2,147,031 pigs and 47,388,869 poultry in 2025 and faces the challenge of ensuring effective surveillance across a vast territory of 903,357 km². In this context, a risk-based active surveillance strategy in rural establishments was implemented in 2023, targeting major diseases absent from the territory, including high-impact transboundary diseases such as foot-and-mouth disease, avian influenza, Newcastle disease and classical and African swine fever, with the objective of increasing surveillance sensitivity and optimizing resource allocation.

Methods

The strategy was structured using epidemiological modelling based on scenario tree modelling. Scenario trees were developed considering the operational characteristics of the surveillance system in Mato Grosso and disease-specific risk factors, combined with stochastic simulations to estimate system sensitivity and corresponding confidence intervals. Rural establishments were selected according to risk profiles associated with disease introduction and spread. Component sensitivity was estimated by aggregating detection probabilities across sampled units under a predefined design prevalence of 1%. Monte Carlo simulations (1,000 iterations) were performed to estimate mean sensitivity and 95% confidence intervals, accounting for parameter uncertainty. Field activities included systematic clinical inspections, standardized data collection and recording in the official animal health information system.

Results

Theme 3

In 2023, 9,861 rural establishments were sampled, of which 9,818 were visited (99.56%), covering all 141 municipalities, with full coverage achieved in 90% (127/141). A total of 814,713 cattle, 1,415,440 poultry and 149,713 pigs were inspected. In 2024, 10,164 establishments were sampled and 10,140 were visited (99.76%), with full coverage in 91.5% (129/141) of municipalities. Inspections included 713,551 cattle, 2,020,426 poultry and 308,044 pigs. In 2025, 10,112 establishments were sampled and 10,096 were visited (99.84%), achieving full coverage in 95.0% (134/141). Inspections included 857,520 cattle, 931,248 poultry and 225,506 pigs.

Assuming a design prevalence of 1%, annual sensitivity in 2023 was 0.9999 (95% CI: 0.9999–1) for foot-and-mouth disease, 0.9906 (95% CI: 0.9644–0.9986) for classical and African swine fever and 0.9994 (95% CI: 0.9910–0.9999) for avian influenza. In 2024, sensitivity was 0.9999 (95% CI: 0.9999–1) for foot-and-mouth disease and 0.98 (95% CI: 0.96–0.99) for classical and African swine fever. In 2025, sensitivity was 0.9999 (95% CI: 0.9999–1) for foot-and-mouth disease, 0.976 (95% CI: 0.9325–0.9963) for classical and African swine fever and 0.9961 (95% CI: 0.9675–0.9998) for avian influenza.

Discussion

Scenario tree modelling combined with stochastic simulation enabled quantitative assessment of surveillance sensitivity, providing robust evidence for system performance evaluation. The risk-based approach improved resource allocation efficiency by targeting epidemiologically relevant units without compromising coverage. The strategy enhanced spatial coverage, reduced redundant visits to low-risk establishments and strengthened integration between active and passive surveillance through increased engagement with livestock producers and improved early reporting. These results support the effectiveness of risk-based surveillance in large-scale livestock systems.

Keywords: Risk-based surveillance, Scenario tree modelling, Surveillance, Sensitivity, Animal.

Assessing the quality of livestock registry data using risk-based surveillance in Mato Grosso, Brazil

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Introduction

Livestock registries are the primary source of information used by official veterinary services and are essential for surveillance planning, sampling strategies, prioritization of establishments, and targeting of inspection and monitoring activities. In Mato Grosso, Brazil, this database includes 128,044 rural establishments and 156,787 active livestock holdings registered in the official animal health information system (SINDESA), highlighting its role as a strategic tool for animal health management. The consistency of these data is critical for the effectiveness of risk-based surveillance, as incomplete or inaccurate information may compromise epidemiological analyses and decision-making. This study aimed to assess the consistency of the registry and its ability to reflect field conditions in rural establishments by comparing registry data with field observations.

Methods

A comparative analysis was conducted between data recorded in SINDESA and information collected during field visits using a structured risk-based surveillance questionnaire applied by official veterinarians. Registry data are collected during annual livestock inventory campaigns conducted in May and November, based on epidemiological questionnaires completed by producers or official staff. For validation, field data were collected during routine surveillance visits, allowing direct comparison between registered and observed variables. Data

Theme 3

from 3,369 rural establishments visited in the second semester of 2025 were analysed. Variables included structural characteristics, environmental conditions, and management practices. Agreement between registry and field data was assessed using confirmation and omission rates, and results were also evaluated according to the source of data entry.

Results

High levels of agreement were observed for structural variables, including cattle presence (97.39% confirmation; 0.12% omission), pasture area (91.5% confirmation; 8.5% omission), backyard poultry (87.3% confirmation; 12.7% omission), aquaculture (81.6% confirmation; 7.9% omission), and backyard swine (79.6% confirmation; 20.4% omission), indicating that the registry adequately reflects key structural aspects of production systems. Intermediate performance was observed for variables such as presence of multiple poultry species (72.9% confirmation; 10.0% omission) and cattle feedlot systems (54.8% confirmation; 6.0% omission). Higher omission rates were identified for variables related to environmental conditions and management practices, including use of feed (39.4% omission), contact between domestic and wild birds (33.4% omission), and presence of dairy cattle (30.3% omission).

Discussion

Some discrepancies may be explained by the dynamic nature of livestock production systems, as activities can change between registry updates and field visits. Differences according to the source of data entry were limited, although higher agreement was observed when data were recorded by official staff. The results highlight that livestock registries should be considered not only administrative tools but also strategic components for risk analysis and surveillance planning. Improving data quality through enhanced field data collection, better reporting tools, and development of quality indicators is essential to strengthen risk-based surveillance and support early disease detection.

Keywords: Livestock registry, Data quality, Risk-based surveillance, Animal health, Epidemiological data.

Theme 4

Theme 4: Innovations, Artificial Intelligence and data integration in surveillance

Oral presentations

Beyond human vision – validating camera vision systems in meat inspection

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Summary

Camera vision systems (CVS) are being developed and used in many areas of society. Lately, CVS are also being developed for use in meat inspection, but there has been – and is - concern about their validity. In this paper, we show how CVS can be validated against the existing meat inspection using Bayesian latent class modelling. Hereby, we compare meat inspection findings with those of the CVS, while assuming that both ways of detection are imperfect. We present two examples of this, where both deal with the use of CVS in post-mortem inspection of finishing pigs: 1) carcass contamination, which is a food safety issue, and 2) chronic pleurisy, which is an animal health issue. It is concluded that the CVS have a higher sensitivity than the meat inspectors, and that the meat inspectors have a slightly higher specificity than the CVS. We also briefly discuss the use of CVS and similar technologies in meat inspection of broilers and bovines.

Introduction

Slaughter animals arriving at the abattoir are first subjected to an ante-mortem (AM) inspection to check that the animals are fit for human consumption, implying that they appear normal and do not exhibit indications of animal welfare issues or disease. If the animals can be accepted at the AM inspection, they will be slaughtered. After slaughter, carcasses and organs are subjected to a post-mortem (PM) inspection, where the aim again is to check whether they are fit for human consumption. The inspection is done by either an official veterinarian or an official auxiliary working under the responsibility of the official veterinarian. These persons are trained to identify disease and welfare issues as well as contaminations and defects in carcasses. This human-based approach forms the cornerstone of food safety practices, although it is known that meat inspector assessments are inherently subjective and influenced by factors such as experience, fatigue, and environmental conditions. Another challenge is a shortage of personnel observed in many European countries, as many of the official veterinarians/auxiliaries are retiring, while recruitment is becoming more difficult (1).

Computer vision systems (CVS) are being used in several places in society, including when interpreting X-ray pictures in relation to cancer diagnoses and treatment. This involves cameras taking photos that are subjected to automated image analysis using advanced algorithms in the decision-making process. Computer vision systems are also already being used in multiple processes during slaughter. However, currently not directly in the PM inspection of pigs and bovines, even though this could potentially enhance the quality and scalability of inspection. The acceptance of using CVS directly in the official meat inspection of pigs and bovines requires regulatory approval. This would imply the generation of solid evidence demonstrating that CVS outputs meet or exceed the accuracy and reliability of the existing meat inspection.

Materials and methods

Theme 4

The question is, therefore, how to evaluate the performance of such systems, which one could say go beyond human vision. Textbooks would suggest a comparison with a gold standard. However, such validation is challenging in meat inspection due to the absence of a definitive gold standard. The meat inspector's judgement contains inherent uncertainties, as described further up. Moreover, it would be impractical, unreasonable and potentially misguiding to compare the CVS results with a thorough pathological examination, as time constraints are an inherent part of the inspection. The solution, we suggest, is making use of Bayesian latent class modelling, a statistical approach, wherein the CVS's performance is compared with that of the meat inspectors under the assumption that both tests are imperfect. Our two recent scientific publications contain examples of this approach using real life data from a Danish pig abattoir. Our focus has been on detection of 1) faecal contamination of the carcass – a food safety issue and 2) chronic pleurisy – an animal health issue. For more details, please see Lund et al. (2,3).

The CVS used for both case studies was developed by the Danish Technological Institute. It has been in place for more than a decade in a large Danish pig abattoir, slaughtering finishing pigs only. The CVS is integrated directly into the slaughter line before the PM inspection, and it is called VISION. The early 2024 version employed a combination of red-green-blue (RGB) and near-infrared (NIR) cameras, generating 24 composite images per full carcass used for the subsequent processing (Fig. 1). In late 2024, the infrared cameras and lighting were replaced by broad-spectrum white LED lighting and additional cameras. The updated system uses 16 individual images (eight from each carcass half) to detect chronic pleurisy. The data for both case studies were collected from the abattoir. For the study of faecal contamination, 16 days of data were used from early 2024, encompassing 69,215 carcasses, whereas for chronic pleurisy, data from late 2024 were used, encompassing 89,613 carcasses slaughtered over 16 days. For each carcass, the VISION results regarding faecal contamination / chronic pleurisy were compared with those from the meat inspectors, where the meat inspector data also included other findings than faecal contamination and chronic pleurisy.

To validate the VISION, we used a Bayesian latent class statistical model that compares patterns in results from both VISION and the veterinary inspectors. Since neither method is perfect, and the true status is unknown, the model treats the status (faecally contaminated /chronic pleurisy) as a latent (unobserved) variable. Each slaughter day is treated as a separate population. The statistical model examines where the two methods agree or disagree to estimate how good each is at correctly identifying contamination. This includes estimating the sensitivity (how often contamination/chronic pleurisy is correctly detected when present) and specificity (how often a carcass without contamination/chronic pleurisy is correctly identified). The model runs hundreds of thousands of simulated scenarios based on the observed data and uses the most consistent patterns to estimate the true performance of VISION as well as the meat inspectors. For more details, please see Lund et al. (2,3).

Results

The descriptive analyses, done in the faecal contamination study, prior to the modelling, revealed that the meat inspection finding “oil contamination" was statistically associated with a 4-times higher probability of VISION detecting faecal contamination compared to carcasses, where the meat inspector did not find oil (RR = 4.1, $P < 0.001$). This showed that VISION could not differentiate oil from faecal contamination. Although faecal contamination is considered worse than oil from a food safety perspective, this is not considered a major problem, because both contaminations must be removed. The outputs from the Bayesian latent class model showed that VISION had a sensitivity of 31% and specificity of 98%, compared to 22% sensitivity and 99% specificity for the meat inspectors (Table 1). Similarly, the chronic pleurisy case study revealed that VISION had a sensitivity of 89.2% and a specificity of 98.8% compared to a sensitivity of 79.4% and a specificity of 99.4% for the meat inspectors. Please, see Lund et al. (2,3) regarding the positive and negative predictive probabilities, validation of the models and sensitivity analyses related to both case studies.

Discussion

Our two examples show that VISION's strength lies in the ability to detect lesions and contaminations, whereas the meat inspectors can rule out false positives. We find that Bayesian latent class modelling is suitable for evaluating CVS against meat inspectors. Moreover, the results are intuitively easy to understand for meat inspectors, such as sensitivity and specificity and relation to other codes. In conclusion, Bayesian latent class modelling offers a robust and flexible framework for evaluating CVS, without requiring a gold standard.

Theme 4

However, CVS are not yet allowed for use in PM inspection of pigs and bovines in the European Union (EU), hence, there is a need for updating this legislation. The EU Hygiene Package legislation from 2004 is a cornerstone for public health and consumer confidence (Food hygiene - European Commission). Since this legislation came into force, only minor updates have been made, while e.g., the technological development within CVS has been ground-breaking. As described by Sandberg et al. (4), new technologies for use in meat inspection have either been developed or are in the pipeline. Similarly, citizens are getting acquainted with camera-equipped smart phones capable of recording high quality footages, and several cell phone applications require facial recognition through the camera when operating. So, why not use these technologies in meat inspections as effective means of ensuring food safety as well as animal health and welfare?

Therefore, we recommend a revision of the current meat inspection legislation to allow use of CVS not just as support for meat inspectors in their decision-making but also to replace the meat inspectors in parts of meat inspection, where this makes sense. Apart from our two examples, CVS detection of enlarged testicles on male pigs that are not surgically castrated would make sense because it makes little sense to insist on having an inspector to manually check all testicles (5). Instead, the CVS could act as the prolonged eyes of the meat inspector, only directing carcasses with faecal contamination, chronic pleurisy or enlarged testicles for individual inspection in the rework area. A third example is the use of video recordings using smartphones for remote online AM inspection in case of emergency slaughter of a bovine that has had a hip dislocation or similar, disabling it from standing and walking, and hence, from being transported to the abattoir, as suggested by Poulsen et al. (6).

The use of CVS could potentially enhance the quality and scalability of meat inspection, among others, because the judgement could be harmonised, not just at an individual abattoir plant, but also between plants and between EU Member States. The latter would require harmonisation of the meat inspection code lists, because currently these differ substantially between the countries (7). Moreover, the condemnation criteria should be harmonised, implying deciding when a finding is so serious that it should be registered and result in condemnation, as suggested by Vieira-Pinto et al. (8). Inspiration for this can be found in the work done by Majewski et al. (9), who developed a harmonised code system for poultry, consisting of 13 codes. Poultry will likely be the first species for which CVS will be used in meat inspection, because the current speed of slaughter implies that the meat inspector is supposed to check around three broilers per second, which sounds like an impossible task. This challenge has already been recognised in the EU legislation. Therefore, the use of CVS is, in principle, already allowed for PM inspection of poultry in the EU. Outside PM inspection, CVS is also being developed and implemented, e.g., to measure tail lengths and detect tail lesions (10).

It would make sense to define criteria, for when CVS have acceptable performance, so the developer would know what work to undertake. For use of CVS in PMinspection, we recommend that the CVS is validated prior to their implementation. Moreover, we recommend that this includes a comparison with the existing way of undertaking meat inspection, e.g., using Bayesian latent class modeling, and that the validation shows acceptable results. Finally, to ensure transparency and acceptance, a requirement could be to have validation results published in a peer-reviewed scientific journal.

Our work was presented to the EU Commission's Expert Group on Food Hygiene and Control of Food of Animal Origin on 23 May 2025. We would like to encourage more developers to present their work to this Committee, as it will show the plethora of tools that are in the pipeline. Next, it would be valuable to open legislation to allow wider use of CVS in the meat inspection of pigs and bovines, as it is in poultry today. Initially, the use of pilot projects at the abattoir should be allowed, while following the instructions given in Article 18.9 of the EU Regulation 2017/625. Hereby, meat inspectors and food business operators can gain experience in understanding how to make meat inspections better and more efficient and define exactly which criteria should be met to allow for replacing specific areas of physical inspection with CVS.

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Theme 4

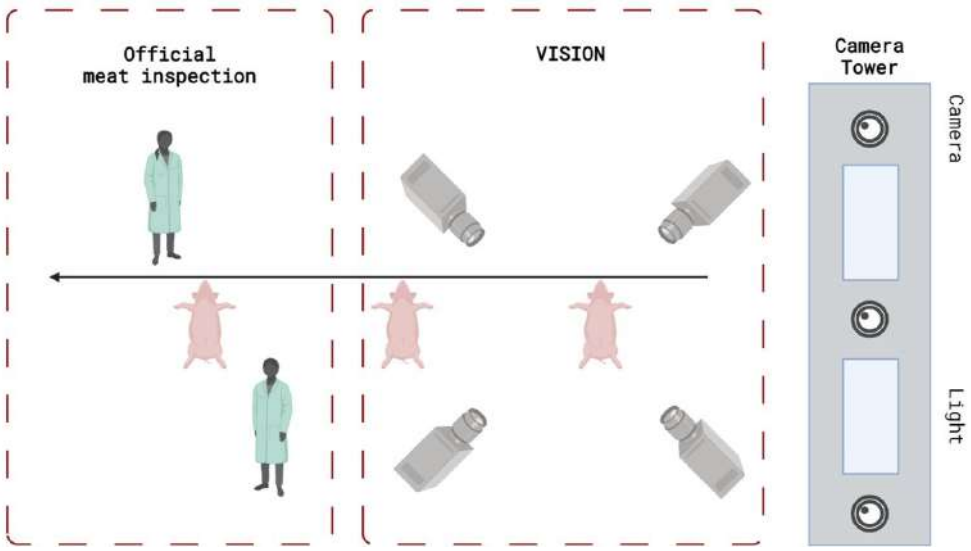


Figure 1. Graphical depiction of how the CVS called VISION works at the abattoir. Source: Lund et al. (2)

Keywords: Innovations, Artificial Intelligence, Data integration.

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Monitoring welfare in dairy farms: analysis of census-level welfare assessment protocols reveals farm characteristics associated with reduced or improved welfare levels

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Summary

In 2016, the Dutch dairy industry introduced the Welfare Monitor, a welfare assessment protocol to give dairy farmers insight into the welfare of their animals and identify any areas for improvement (1). The Welfare Monitor (WM) is a practical and pragmatic implementation of the WelfareQuality® protocol, annually filled by the veterinary practitioner of dairy farms. In the WM, all observations of the practitioner are translated into 12 (numerical) criteria via a set of calculation rules, which in turn result in a 0-100 score for each of four welfare principles: Nutrition, Housing, Health, and Behaviour. Since 2020, the WM has a 95% participation rate among dairy farmers. The aim of this study was to analyse variance components of WM scores within- and between herds and to assess associations with farm characteristics. Results showed significant differences in the variation in scores between farms, and within farms over the analysed period. Highest variation between farms

Theme 4

was observed in the principles Nutrition and Behaviour. Apparently, some farmers succeed in performing well within these principles, while a substantial number of farms score low. Multivariable analysis of WM scores in relation herd characteristics provided insight in the profile of dairy farms that either scored high or low in the WM. For instance, having a favourable certified health status (IBR, paratuberculosis, salmonella) was associated with higher WM scores. Also, there are indications that farmers striving for higher longevity of their herd achieve higher WM scores. Why some farmers succeed well in maintaining a high level of welfare in their herds, where others do not, is complex and needs further research. It is also recommended to investigate whether the presentation of the Welfare Monitor to farmers can be optimized, e.g. with national benchmark values and graphics providing insight in farm-level trends over time.

Methods

Yearly WM scores from all dairy herds in the period 2020 to 2023 were provided by ZuivelNL, the organisation of the Dutch dairy supply chain. The measurements per welfare criteria are summarized below. Details on the measurements and criteria that define the WM protocol are described in detail by (1).

Measurements per welfare principle in the Dutch Welfare Monitor for dairy herds:
Nutrition

- -Extreme body condition scores (BCS 1 or 5)
- -Water supply (quality, quantity, accessibility)

Housing

- -Comfort (freestall dimensions, bedding, softness)
- -Cow hygiene
- -Freedom of movement (access to pasture)
- -Barn conditions (daylight, ventilation, cow brushes

Health

- -Lameness (locomotion score)
- -Wounds, swelling, hock and knee injuries
- -Mastitis incidence and other diseases (respiratory/metabolic/fertility)
- -Dehorning (with/without pain mitigation)

Behaviour

- -Ability to express natural behaviour (access to pasture)
- -Avoidance distance at the feeding fence

Farm characteristics describing herd size, replacement rates, open/closed farming system and geographical location (postal code area) were provided by the Netherlands Enterprise Agency (Assen, the Netherlands). Herd health certification statuses (BVD, BoHV-1, MAP, salmonellosis and leptospirosis, see (2) for a program details) were available at Royal GD (Deventer, the Netherlands). Farm identification numbers were anonymized in all datasets prior to data transfer to Royal GD.

Analysis

All analyses were performed using Stata software (StataSE, version 18). Descriptive analyses involved the quantification of within-herd (year-to-year) and between-herd variation in scores for each welfare principle between 2020-2023. For this purpose, the 'within-subject' and 'between-subject' variance was estimated for each welfare principle via linear regression models including a random herd effect. By dividing these by the long-term average of the welfare principle, a coefficient of variation (CV) was calculated, which allows for the comparison of variation amongst welfare principles. In-depth analyses involved multilevel multivariable logistic regression analyses per welfare principle, to assess the association between farm characteristics and the probability of an either high score (>75th percentile of the population) or low score (<25th percentile of the population) for each of the four principles.

Results

The dataset contained 54,208 annual entries from 14,624 different dairy farms over the period 2020-2023. WM scores for all four years were available for 12,135 farms (83% of all dairy farms). Most farms were assessed by their practitioner in the period October to December (~60% of the farms).

Within- and between-herd variation in scores

Theme 4

The average score per principle varied over the analysed period from 51.5 points for Health to 78.5 points for Nutrition (Table 1). The principles Nutrition and Behaviour showed most variation between farms; the CV varied between 25.8% and 31.8% of the population average, respectively (Table 1). The scores for the principle Health varied the most from year to year within the same farm, with a CV of 17.7%.

Associations with farm characteristics

This in-depth analysis provided insights into the profile of a dairy farm with a low or high score for each of the four welfare principles within the WM. Significant associations (p-value <0.05) are summarized below per farm characteristic.

IBR status: Herds with a IBR-free certificate have higher Nutrition, Health and Behaviour scores;
Salmonella status: Herds with a favourable Salmonella certificate have a higher Nutrition score;
MAP status: Herds with a favourable MAP certificate have a higher Nutrition score;
Leptospirosis status: No associations found;
BVD status: No associations found;
Grazing: Herds that apply grazing have higher Health scores;
Herd size: Larger herd sizes (99-191 cows and >191 cows) are associated with higher Housing scores. Smaller herd sizes (<49 cows and 49-98 cows) are associated with higher Behaviour scores
Replacement rate: Low replacement rates (<16% of cows per year) are associated with higher Behaviour and Health
scores;
Mean cow age: Herds with a high mean age (>52 months) in their herd have higher Health scores yet lower Housing
scores. Herds with a very low mean age (<35 months) in their herd have higher Health scores;
Month of assessment: Herds that were assessed early in the year (January/February) have higher Health scores, yet lower
Nutrition and Housing scores.

Discussion

Results of this study showed significant differences in the level of each welfare principle with the WM (Health, Nutrition, Housing, and Behaviour) and the variation between farms and within farms over the analysed period. Most differences between farms were observed in the principles Nutrition and Behaviour. Apparently, some farmers succeed in performing well within these principles, while a substantial number of farms score low on these principles. A note here is that these two principles are each based on only three criteria, so not having one of the measurements in order has a greater impact on the principle score than in a principle composed of five criteria. The in-depth analysis provided some insight into the profile of dairy farms that score high or low in the WM. For instance, favourable herd health statuses were associated with a high Nutrition score. Additionally, there are indications that farmers striving for longevity of their herd, in the form of a low replacement rate and/or high average age of the herd, achieve higher scores in Behaviour and Health. In a few cases, conflicting results were found between farm characteristics and the different principle scores. For example, larger dairy farms scored higher on the principle of Housing, but lower on Behaviour. It is also noteworthy that the month of the year in which herds were assessed influenced some principle scores, which could be due to factors associated with winter housing period versus grazing period (such as cow hygiene). Also, it is assumed that veterinarians conduct assessments consistently throughout the year, yet variation between veterinarians (or veterinary practices) cannot be ruled out.

Conclusion

This study provided a first overview of the national animal-based WM scores in dairy herds in the Netherlands and revealed where most variation between farms exist and thus, where potential for improvement can be found. Why some farmers succeed well in maintaining a high level of welfare in their herds, where others do not, is complex and needs further research. It is also recommended to investigate whether the presentation of the WM to farmers can be optimized, for example by including national benchmark values and graphics that provide insight in farm-level trends over time.

Theme 4

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Statistic	Nutrition	Housing	Health	Behaviour
Mean	78.5	64.9	51.5	71.1
Median	89.0	65.0	50.0	78.0
Standard deviation	23.3	9.5	13.4	24.2
Range	0-100	34-98	0-100	19-97
Between herds CV	25.8%	13.9%	19.1%	31.8%
Within herds CV	14.9%	4.71%	17.7%	12.6%

Table 1. Descriptive statistics per welfare principle within the Welfare Monitor over the period 2020-2023, with between- and within-herd variation expressed as coefficient of variation (CV).

Keywords: Welfare, Dairy farms, Monitoring.

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European benchmarks for AI based detection of broiler carcass lesions and insights from official veterinarians on broiler post mortem inspection

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Summary

The study developed European benchmarks for AI assisted detection of broiler carcass lesions and explored factors influencing official veterinarians' (OVs) post mortem inspection (PMI) decisions. Using an online survey across 14 countries, researchers defined severity based cutoff points for six lesions to support validation of the VetInspector computer vision system (CVS). Responses revealed variability in inspection practices, communication, training, and decision making, highlighting the need for clearer guidelines and technological

Theme 4

support. Harmonised PMI criteria and CVS implementation could improve inspection consistency, manage high line speeds, and enhance welfare and food safety monitoring.

Introduction

Official meat control in the European Union (EU) consists of ante-mortem inspection (AMI) and PMI [1]. Currently PMI in broilers is based on a visual assessment of carcasses and accompanying organs, usually performed by OVs, official auxiliaries or abattoirs staff working under supervision of the OV. In the modern slaughter lines, the high line speed implies that the four broiler carcasses are supposed to be inspected per second. In the future, an expected even higher slaughter speed challenges the quality of the meat inspection.

Implementation of CVSs, like VetInspector, could solve this concern. In the EU, CVSs were allowed to be used as assisting tools in poultry PMI. The VetInspector system includes four camera stations: footpad dermatitis scoring, external surface assessment before evisceration, evaluation of internal organs, and verification of carcass hygiene after evisceration. Adoption of a CVS tool would allow for a higher quality of the PMI as well as more precise and detailed data collection and analysis. Additionally, several findings could be registered for individual broilers, enabling the setting of more accurate diagnoses for affected flocks. This could result in a more targeted disease prevention and faster welfare issues detection at farm level. However, before being adopted, a standardisation of the PMI procedures is required. First, it is necessary to harmonise the codes corresponding to the findings detected in the PMI for broilers in Europe. Next, we need to agree on the severity criteria used for each of the codes. This could be agreed on at a national or EU level, the latter allowing higher transparency among trade partners.

The aim of this study was to develop an AI model test dataset (benchmark) for the six codes used in PMI of broiler before evisceration of the carcasses and to determine the factors influencing the decisions made by OVs when performing duties related to PMI of broilers.

Methods

An online questionnaire to gather information on how European OVs currently perform PMI of broiler carcasses was created in SurveyXact (https://rambollxact.com/surveyxact). The survey was available in multiple European languages. The survey participants were OVs working daily in broiler abattoirs and recruited through national competent authorities (CA). Countries included in the study (Denmark, France, Germany, Greece, Italy, Latvia, Netherlands, Norway, Poland, Portugal, Slovenia, Spain, Sweden, and the United Kingdom) covered all regions of Europe. Data were collected between 1 October and 1 December 2025. Participation was voluntary and anonymous. Due to guaranteed anonymity, cross-country comparisons were not aimed for.

In the first section of the survey, participants were asked to determine the threshold at which a carcass should be considered unfit for human consumption based on photos showing increasing lesion severity on external carcass surfaces. The assessed lesions included emaciation, dermatitis, ascites, bruising, processing-related damage, and hock burn. Each lesion was presented with pictures representing the subsequent degrees of severity, from complete absence of anomaly (severity level 1), through mild (2), moderate (3-4), severe (5-6) and extremely severe (7).

The responses were presented in terms of cumulative severity levels. For example, selecting level 3 meant that all higher levels (4 to 7) were also considered unfit. Using these responses together with the accompanying risk assessment, we established evaluation benchmarks for each lesion type. The cutoff point was defined as the severity level at which most respondents, representing two-thirds (66.7 ± 1%), classified the carcass as unfit for human consumption.

In the second part, the OVs' perceptions, training, daily tasks, communication, and factors influencing their PMI decisions were explored. The questionnaire aimed to identify what shapes OVs' decisions during broiler PMI and how training, guidelines, and personal perceptions contribute to these assessments. The analysis of responses followed a modified and simplified protocol for practical thematic analysis. The analysis was conducted by six team members with experience in veterinary epidemiology, poultry pathology, and meat inspection.

Results

Theme 4

A total of 155 respondents participated in the survey. Responses were recorded after each question, so partial data from incomplete surveys were also included in the analysis. Among all respondents, 119 (76.8%) completed all quantitative questions, and 69 (44.5%) took part in the second section containing open-ended questions. Median experience of the respondents in PMI of broilers was 5 years.

Table 1 presents severity level benchmarks for external broiler carcass lesions based on when at least two thirds (>66.7%±1%) of veterinarians judged a carcass unfit. Most respondents assigned severity levels that clearly indicated pathological change visible in the picture presenting the lesion. This included choosing level "5" for emaciation, hock burn, bruises, and wooden breast. For ascites and dermatitis/cellulitis, respondents tended to rate lesions more severely, selecting level "4" more frequently, while for superficial dermatitis they more often chose level "3". Surprisingly, respondents were the most strict regarding muscle damage during post-slaughter processing of meat, indicating even minor damage (level "2") as a reason for considering the carcass unfit.

Open-ended questions section

The simplified thematic analysis process resulted in the identification of five themes, which are described in detail below.

Abattoir capacity and OV work hours
The 69 respondents who answered the open-ended questions in the second part of the survey consisted of OVs performing inspection in a wide range of abattoirs, from small-capacity plants to large-scale enterprises slaughtering up to 370,000 birds during a single working day. An identical proportion of OVs worked full time and part time in abattoirs (43% each). Among those working part time in smaller facilities, most contributed only a few hours per week (28%), while a smaller group worked several dozen hours weekly (16%). The remaining respondents either did not report their working hours (10%) or were not currently employed in a slaughterhouse (4%).

Decision making and operational practices in broiler post-mortem inspection
The PMI of broilers is mainly a visual assessment of carcasses and organs, with palpation or cutting used only when necessary, and additional necropsy is performed by OVs for doubtful cases. Although the OVs can inspect all carcasses, the PMI is usually carried out by an OA or abattoir staff under the OVs' supervision, with OVs verifying only a portion of each flock. The PMI station setup varied because EU regulations do not define a precise PMI location, and on many abattoirs early inspection point to detect lesions was located before evisceration. Decisions on carcass fitness relied on national guidelines based on the EU law, though clarity varied, and inspectors often based their decision on lesion type, its severity, presence of contamination, and overall flock condition. In borderline cases, respondents frequently prioritized public health protection by condemning carcasses whenever potential risk could not be excluded.

Communication of inspection findings to stakeholders
Communication of PMI results varied widely and depended on national rules and inspection procedures. The OVs used official channels such as certified paper documents or approved electronic systems, but they often also relied on informal methods, including regular email, phone calls, online communicators, and in person discussions with abattoir representatives to address issues promptly. PMI findings were usually communicated to the Food Business Operator (FBO) and, indirectly, to the poultry producer. Some OVs occasionally reached out to the flock veterinarian. Several respondents also routinely reported to the CA departments, and serious issues triggered immediate notification. One respondent noted that OVs had limited interaction with the stakeholders, except the transport companies, which often participated in operational meetings and were informed immediately when non-compliance occurred.

Training and support needs for performing PMI
Respondents stated that veterinary studies gave them a solid basis, which was supplemented by additional theoretical and practical training (a few days to several months), provided by the CA at the start of their employment. Ongoing mentoring, self directed learning, and optional courses were also important. Some OVs received regular training through courses organized by the CA or relevant ministry, delivered in person or online, while others reported irregular training and a clear need for further education, especially in food safety, broiler welfare, and broiler health.

Most respondents felt adequately supported in performing PMI, citing access to training, modern equipment, and good collaboration with colleagues, authorities, and the FBO. Others, however, reported limited support and relied mainly on personal experience and guidance from senior colleagues. Several OVs described challenging working conditions, including insufficient space and inconsistent inspection standards across abattoirs. They

Theme 4

emphasized the need for updated practical PMI guidelines with clear visual examples, more opportunities to exchange experiences with OVs from other plants, and greater use of technologies such as AI supported CVS and automated data collection. Respondents also called for regular training and better access to official laboratories. Despite these concerns, most OVs still considered the existing support sufficient.

Impact on public health and consistency of inspection decisions
Respondents emphasized that PMI played a key role in public health by preventing the entry of meat from sick animals, carcasses with residues of antimicrobials, or those produced under poor hygiene, and highlighted the importance of food chain information, AMI, and PMI in safeguarding food safety. They also recognized the strong link between PMI findings and broiler welfare, noting that many causes of condemnation reflected poor on farm conditions and that welfare assessments extend across transport, handling, stunning, and slaughter. While actions were sometimes taken when welfare related non compliances occurred, respondents felt that the consequences for the broiler producers were often limited and that stronger incentives for improvement were needed. Although the EU rules require only healthy birds to be sent to slaughter, OVs noted that PMI still provided insight into flock health, biosecurity, and the effectiveness of modern poultry production, which had reduced many historical diseases. Respondents stressed that consistent inspection decisions were essential, supported by clear guidelines, training, and communication among inspectors, although uniformity can be affected by factors such as line speed, lighting, fatigue, motivation, and variable interpretation when guidelines are lacking.

Discussion

Currently, there is no standardized European guideline of PMI for broilers that specifies which lesions to register and associated severity criteria for the individual lesions. To harmonize PMI in EU and to support VetInspector implementation, a risk-based condemnation code set, consisting of 13 findings related to broiler welfare, health and food safety has been developed [2]. Based on the OVs' responses, an attempt was made to establish risk-based condemnation criteria for six lesions detected in broiler carcasses. In the case of bruises, wooden breast and hock burn, most respondents decided that the carcass shown in photo number “5” should be considered unfit, which corresponds to an advanced degree of severity. Given that these anomalies typically do not impact food safety, carcasses with barely noticeable symptoms should not be rejected [3]. A similar issue occurred with emaciation/generalized disease, where diagnosis is difficult due to the varied causes of these findings. Emaciation alone may present only as smaller, thin carcasses that can still be approved for consumption, whereas disease-related cases may also show altered skin color or meat texture, which must be considered when assessing fitness. Surprisingly, many respondents were highly restrictive toward processing related skin and muscle defects that do not affect food safety or animal welfare. Even minor muscle damage (photo number “2”) was judged as reason for condemnation by a notable share of respondents. In the case of skin diseases and ascites, respondents showed a much more restrictive approach to the condemnation of carcasses with moderate lesions. Ascites is a major cause of carcass condemnation in abattoirs and impairs broiler welfare [4].

Respondents received guidance on the scoring procedure at the beginning of the survey. However, some seemed to have slightly misunderstood the instructions, since a few selected photo number “1,” which showed a completely normal carcass, as unfit for human consumption. Also a small number of respondents indicated some of the lesions as insignificant in the PMI of broilers.

Data from the open-ended questions clearly showed that most OVs were well trained to perform and supervise broiler meat inspection. At the same time, some respondents highlighted differences in the way PMI is carried out between different inspectors, especially working in different abattoirs. The decision regarding meat fitness, particularly in borderline cases, depended mainly on the inspector's experience, the public health relevance of the finding, and the overall condition of the flock, all of which may influence the final judgement.

One of the needs the respondents reported was the introduction of new technologies, in particular camera-based systems, to improve PMI, make it more sustainable and to ensure the repeatability of decisions between different meat inspectors and abattoirs. A similar but larger dataset could be used to test that the CVS is continuously working.

Conclusion

Harmonizing broiler PMI codes and defining benchmarks would allow proper validation of the VetInspector CVS. VetInspector can manage high slaughter speeds, reducing capacity limitations of manual PMI without

compromising inspection quality and could provide unbiased, bird level inspection across abattoirs. In this study, benchmarks were developed for codes detected by the VetInspector external station. The next steps include creating benchmarks for the remaining stations, covering meat hygiene, footpad dermatitis and visceral lesions.

Lesion	Camera view	Severity level (cumulative % of respondents)							
		NA	1	2	3	4	5	6	7
Emaciation/generalized disease	Front	0	3.2	9.0	21.3	45.2	79.4	94.8	100
Dermatitis	Front	0	10.5	50.0	66.4	80.9	87.5	97.4	100
	Top	2.0	10.7	32.9	56.4	79.9	89.9	93.3	98.0
Superficial dermatitis	Front	6.1	4.7	37.2	66.2	74.3	84.5	87.2	93.9
Ascites	Front	0.7	4.1	19.0	45.6	70.7	84.4	91.8	99.3
Bruises on breast muscle	Front	1.4	0.7	5.4	20.4	45.6	88.4	95.9	98.6
Bruises on legs	Front	4.9	2.1	7.6	19.4	34.7	87.5	93.1	95.1
Wooden breast	Front	8.4	2.1	11.9	24.5	49.7	80.4	88.8	91.6
Processing related skin defects	Front	1.4	2.8	12.6	36.4	75.5	85.3	95.8	98.6
Processing related muscle defects	Front	0.7	7.0	68.5	76.9	87.4	97.9	98.6	99.3
Hock burn	Back	9.2	2.1	5.6	13.4	42.3	70.4	81.0	90.8

Table 1. Benchmarks for the lesions to external surfaces of broiler carcasses based on respondent-indicated threshold points, using 66.7±1% as the indication of the agreed threshold

Keywords: meat inspection, official veterinarian, computer vision system, broiler.

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Short oral presentations

FarmVetCare app: A digital approach to improving disease reporting and surveillance for livestock farmers and authorities

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Introduction

The livestock sector is vital to Vietnam's rural livelihoods, food security, and agricultural productivity. Livestock farmers, however, face persistent animal health challenges, including recurrent disease outbreaks, limited access to veterinary services, and weak surveillance systems, which are exacerbated by delayed information flows that hinder outbreak response. To address these gaps, a mobile application is essential to engage livestock farmers, veterinarians and authorities in participatory-based surveillance, including reporting symptoms, early warnings and scheduled vaccinations, maintaining health records, and accessing professional guidance for improved farm and animal health management.

Materials and Methods

FarmVetCare is a mobile application which has been developed and implemented in Lao Cai and Phu Tho provinces under the ICT4Health project. FarmVetCare included one app for farmers, one app for veterinarians,

Theme 4

and one website to manage app information. It serves as a digital platform for farmers to exchange information, report on animal health situations, keep farming records and rapid access to professional consultation. Through the app interface, farmers are offered free support and advice about disease diagnostic, treatment, disease notification, livestock care… from the local veterinarians and automatically Artificial Intelligence responses.

Results

To date, under pilot stage between Sep 2025 and Apr 2026, over 1,000 users, including 969 farmers and 36 local veterinarians, were installed and trained about the app.

Participating farmers actively use the app to report and seek support about clinical signs of suspected cases, as well as record their animal numbers. During follow-up surveillance, 10 reported cases from pig farms in Phu Tho and Lao Cai provinces were tested and positive with ASFV; two cases from chicken farms in Phu Tho provinces were positive with avian influenza type A/H5 virus, and two cases from pig farms in Phu Tho were positive with both CSFV and PRRSV.

From the reported and tested cases, farmers have received timely advice and consultations of local authorities to response and control the disease at early stage. Diverse information about livestock breeds, market price, vaccination and disease prevention, animal husbandry techniques, disease situation around their areas have been asked, exchanged and addressed through the app.

With the support from local authorities and veterinarians in the two studied provinces, the project will expand number of users to 10,000 livestock farmers in the 2ndhalf of 2026 to facilitate better digital application and effectiveness in livestock management, disease surveillance, prevention and control.

Conclusions

By enabling direct interaction and participation among farmers, veterinary staff and authorities, the app strengthens information flow, early reporting of animal health issues, and responses to disease threats. Given its low cost, ease of implementation, the FarmVetCare app shows a strong potential for better disease surveillance system and is well positioned for scaling to larger number of livestock farmers and areas.

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Keywords: FarmVetCare, Digital tool, Livestock, Disease reporting, Surveillance.

Bibliometric mapping of the wild-domestic animal interface and pathogen spillover research

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Zoonotic spillover risk emerges as wildlife, domestic animals and humans share environments more frequently at the wildlife-domestic animal interface. Here we analyse research on the wild-domestic animal interface to identify unifying themes and metrics, examining temporal and collaboration trends and highlighting research priorities revealed by a bibliometric analysis. Bibliometric mapping analyses the structure of scientific literature using information on authors, citations, and focus topics shared. Specifically, we asked two questions: 1) How has the scientific production around the investigation of the wild-domestic animal interface related to infectious disease spillover risk changed through time? 2) How has the wild-domestic animal interface been discussed and what does it say about biosurveillance? Four databases (CAB, PubMed, MedLine, Google Scholar) were searched

Theme 4

using the terms <interface> AND <animal> AND <domestic> AND <wild>. After manual screening, publications were reviewed throughout a supervised text review via programming custom functions in R, pdftools, rcrossref, large language models and researcher-validated data. From the review of 270 eligible publications, there were 252 indexed and traceable for bibliometrics (93%). Our findings highlighted that from 1993-2025 there was a general yearly increase in publications and an expected decrease in citations for recent years. The majority of publications (N=233, 86%) were journal articles, followed by book chapters (N=18 indexed), and other posted content (N=20 non-traceable local journals, proceedings, and preprint repository). The average yearly number of indexed citations since publication was 5 citations/year ranging from zero (N=14) to 246. The global average was 35 citations/publication (median=15) and a maximum of 648 total citations for a single publication. Top journals where articles were published were Transboundary and Emerging Diseases (N=24), Frontiers in Veterinary Science (N=13), Preventive Veterinary Medicine (N=10), Viruses (N=9) and One Health (N=7). Top words from titles, excluding our focus terms (interface, wildlife, livestock, domestic, wild), were influenza (N=38), virus (N=38), disease (N=36) and transmission (N=36). Surveillance was a main focus for only 3% of articles (N=10) but with a higher number of citations (48/publication) compared to the global average (35/publication). Moreover, journal articles were cited 4x more than book chapters. We found an increase in the number of authors per publication through time, estimated at 10 authors per publication for 2025 (above the mean of 7 authors/publication). Collaboration size did not seem to influence the number of citations a publication received, but care should be taken when considering only the number of citations as impact. The five most cited articles had between 4-15 authors. Our results highlight how surveillance has not been integrated in spillover risk research at the wild-domestic animal interface and draws attention to research opportunities, including knowledge synthesis of definitions applied. The metrics provided by our bibliometric mapping can help researchers, funding agencies and governance to tailor projects that reach intended readership and impact for actionable science. Our findings can help stakeholders to integrate biosurveillance implementation and One Health operationalization at the wild-domestic animal interface.

Keywords: zoonotic risk, infectious disease surveillance, research collaboration, research impact, knowledge synthesis.

Poster presentations

Towards LLM-Enhanced Epidemic Intelligence: Opportunities for animal disease surveillance in Vietnam

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Emerging and transboundary animal diseases (TADs), including African swine fever (ASF), highly pathogenic avian influenza (HPAI), and rabies, continue to challenge animal health, food security, and livelihoods in Vietnam. The country's livestock sector, characterized by a high density of smallholder farms, informal value chains, and frequent animal movement, increases vulnerability to disease emergence and spread. Strengthening epidemic intelligence (EI), which integrates data collection, analysis, and interpretation for early detection and response, is therefore essential. While Vietnam has made progress in indicator-based surveillance through national reporting systems and laboratory networks, challenges remain in integrating and analyzing diverse and unstructured data sources in a timely manner.

Recent advances in artificial intelligence, particularly large language models (LLMs), present new opportunities to enhance EI. LLMs can process multilingual, unstructured data and provide context-aware interpretation, making them particularly relevant in Vietnam, where disease-related information is dispersed across official reports, provincial communications, online media, and social networks. This paper explores how LLMs can be integrated into animal disease surveillance, with a primary focus on strengthening Event-Based Surveillance (EBS) through three key areas: (1) Early Detection: LLMs enable automated screening of local-language reports to capture "weak signals"—such as unusual morbidity or mortality events—that often precede official notifications. (2) Data Structuring: They can efficiently extract and structure epidemiological information (e.g., disease type, host species, geographic location, and temporal patterns), facilitating faster data integration and analysis. (3) Operational Efficiency: LLMs assist in generating real-time situation reports and risk summaries,

Theme 4

reducing the administrative burden on surveillance officers and improving communication across all levels of the veterinary system.

Despite these opportunities, several limitations must be considered. LLMs may produce inaccurate or fabricated outputs (hallucinations), posing risks in high-stakes surveillance contexts. Their performance depends heavily on data quality and may be affected by bias or inconsistencies in source information. Moreover, LLMs lack domain-specific epidemiological reasoning and require expert validation to ensure reliability. Challenges related to data governance, confidentiality, and integration with existing national systems also remain significant, particularly in resource-constrained settings.

To address these limitations, this paper proposes a hybrid approach in which LLMs are integrated within existing surveillance frameworks and combined with human expertise. Such an approach can leverage the strengths of LLMs in processing unstructured data while ensuring validation and contextual interpretation by veterinary professionals. In the context of Vietnam, this hybrid model offers a feasible and scalable pathway to enhance early warning capacity, improve data utilization, and support more proactive disease control. Further research and pilot implementation are needed to assess operational feasibility and inform policy development for LLM-enhanced epidemic intelligence.

Taken together, these advances position large language models as a paradigm shift in epidemic intelligence, enabling context-aware extraction and interpretation of unstructured data at scale. However, their effective deployment depends on integration within hybrid surveillance systems, where human expertise remains essential for validation, contextualization, and informed decision-making.

Keywords: large language models, epidemic intelligence, Event-Based Surveillance, animal disease surveillance, Vietnam.

Utilizing internet-based data for early detection of African Swine Fever in Viet Nam

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Introduction

Viet Nam has implemented the Vietnam Animal Health Information System (VAHIS) for reporting animal diseases. Access to VAHIS is restricted to veterinary authorities. Moreover, outbreak data are not always collected in time. While a wealth of publicly available ASF-related information exists online. This internet-based data could serve as a complementary source to capture ASF outbreaks.

Methods

From Jan to Jun 2024, we conducted daily internet searches using keywords related to ASF outbreaks. Relevant outbreak information was extracted and incorporated into Excel spreadsheet. Outbreaks were included if they met the following definition: the occurrence of one/more confirmed or suspected ASF cases in domestic pigs within a commune. ASF outbreaks were classified based on case confirmation and information source: outbreaks, with laboratory- or POC-confirmed case(s), reported by official government websites were labelled as confirmed; all others were considered suspected.

ASF outbreaks, occurring from Jan to Jun 2024, reported by government authorities to WAHIS were collected.

Outbreaks captured on the internet and official outbreaks reported to WAHIS were manually cross-referenced and a Venn diagram was created to assess the completeness. Gaps between the onset date (as reported in WAHIS) and the online reporting date were calculated and analysed to determine the timeliness. Pearson's correlation test was used to determine the correlation between the number of outbreaks that occurred and the number reported on the internet by province.

Theme 4

Results

Between Jan and Jun 2024, 293 ASF outbreak reports were collected from internet sources. 571 ASF outbreaks occurring in the same period was captured by government authorities and subsequently reported to WAHIS. Of the 571 outbreaks assessed, 36% were also reported on the internet, while 31% of the internet-detected outbreaks were not documented in WAHIS. A strong correlation ($R = 0.75$, $p < 0.05$) was observed between the number of outbreaks reported in each province by internet sources and government authorities. The mean time to notify was 16.46 days.

Conclusion

This study provides evidence supporting the use of internet-based surveillance for monitoring ASF in Viet Nam. This proactive approach may also help to identify ASF epidemic situation missed or lagged by VAHIS/WAHIS. Future developments should focus on automating open-source data tracking to improve efficiency and accuracy.

Keywords: African Swine Fever, Viet Nam, Internet-based monitoring, early warning, ASF.

Theme 5

Theme 5: Integrating environmental and wildlife surveillance in a One Health framework

Oral presentations

Mapping of wild meat supply chains in relation to zoonotic disease transmission in selected provinces in Viet Nam

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Background:

Southeast Asia, including Viet Nam, is a global hotspot for emerging infectious diseases due to dense human populations, rapid land-use change, and frequent interactions among wildlife, livestock, and people. The increasing demand for wild meat (Shairp, 2016)—driven by rural dependence on protein sources and urban consumption linked to social status—drives increased activities in both legal and illegal value chains (hunting, farming, trade), contributing to biodiversity loss and zoonotic spillover risks (Latinne, 2023). Viet Nam also plays a central role in transboundary illegal wildlife trade, with seizures involving thousands of individuals and tons of wildlife products despite strengthened regulations. Evidence shows pathogens such as coronaviruses can amplify along wild meat supply chains (Huong, 2020), yet empirical data on these dynamics remain scarce. Addressing this knowledge gap is critical for balancing biodiversity conservation, food security, and livelihood resilience while mitigating pandemic risks.

Methods:

The study employs a mixed-methods approach combining desk reviews, stakeholder interviews, and online surveys/media scanning to generate a comprehensive picture of wild meat supply chains in Viet Nam. Desk reviews provide a national and provincial-level overview of wildlife hunting, poaching, and farming practices, establishing the structural context of supply chains. Interviews and consultations with rural communities and provincial stakeholders add depth by verifying local drivers of hunting and poaching, while also capturing socio-cultural and livelihood dimensions often absent from official records. Online surveys and media scanning complement these by quantifying the flow of selected species—particularly those farmed but potentially of wild origin—into and out of supply chains, offering insights into consumer demand and market dynamics. Together, these three methods reinforce one another: desk reviews identify broad patterns, interviews ground these patterns in lived realities, and online surveys/media scanning provide quantitative evidence of trade volumes and trends. This triangulation ensures that the mapping of wild meat value chains is both empirically robust and contextually nuanced, enabling identification of critical nodes where zoonotic disease risks are most likely to emerge and where interventions can be most effective.

Results:

Data collection is still underway, but preliminary findings indicate that human–wildlife interactions along Viet Nam's wild meat supply chains create multiple opportunities for zoonotic spillover. Early mapping of stakeholders highlights critical nodes where risks are concentrated, including hunting and poaching sites, wildlife farms, and points of sale to urban consumers. These insights are already raising awareness among provincial stakeholders about the interconnectedness of biodiversity loss, food security, and public health. The final results, to be presented at the conference, will provide a more complete picture of national wild meat supply chain dynamics and inform targeted recommendations for policy and practice to reduce zoonotic disease transmission and biodiversity loss.

Conclusions:

Theme 5

Wild meat supply chains in Viet Nam present an increased risk for zoonotic spillover and threaten biodiversity. Final data analyses, completed ahead of the conference, will provide empirical evidence to inform sustainable wildlife management models that balance biodiversity conservation with food security and livelihood needs, while mitigating zoonotic disease risks. This study will provide dynamic mapping of wild meat value chains that generate actionable insights for pandemic prevention, conservation, and livelihood resilience in Viet Nam.

Keywords: wild meat, zoonotic disease, wildlife trade, supply chains.

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Are we targeting the right animals? Validating network centrality as a proxy for disease risk across contrasting wildlife systems

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Contact network analysis is increasingly used in wildlife disease studies. Centrality metrics such as degree, betweenness, and closeness are widely applied as proxies for individual disease risk and could be used to inform surveillance efforts. The foundational assumption is that animals in central positions in a contact network are more likely to be exposed to pathogens and spread pathogens. However, there are a lack of empirical studies supporting this assumption in real wildlife systems. If centrality poorly predicts infection status, surveillance strategies built on network-derived risk scores might be misdirecting effort.

We present a cross-species pilot study to test this assumption using GPS telemetry data from two contrasting wildlife populations: 11 feral pigs (*Sus scrofa*, an invasive species) with linked serological results in Queensland, Australia; and 15 Baird's tapirs (*Tapirus bairdii*, an endangered species) in Costa Rica with GPS collars deployed and serological testing ongoing. These species contrast markedly in ecology, social structure, and conservation context, providing a meaningful cross-system test of whether centrality-infection relationships are generalisable.

For each species, we construct two network types: a proximity network using fine-scale spatiotemporal co-occurrence thresholds, relevant to directly transmitted pathogens such as ASF and *Brucella suis*, and a co-occurrence network using shared space use over broader temporal windows, relevant to environmentally persistent pathogens such as *Leptospira* spp. For feral pigs, we test centrality against *Brucella* spp. seropositivity using logistic regression with permutation-based null models, and against *L. pomona* antibody titre using linear regression on log-transformed values, to account for the high prevalence of this pathogen in the study population.

Preliminary results from the feral pig dataset show variable pathogen prevalence: all animals tested seropositive to *L. pomona*, 82% to Japanese encephalitis virus, and 27% to *Brucella* spp. Centrality metrics from neither the proximity nor the co-occurrence network predicted *Brucella* seropositivity. Similarly, neither network type predicted *L. pomona* titre. These results suggest that network position alone might not reliably identify animals at higher disease risk. Tapir results will be presented and will provide a critical cross-species comparison.

There is a lack of empirical evidence to support or challenge the assumptions that underpin network-based wildlife surveillance. This work addresses that gap and presents a replicable analytical framework applicable across species, pathogens, and surveillance contexts. The framework is designed to be tested in other systems

Theme 5

and adapted where data limitations apply. These findings highlight the need to validate our strongly-held network-based assumptions before applying centrality metrics to guide surveillance efforts at the wildlife-livestock interface.

Keywords: GPS telemetry, Contact network analysis, Pathogen exposure, Wildlife-livestock interface, Wildlife disease surveillance.

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Environmental Monitoring of Avian Influenza Virus in Scotland: Insights into Molecular Evolution and One Health Dynamics

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Avian Influenza Virus (AIV) is a highly diverse and rapidly evolving pathogen with significant implications for animal and public health. Wild waterbirds, particularly *Anseriformes* and *Charadriiformes*, act as natural reservoirs, facilitating viral maintenance and transmission across ecosystems. However, traditional surveillance systems—largely based on direct sampling and opportunistic carcass detection—face logistical, financial, and biosecurity constraints, potentially limiting early detection and underestimating viral circulation.

Here, we evaluate environmental sampling as a complementary, non-invasive surveillance strategy to improve AIV detection in wild bird populations. Between 2024 and 2026, a total of 3,500 environmental samples (faecal, sediment, and water) were collected from 20 sites across Scotland, targeting key habitats of *Anseriformes* and *Charadriiformes*, alongside opportunistic carcass sampling. RNA was extracted and screened using a nested PCR assay targeting the AIV matrix gene (Segment 7), followed by Sanger sequencing. Selected positive samples were further analysed using whole-genome sequencing with Oxford Nanopore Technology.

AIV RNA was detected across multiple sites and environmental matrices, with detections occurring at different time points, including periods of increased viral activity. These findings highlight the ability of environmental surveillance to capture otherwise undetected viral circulation. Faecal sampling yielded the highest detection success and proved operationally efficient, while consistent longitudinal sampling was critical for viral recovery and downstream genomic analyses. Whole-genome sequencing enabled recovery of viral genomic data, although with variable segment coverage. Phylogenetic analysis showed that environmental sequences clustered with recently reported sequences in Scotland, indicating the presence of currently circulating reassortant viruses in environmental samples.

These findings demonstrate that environmental sampling can enhance existing AIV monitoring systems by providing a scalable, non-invasive early warning tool. Integrating environmental and wildlife surveillance within a One Health framework improves disease monitoring, supports phylogenetic and epidemiological analyses, and strengthens preparedness for emerging zoonotic threats at the human–animal–environment interface.

Theme 5

Strengthening wildlife interface viromic surveillance for emerging infectious disease detection in Southeast Asia

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Emerging infectious disease (EID) events present a one health risk, with many originating from animal and wildlife reservoirs. As interactions among wildlife, livestock, and human populations continue to intensify, Southeast Asia has been identified as a global hotspot for EID emergence. Despite this elevated risk, regional capacity for surveillance, early detection of zoonotic pathogens, and outbreak preparedness remains limited. The Wildlife Interface Viromic Regional Emerging Infectious Disease Surveillance (WIViREIDS) project, led by the CSIRO Australian Centre for Disease Preparedness (ACDP), was established to strengthen active pathogen genomic surveillance capacities across Indonesia, Cambodia, Lao PDR, and the Philippines through the integrated workflows for field sampling, animal health laboratory diagnostics, pathogen genomic sequencing, and EID bioinformatics. Between 2024 and 2026, project partners collected thousands of environmental samples from wildlife, wet markets, and associated interfacing environments using country-specific surveillance strategies. Harmonized workflows for wildlife and environmental surveillance were implemented across participating laboratories, incorporating targeted molecular screening and Oxford Nanopore sequencing technologies.

By combining field-based surveillance with standardized diagnostic workflows across the participating countries, WIViREIDS has enhanced pathogen detection capabilities and increased the generation of genomic data to support regional EID risk assessment and preparedness. The project highlights the value of a regionally coordinated One Health approach for understanding pathogen diversity to support regional health security and diagnostic preparedness to future emerging infectious disease threats.

Short oral presentations

Distribution of ESBL producing E. coli and resistance pattern in riverine and wastewater system of Kathmandu Valley

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Summary

The environmental waster is recognized as a critical but underexplored reservoir for resistant bacteria. Urban rivers in rapidly growing cities are increasingly shaped by human activity, receiving continuous inputs of domestic sewage, hospital effluents, animal farm drainage, and urban runoff (1, 2). In order to assess the prevalence, antimicrobial sensitivity, and ESBL-producing patterns of *E.coli* in environmental water, a longitudinal study was conducted in the major three river basins (Bagmati, Manohara, and Nakkhu) of the Kathmandu Valley (KV). This study reported that *E.coli* was detected consistently across all sources of environmental water (river water, and wastewater from animal farm and hospital), in all seasons, all gradient of

Theme 5

river, and all types of rivers (Bagmati, Manohara and Nakkhu). Comparatively, prevalence of *E.coli* has been reported higher in river water, but multidrug resistance (MDR) *E.coli* and ESBL-producing *E.coli*(ESBLEC) reported higher in hospital and animal farm, respectively. Similarly, prevalence rate of ESBLEC and MDR was found moderate but increasing trend of their prevalence was reported higher in downstream of river gradient. Ceftriaxone and ciprofloxacin exhibited the highest resistance, while carbapenem and colistin resistance were either absent or rare. These findings indicate widespread environmental dissemination of AMR *E.coli* in KV in a One Health interface.

Methods

From November 2024 to October 2025, a longitudinal study was conducted in river basin of the KV, Nepal. Over four seasons, a total of 276 water samples were collected from hospitals (n = 36), animal farms (n = 95), and rivers (n = 145) across KV, covering 33.5 km of the Bagmati river, 22.7 km of the Manohara river, and 16.2 km of the Nakkhu river basin. Sampling sites were chosen based on the intensity of human–animal interaction, accessibility, wastewater discharge points, and river basin mapping. Water samples were collected aseptically, transported under cold chain conditions, and processed within 24 hours. The isolation and confirmation of *E.coli* were accomplished using conventional microbiological techniques, such as enrichment, membrane filtration, culture, biochemical testing, and MALDI-TOF MS. The Vitek Compact 2 system was used to perform antimicrobial susceptibility testing (AST), and combination disk diffusion test were used to evaluate ESBL production. STATA 14 was used to conduct descriptive statistics and chi-square tests, with a significance level of p-value < 0.05. The Central Veterinary Laboratory's Institutional Biosafety Committee (IBC 03-082/83) has reviewed and approved the study protocol.

Results

Prevalence of E. coli across, river, source, season, location

Among 276 environmental water samples, prevalence of *E.coli* was 86.9% (240). *E.coli* was highly prevalent in both river water (86.9%) and hospital effluent (86.1%), whereas a substantially lower prevalence was observed in animal farm wastewater (52.6%). *E.coli* showed consistently high prevalence across all seasons, ranging from 84.1% in summer to 91.3% in winter, indicating year-round fecal contamination and persistent with a slight increase during winter. *E.coli* was highly prevalent in all rivers (85.3–90.6%), with the highest level in Manohara (90.6%). *E.coli* prevalence varied along the river stream. *E.coli* was consistently high across different stream (86.0-88.0%).

Prevalence of ESBLEC

Among the *E.coli* isolates (n = 240), 28.3% (68/240) were identified as ESBL producers. Source-wise, the highest ESBL prevalence was observed in animal farm wastewater (36.1%), followed by hospital wastewater (25.8%) and river water (23.8%). Seasonal variation was evident, with the highest proportion of ESBL-producing *E.coli* detected in spring (36.7%) and the lowest in summer (17.2%). Among rivers, the Bagmati River had the highest ESBL prevalence (32.1%), followed by the Manohara River (29.3%) and the Nakkhu River (17.6%). By river section, ESBL prevalence was highest in downstream sites (33.7%), compared with upstream (27.3%; 24/88) and midstream (22.7%) sites.

Antimicrobial resistance in E. coli

The MIC value of different 17 types of antibiotics for *E.coli* isolates from water sample was calculated. Resistance among *E.coli* isolates (N = 240) was highest to ciprofloxacin (19.2%) and ceftriaxone (21.3%), followed by trimethoprim–sulfamethoxazole (15.0%), and cefuroxime (12.1%). Moderate resistance was observed to amoxicillin/clavulanate and piperacillin/tazobactam (each 8.3%) and cefepime (7.5%). Lower resistance rates were detected for amikacin (3.8%), tigecycline (3.3%), and fosfomycin (7.1%). Resistance to carbapenems was absent for ertapenem and meropenem, while imipenem resistance was observed in 10.0% of isolates. Colistin resistance was rare (0.4%).

Antimicrobial resistance in E. coli by river

The Bagmati river showed the highest and most diverse resistance, including ceftriaxone (22.9%), ciprofloxacin (18.3%), and trimethoprim–sulfamethoxazole (15.3%), with rare resistance to colistin (0.8%). The Manahara river exhibited moderate resistance but the highest ciprofloxacin resistance (29.3%), with ceftriaxone at 22.4%. In contrast, the Nakkhu river showed a narrower profile but very high trimethoprim–sulfamethoxazole resistance (36.1%), alongside ceftriaxone (22.2%) and ciprofloxacin (13.9%).

Theme 5

Antimicrobial resistance in E. coli by river gradient

Upstream sites showed comparatively lower resistance, notably to ceftriaxone (13.6%), ciprofloxacin (18.2%), and trimethoprim–sulfamethoxazole (11.4%), indicating limited anthropogenic impact. Midstream sites demonstrated higher resistance, particularly to ceftriaxone (22.7%), ciprofloxacin (22.7%), imipenem (15.2%), and trimethoprim–sulfamethoxazole (16.7%). Downstream sites exhibited the highest resistance overall, especially to ceftriaxone (27.9%), cefuroxime (16.3%), and trimethoprim–sulfamethoxazole (17.4%).

Antimicrobial resistance in E. coli by season

Seasonally, ceftriaxone resistance peaking in autumn (35.6%) and remaining lower in summer (8.6%). The cefuroxime showed relatively stable resistance across seasons (8–14%). Resistance to β-lactam/β-lactamase inhibitor combinations was generally low, except for piperacillin/tazobactam, which showed a marked increase in spring (25.0%). Among fluoroquinolones, ciprofloxacin resistance was consistently high, particularly in spring (26.7%) and autumn (22.0%), with a noticeable decline during summer (10.3%). Carbapenem resistance was rare, with no resistance detected to ertapenem or meropenem in any season and low, seasonally variable resistance to imipenem.

Antimicrobial resistance in E. coli by sample source

Overall, resistance was most pronounced in hospital source, followed by animal, with the environment acting as a reservoir linking both sectors. Hospital wastewater isolates showed the highest resistance to ceftriaxone (29.0%), cefuroxime (25.8%), and trimethoprim–sulfamethoxazole (32.3%). Animal farm wastewater isolates had the greatest resistance to ciprofloxacin (26.5%), ceftriaxone (24.1%), and trimethoprim–sulfamethoxazole (18.1%). River water isolates exhibited moderate but widespread resistance, particularly to ceftriaxone (17.5%) and ciprofloxacin (14.3%). Carbapenem resistance was absent across all sources.

Prevalence of MDR bacteria according to source and river location

Of 240 *E.coli* isolates, 50 (20.8%) were multidrug resistant. MDR prevalence was highest among hospital wastewater isolates (32.3%), followed by animal farm wastewater (22.9%) and river water isolates (16.7%). Seasonal variation was evident, with higher prevalence in autumn (25.4%) and lower prevalence in summer (12.1%). Among river systems, the Bagmati had the highest proportion of MDR isolates (32.1%), followed by the Manohara (29.3%) and Nakkhu (17.6%). A gradual increase in MDR prevalence was observed from upstream (18.2%) to downstream (23.3%) river sites.

Discussion

This study demonstrates a high prevalence of *E.coli* (86.9%) in river and wastewater sources of KV, indicating widespread fecal contamination. Previous investigations in the Bagmati River reported *E.coli* detection in 76.9% of water samples, confirming persistent contamination of river systems due to anthropogenic activities (3). The slightly higher prevalence might be due to limited sample size and sampling point. The prevalence of ESBLEC (28.3%) in this study was lower than that reported in recent studies from the Bagmati river, where prevalences of 91.0% and 33.3% were recorded (4). Earlier studies were limited to river water samples, had relatively small sample sizes, and were conducted only during the winter season, while the present study incorporated a longe river stretch and more diverse sample set, including multiple environmental sources and more upstream sites. Despite the lower overall prevalence, the downstream increase in ESBLEC identified in this study supports previous evidence that AMR bacteria accumulate along river stretches receiving untreated or poorly treated wastewater inputs (3, 4).

The observed MDR prevalence (20.8%) is comparatively lower than earlier reports from Nepal, where MDR among riverine *E.coli* isolates reached up to 80% (3). This variation may reflect differences in antimicrobial selection pressure, temporal changes, and methodological approaches. Nonetheless, the higher MDR burden in hospital wastewater compared with animal and river sources in this study is consistent with previous findings highlighting hospital effluents as major reservoirs of resistant bacteria (5). Similarly, the gradient increase in resistance from upstream to downstream sites supports the concept of rivers acting as conduits for AMR dissemination (3).

The AMR patterns observed in this study, particularly high resistance to third-generation cephalosporins and fluoroquinolones, are in line with national and regional reports from Nepal, which indicate widespread resistance to these commonly used antibiotics, while carbapenem resistance remains low or absent (5). Resistance to β-lactam/β-lactamase inhibitor combinations was generally low and stable across seasons, although the spring increase in piperacillin/tazobactam and persistently high ciprofloxacin resistance, particularly in spring and

Theme 5

autumn, suggest seasonal influences of wastewater discharge, and reduced dilution during drier periods (6). In contrast, carbapenem resistance remained rare, with no resistance to ertapenem or meropenem and only occasional imipenem resistance, indicating limited circulation of carbapenem-resistant *E.coli* in the environment, though even sporadic detection remains a public health concern (7).

Conclusion

This study revealed widespread contamination of rivers and wastewater sources in KV with *E.coli*, including ESBL-producing and multidrug-resistant strains. Resistance was highest in hospital and animal farm wastewater and increased from upstream to downstream river sites, indicating the role of wastewater discharge in environmental AMR dissemination. High resistance to cephalosporins and fluoroquinolones, despite low carbapenem and colistin resistance, raises important One Health concerns. These findings underscore the need for integrated AMR surveillance, effective wastewater treatment, and strengthened antimicrobial stewardship to mitigate environmental transmission of resistant and ESBLEC in urban city, Kathmandu.

Keywords: Antibiotic resistance, *E.coli*, environmental wastewater, ESBL, Kathmandu Valley.

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Theme 5

Poster presentations

More than just a catch: Unveiling Parasites in Wild and Market Fish with One Health Implications

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Fish are an essential source of food and livelihood, yet parasitic infections in both freshwater and marine species pose significant risks to public health and food security. This study aimed to determine the prevalence of parasites in wild-caught freshwater fish from Bukidnon rivers and marine fish sold in local wet markets. A total of 614 fish samples were collected and examined for parasitic infection. Results revealed an overall prevalence of 42.3%, with higher infection in marine/market fish (57.3%) compared to river fishes Tilapia (30.1%) and Paitan (25.3%). Further, *Katsuwonus pelamis* showed the highest infection rate for non-zoonotic infection (96.67%), followed by *Auxis thazard* (83.33%), then *Sardinella* spp. (58.33%), *Exocotidae* (45.00%), *Oreochromis niloticus* (12.00%), and *Decapterus* spp. (1.60%). Meanwhile, *Barbodes* spp. exhibited a high zoonotic infection (30.10%), followed by *Orechromis niloticus* (25.30%). Zoonotic (*Heterophyes* spp., *Ascaris* egg, *Procerovum varium*, *Prohemisomum vivax*, *Haplorchis* spp., *Capillaria* spp., *Centrocestus* spp., *Cyathocotilidae*, and *Anisakis* larvae) and non-zoonotic parasites (*Torticaecum* spp., *Didymocystis* spp., *Goussia* spp., *Trichodina* spp., *Dactylogyrus* spp., Unidentified Coccidia, *Piscinoodinium* spp., *Chilodinella* spp., *Lobatozoum multisacculatum*, *Rhadinoynchus* spp., *Lecithaster* spp., and Didymozoids) were identified, with potential implications for gastrointestinal illness, malnutrition, fish mortality, and reduced aquaculture productivity. This study reinforces the importance of the One Health approach, calling for collaborative actions among veterinary, medical, and environmental sectors. Safe handling, proper cooking, and sustained awareness campaigns are vital to minimizing the risk of fish-borne parasitic infections in vulnerable populations

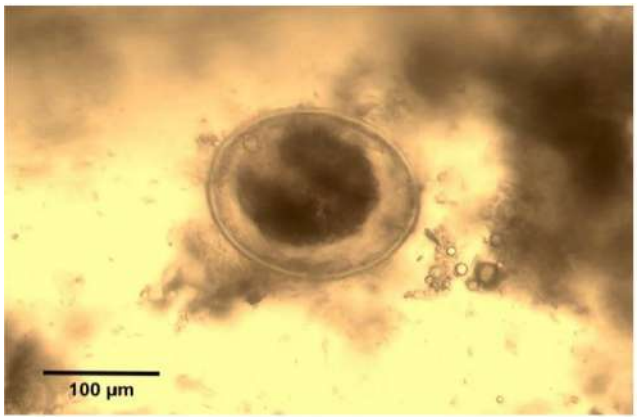


Figure 1. Heterophyid metacercaria consistent with *Heterophyes heterophyes* (size: 128.13 x 111.11 µm) (100x: LPO)

Keywords: metacercaria, fish-borne parasites, heterophyid, food safety.

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Theme 6

Theme 6: All about AMR

Oral presentations

Designing an Antimicrobial Resistance Surveillance System for Healthy Pet Dogs and Cats

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Introduction

Antimicrobial Resistance (AMR) is a global One Health challenge. Surveillance is an essential tool for addressing this challenge, as it is only with regular collection and interrogation of high-quality data that we can obtain a clear picture of baseline AMR levels in different populations, trends or changes over time, and the effects of interventions designed to mitigate risk.

Close contact between people and animals, as occurs in households with pets, is an opportunity for cross species AMR transmission. Understanding AMR in dogs and cats, the most common UK pets, is essential for understanding the risk of AMR transmission to the health of dogs and cats, their owners, other human contacts and the environment. In the UK the information needed to fully understand and mitigate these risks is lacking. Although AMR surveillance of clinical samples from dogs and cats occurs (1), AMR surveillance of healthy UK dogs and cats is absent.

Surveillance capable of providing AMR prevalence estimates that are generalizable to populations of dogs and cats requires collection of representative samples, ideally through random sampling of the population under surveillance. Collecting a random sample from a population requires that all animals in the population are a) identifiable and b) accessible for sampling. Neither of these are straightforward for all dogs and cats in the UK because there are no single, authoritative registries of all UK dogs or cats, sampling locations where the entire populations can be accessed are few, and there are few studies reporting the structure and distribution of the UK dog and cat populations in their entirety. While there are surveys of AMR in healthy pets (2), there are no operational national healthy pet AMR surveillance systems (3).

There are other methods for collecting samples that are considered acceptable by the surveillance community for making valid inferences about populations or their subpopulations (hereafter referred to as compartments). Examples for animals include random surveys of carcasses at abattoirs (e.g. the PATH-SAFE funded survey of AMR in prime cattle at slaughter in GB), the approach used for Bovine Spongiform Encephalopathy (BSE) surveillance where the population is divided into compartments and different approaches for selecting animals are used in each compartment (WOAH), and risk-based surveillance (4). Compartments or high-risk areas are often not representative of the entire population. However, if individuals within compartments can be selected using randomization methods, surveillance samples can be collected that are representative of the compartment, and parameters can be estimated that are representative of the subpopulation within that compartment.

This project aims to provide sufficient information to design surveillance to produce representative estimates of AMR in commensal *Escherichia coli* (*E.coli*) in healthy UK dog and cat populations. When operational, the surveillance is expected to produce information about emerging AMR issues, changes in AMR trends, and to have the ability to estimate changes in AMR trends following interventions aimed at reducing AMR. The key challenges are 1) the characterisation of the UK dog and cat populations at sufficient resolution to design a strategy for collecting representative samples from the populations, and 2) the collection and delivery to the laboratory of faecal samples of sufficient quality to allow the use of European Committee on Antimicrobial Susceptibility Testing (EUCAST) methods to produce AMR surveillance information that is consistent with that

Theme 6

routinely reported by the UK Veterinary Antimicrobial Resistance and Sales Surveillance (VARSS) livestock programme.
This paper outlines our overall approach for designing a surveillance system for AMR in healthy UK dog and cat populations and describes the outcomes of two activities completed to date – a representative survey of UK dog or cat-owning households and collection for AMR testing of faecal samples submitted from dogs and cats owned by a subset of respondents to that survey.

Materials and Methods

Defining information needs from an operational pet dog and cat AMR surveillance system.
A workshop with participation from the project team and members of the Veterinary Medicines Directorate (VMD) an executive agency of the UK Department for Rural, Environment, Food & Rural Affairs (DEFRA) was held to define surveillance objectives and identify information needed from an operational surveillance system. To ensure that an operational surveillance system will be useful, the outputs of the workshop will be used to guide the design of the new surveillance system.

Identification and characterisation of the UK dog and cat populations and their compartments.
We divide UK dog and cat populations into compartments based on available information about size and degree of human control over that compartment which influences the accessibility of animals for sampling. We then explore different approaches for collecting representative samples from each compartment. This approach will allow monitoring of each compartment independently over time, estimating the current and changing AMR prevalence in compartments, estimating the AMR risk to the health of people and animals from each compartment, targeting higher risk compartments for more intensive surveillance, and estimating overall AMR prevalence or risk by weighting the estimates from each compartment by size and precision, and combining them.

Three population compartments have been adopted for our surveillance system design: 1) owned and controlled (O&C) dogs and cats, which are those that are owned and live in people's homes, 2) unowned and controlled (U&C) dogs and cats, which are those that are temporarily in local authorities or shelters before being returned or re-homed, and 3) unowned and uncontrolled (U&U) dogs and cats, such as stray or free-ranging dogs and cats (5). There is empirical evidence that the uncontrolled compartment of cats in the UK is larger than the equivalent dog compartment, as the UK has negligible free-roaming dogs, but stray and feral cats are considered relatively numerous.

We reviewed scientific and grey literature to produce updated estimates for the size and distribution of the UK dog and cat populations across the compartments described above. Where feasible, we will use random selection of dogs and cats proportional to the subpopulation size in each compartment to allow the surveillance samples to be as representative as possible of the subpopulation in each compartment.

For O&C dogs and cats, we explore 3 sampling approaches: 1) a nationally representative survey of a minimum of 1000 dog or cat-owning households; 2) a national veterinary survey, where veterinary surgeries are randomly selected proportional to the human population density and asked to provide samples from a number of dogs and cats that is proportionate to the human population density and national statistics on dog/cat ownership; and 3) a national dog/cat survey, where owners and their dogs/cats are randomly selected from pet identification registries, proportional to regional dog and cat population densities found within those registries, and asked to provide samples. The household survey has been completed in collaboration with an external provider – IPSOS. We have used the IPSOS Knowledge Panel to screen UK households and recruit those owning dogs and/or cats to complete an online questionnaire. The questionnaire gathered information about respondents' dogs/cats, their feeding practices, lifestyle, and interaction with owners and vets. We were provided with the background demographic household data IPSOS used to ensure their UK panel was representative of the UK population.

For U&C dogs and cats, we will create lists of local authorities, shelters and other locations that care for found dogs and cats and explore possibilities for randomly selecting locations to request samples for a national U&C survey.

For U&U cats (and to a lesser extent, dogs) it will be a greater challenge, since little is known about their demographics, and easily accessing them to collect samples may be difficult or impossible. To identify sampling opportunities, we propose consultation and a workshop with people who interact with U&U pets such as community members, workers from shelters, feral cat wardens and others.

Theme 6

The results of all these sampling components will be analysed to estimate potential biases, compliance to requests for samples, ease of sample collection, sample quality at the lab, cost, scalability and whether or not the information produced meets the information requirements defined for the surveillance system.

Collection of faecal samples of appropriate quality for laboratory testing for AMR

Through consultation with colleagues experienced in acquiring samples from cattle for AMR surveillance activities we refined sampling protocols and defined minimum standards for samples, including types of sample vessel, sample volume, transport media, conditions of transport and mechanism of transport, to optimise capacity to culture generic *E.coli* from the sample on receipt at the laboratory. We compiled sampling kits to be sent out along with instructions, such that samples could be collected by participants and posted back to our laboratory. The sample collection process was piloted with 10 "friends and family" testers, who were asked for feedback regarding ease of sample collection and submission. Following this pilot, we invited 100 respondents from the completed household questionnaire to submit a faecal sample from their dog or cat for laboratory AMR testing.

Laboratory processing of samples obtained

We culture all samples received for this project, following standardised protocols, to isolate generic *E.coli*. A single generic *E.coli* isolate per sample will undergo Whole-Genome Sequencing (WGS) and Antibiotic Sensitivity Testing (AST) against a defined panel of antibiotics as specified in Table 2, Annex 1 of the Commission Implementing Decision (EU) 2020/1729, plus three additional antibiotics selected in consultation with the VMD due to their importance as veterinary treatments for dogs and cats. The AST approach will be the Minimum Inhibitory Concentration (MIC) method, using commercially available MIC plates for the defined panel of antibiotics and bespoke MIC plates for the three additional antibiotics. Each sample obtained will also be cultured on selective agar to identify the presence of presumptive Extended-Spectrum Beta-lactamase (ESBL)-producing, AmpC-producing or Carbapenemase (CP)-producing *E.coli*. Any isolates identified from selective agar will subsequently be submitted for WGS to confirm that they are ESBL/AmpC/CP-producing and for bioinformatics analyses.

Results

Workshop participants identified three areas of importance in terms of useful information that should be created by the surveillance system:

- -baselines for AMR carriage in healthy cats and dogs.
- -changes in the AMR carriage over time.
- -patterns of AMR carriage in space and time.

Workshop participants suggested potential uses for this surveillance information including:

- -making comparisons of AMR carriage in pets with humans and other species and across health sectors, regions and nations.
- -understanding transmission patterns among pets and across species.
- -identifying risk factors and opportunities for intervention.
- -informing estimates of AMR risk for humans and other species.
- -informing policy development.
- -leading to new research directions

Other outputs from the workshop included the metadata that should be collected with samples, and data about AMR generated from laboratory analyses.

Sample collection kits were designed and pilot tested with ten friends and family member in November 2025. Feedback received was used to clarify the instructions provided with the sampling kits. Faecal samples collected during the pilot were processed in the laboratory following the planned protocol for the household survey and the testing components will be done later in the project, when other subpopulations have been sampled.

The household survey was available online from February 5th to 11th, 2026 and 1,085 pet-owning UK adults participated. Overall, 48% of respondents owned at least one dog or cat, with 29% owning a dog, and 24% owning a cat. Most respondents had only one dog (80% of dog owners) or cat (60% of cat owners). Over half or respondents (52%) agreed to provide a faecal sample from their pet – 62% for dog owners and 40% for cat owners. We invited 56 dog owners and 44 cat owners to submit a faecal sample from their dog/cat.

Theme 6

At the time of writing, we have received 75 samples in total from the 100 respondents invited to submit a sample and have processed 69% of these. Fifty samples (67%) reached the laboratory within 3 days of sample collection; for the remaining samples it ranged from 4-10 days or is unknown. We isolated generic *E.coli* from 67 samples so far and will carry out AST on these isolates. To date, from the selective agar, we have identified presumptive ESBL/AmpC-producing *E.coli* in eight samples and have not identified any presumptive CP-producing *E.coli*.

Discussion

Preliminary findings suggest that AMR is present in healthy pets, which supports the need for AMR surveillance and the continued conscientious stewardship of antibiotic use in pets. The household survey has been an effective way to access faecal samples from one cohort within the O&C dog/cat subpopulation. Our next steps will be to trial the sampling approach for each of the remaining compartments of UK dogs and cats, beginning with those accessing veterinary clinics and moving on to those living in shelters, before addressing the uncontrolled subpopulations. All this information will feed into a workshop, to be held with the VMD and an expert advisory group, to select the population sampling and animal sampling methods that will form the operational surveillance system. The operational system will be tested at in a national scale pilot with a sample size that will be comparable with the EU and VARSS surveillance of other animals.

Conclusion

For an AMR surveillance system for healthy UK dogs and cats to be sustainable, it is prudent to make use of existing routes of communication with and access to the target populations – where appropriate – to optimise the use of resources in the collection of surveillance samples and data. At this point, we have found that part of the O&C subpopulation can be successfully accessed for sampling purposes through targeted recruitment and a self-directed sampling process, when the necessary materials and instructions are provided. This is a positive finding as the active sampling component of a surveillance system can be resource-intensive, in terms of time and money. We have also demonstrated that the samples returned meet the quality required for AMR testing, making this an effective approach for gathering surveillance data from this important and largest compartment of the UK dog and cat populations. Finally, although laboratory processing is not yet complete, we have identified evidence that the sampled cohort contains bacteria of importance for public health, confirming that this work is a necessary component of national efforts to address the challenge of AMR.

Keywords: Antimicrobial Resistance, Antimicrobial Resistance Surveillance, Dogs and Cats.

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Integrated One Health Surveillance of Salmonella, Antimicrobial Resistance, and Stakeholder Food Safety Practices in Poultry Markets in Mindanao, Philippines

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Salmonella remains a leading global foodborne pathogen, with poultry products serving as major transmission vehicles along the farm-to-market chain, particularly in low- and middle-income countries where informal

Theme 6

market systems and limited biosecurity persist. In the Philippines, integrated surveillance examining pathogen prevalence, antimicrobial resistance (AMR), and stakeholder practices across poultry market systems remains limited. Addressing these gaps requires not only pathogen and AMR surveillance but also an understanding of stakeholder behaviours, including gender roles in egg marketing and handling, to inform effective food safety interventions. This study integrates pathogen detection, antimicrobial resistance profiling, and role and gender-disaggregated behavioural analysis to investigate the prevalence and risk factors of Salmonella contamination in chicken table eggs and spent hens sold in public markets across Mindanao, Philippines, and to assess stakeholder knowledge, attitudes, and practices (KAP) on Salmonella prevention. Sampling covered 25 towns and cities across four regions of Mindanao, yielding 7,200 eggs and 720 spent hens sampled. Egg samples were pooled in groups of ten, with both eggshells and internal contents tested, while cloacal and organ swabs (liver, oviduct, cecum, cloaca) were collected from hens. Isolation using XLD agar and PCR confirmed Salmonella contamination. In Bukidnon, 90 pooled egg samples and 30 necropsied hens were additionally tested for *Escherichia coli*, and AMR profiling of Salmonella isolates was conducted using the Kirby–Bauer disk diffusion method. A total of 960 egg sellers and consumers were surveyed to assess market practices and behavioural risk factors. Salmonella prevalence was 0.9% in eggs and 7.1% in spent hens, with significant variation across locations, egg components, and organs. Eggshells were more frequently contaminated than internal contents, indicating contamination during handling and distribution. Cloacal and oviduct samples showed higher prevalence than liver samples. Significant risk factors included infrequent stall sanitation, frequent egg delivery, sourcing from unregulated suppliers, outsider access to poultry areas, and absence of pest control. Detection of *Escherichia coli* further indicated hygiene deficiencies in market handling. Antimicrobial resistance profiling showed that 90.9% of Salmonella isolates were resistant to at least one of ten commonly used antibiotics, with 81.8% exhibiting multidrug resistance, particularly to ceftriaxone and ampicillin, while all isolates remained susceptible to amikacin. KAP analysis indicated favourable attitudes but low to moderate knowledge and inconsistent practices. Role- and sex-disaggregated analysis showed higher knowledge among consumers than sellers, and among female respondents than male, although overall knowledge remained limited. These findings confirm Salmonella as a persistent food safety and public health concern in poultry market systems in Mindanao, driven by gaps in hygiene practices, informal market conditions, and the emergence of antimicrobial resistance. Addressing these risks requires strengthened farm-to-market biosecurity, improved sanitation in informal markets, enhanced AMR surveillance, and targeted food safety interventions that reflect the roles of key stakeholders in food handling and decision-making. Integrating pathogen surveillance, antimicrobial resistance monitoring, and behavioural insights within a One Health framework provides a practical and scalable approach to improving food safety. Such strategies can support more resilient, equitable, and evidence-based poultry market systems in low- and middle-income settings.

Keywords: Salmonella, AMR, Market Eggs, Spent Hens, Food Safety.

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Hidden Threats in Our Meat: Uncovering Antimicrobial Resistance in Slaughterhouses in Bukidnon, Philippines

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Antimicrobial resistance (AMR) is an emerging threat to food safety and public health, particularly in slaughterhouse settings where humans, animals, and the environment intersect. This study aimed to determine the antimicrobial resistance profiles of Enterobacteriaceae isolates and assess the knowledge, attitudes, and practices (KAP) of slaughterhouse personnel in Bukidnon, Philippines.

A cross-sectional study design was employed, integrating microbiological sampling and structured KAP surveys among slaughterhouse workers. Bacterial isolates were identified and subjected to antimicrobial susceptibility testing using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute guidelines. KAP data were collected using a pre-tested questionnaire and analysed through descriptive and inferential statistics to examine patterns and associations.

Results revealed a high prevalence of antimicrobial resistance among Enterobacteriaceae isolates, including resistance to commonly used antibiotics. A considerable proportion of isolates exhibited multidrug resistance, indicating potential risks for treatment failure and transmission through the food chain. KAP assessment among personnel demonstrated gaps in knowledge and inconsistencies in the implementation of biosafety and hygiene practices. While some workers showed awareness of basic sanitation measures, adherence to standard protocols was variable. Statistical analysis further identified associations between selected demographic characteristics and KAP scores, suggesting that factors such as experience and training may influence compliance and awareness.

These findings highlight slaughterhouses as potential reservoirs and critical control points for AMR dissemination. The presence of multidrug-resistant bacteria, coupled with gaps in personnel practices, underscores the need for strengthened antimicrobial stewardship and stricter enforcement of hygiene and biosafety protocols. Capacity-building initiatives, including targeted training and continuous monitoring, are essential to improve compliance and reduce risks.

This study contributes to the growing body of evidence on AMR in food production systems and emphasizes the importance of a One Health approach in addressing antimicrobial resistance across human, animal, and environmental health sectors.

Keywords: antimicrobial resistance, Enterobacteriaceae, knowledge attitude practices, One Health, slaughterhouse.

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Short oral presentations

AI-Powered Antimicrobial Resistance Surveillance and Management in a One Health context: A Scoping Review and Lessons for Vietnam

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Summary

Background: Antimicrobial resistance (AMR) constitutes a foremost threat to global public health, primarily attributable to the inadequately regulated use of antimicrobial agents across human medicine, animal production, and environmental systems. The implementation of a "One Health" (OH) strategy is therefore essential to mitigate the adverse consequences of AMR.

Objective: This scoping review aims to systematically collate scientific evidence regarding the application of artificial intelligence (AI) in the surveillance, prediction, and management of AMR, with specific emphasis on the OH ecosystem.

Methods: The study adhered strictly to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses extension for Scoping Reviews (PRISMA-ScR) guidelines. A comprehensive search of the peer-reviewed literature was conducted across PubMed, Embase, Scopus, Web of Science, and Google Scholar, supplemented by forward and backward citation tracking.

Theme 6

Results: A total of 549 records were retrieved. Following duplication and preliminary screening, 27 studies fulfilled the inclusion criteria and were incorporated into the analysis. Evidence demonstrates that AI is being actively deployed to combat AMR within a OH framework, with applications spanning detection of resistance determinants, early prediction of resistance phenotypes, real-time surveillance, and clinical decision support. Nonetheless, considerable limitations persist, including heterogeneity in data quality, infrastructural and operational barriers, and unresolved regulatory constraints

Introduction

Antimicrobial resistance has emerged as one of the most critical public health challenges of the twenty-first century, substantially eroding the efficacy of therapeutic regimens and amplifying the global burden of healthcare. Vietnam has long been a hotspot for AMR shaped by the intersection of economic liberalization, weak pharmaceutical regulation, and high infectious disease burden. This has generated strong selective pressure on microorganisms, resulting in documented resistance to a broad range of antimicrobials - including penicillins, quinolones, cephalosporins, aminoglycosides, methicillin, and carbapenems - across multiple pathogens including M. tuberculosis, Streptococcus pneumoniae, gram-negative bacteria, and malaria parasites.

The misuse and overuse of antimicrobials across clinical, agricultural, and environmental settings have driven the rapid emergence and spread of resistant pathogens. Compounding this, resistant bacteria discharged from pharmaceutical facilities, hospitals, farms, and untreated wastewater accumulate in environmental reservoirs, where resistance genes persist and proliferate. These genes can subsequently transfer to human pathogens through contaminated water, soil, and food chains, further amplifying the AMR threat across human, animal, and environmental health - a phenomenon that underscores the urgency of a coordinated OH response. This framework acknowledges the profound interdependence among human, animal, and environmental health, and recognises that AMR cannot be effectively controlled by addressing any single domain in isolation. OH approach, however, necessitates the integration and analysis of highly diverse and heterogeneous data streams, presenting considerable difficulties for the development of coordinated AMR response strategies. The rapid expansion of AI has supplied superior automated analytical tools for understanding and combating AMR. Despite this potential, research on AI applications in AMR control remains fragmented and dispersed across numerous disciplines. This scoping review was therefore conducted to synthesise and critically evaluate the existing evidence on AI in AMR response, identify breakthrough directions, and delineate persistent knowledge gaps.

This review aims to address the following questions:

- What AI applications have been explored for AMR control across human, animal, and environmental health globally and in Vietnam?
- What challenges are currently faced in applying AI to AMR prevention within a OH framework?
- What measures can be proposed to promote the application of AI in OH-integrated AMR prevention in Vietnam?

Methods

This study was developed in strict accordance with the PRISMA-ScR (1) criteria, specifically designed for scoping reviews.

Search Strategy:

Studies were identified through a systematic and comprehensive search of established academic databases - PubMed, Embase, Scopus, Web of Science, and Google Scholar - supplemented by citation tracking. The following search terms were applied in various combinations: "artificial intelligence", "machine learning", "deep learning", "neural network", "global health", "antimicrobial resistance", "antibiotic resistance", "drug resistance", "OH", "animal health", "human health", "environmental health", "human-animal-environment interface", and "Vietnam". All retrieved citations were imported into EndNote for retrieving duplication. Two independent reviewers subsequently conducted study selection in two sequential stages: an initial screen based on titles and abstracts, followed by full-text evaluation of all records satisfying the first-stage criteria.

Eligibility Criteria:
Studies were eligible for inclusion if they met all of the following criteria:

- Original research published in peer-reviewed journals, conference proceedings, or book chapters.

Theme 6

- Studies examining the application of AI tools and techniques to AMR within a OH scope.
- Published between 2020 and 2025.
- Written in English.

Results

Search Outcomes

The initial search yielded 549 potentially eligible records. Following deduplication and manual screening, 27 studies met the inclusion criteria and were retained for synthesis. Collectively, these studies addressed AMR prevention and control through a OH model, consistently emphasising the close linkages between human, animal, and environmental health.

Clinical Applications:

Rapid characterisation of bacterial antimicrobial susceptibility profiles is of paramount importance in clinical management. One study applied five machine learning (ML), a developing branch of AI algorithms - including XGBoost, LightGBM, Random Forest, AdaBoost, and Ridge Logistic Regression - to electronic medical records (EMRs) of intensive care unit (ICU) patients across two Vietnamese hospitals to predict AMR of key bacterial pathogens and antibiotic families. Using demographic, clinical, and laboratory data from 1,296 patients collected between 2020–2022, models were evaluated across multiple performance metrics, yielding promising results. The authors highlighted that ML-driven AMR prediction could support timely empiric antibiotic decision-making in resource-limited settings where culture results require 36–72 hours (2). Concurrently, natural language processing (NLP) algorithms have been applied to veterinary data platforms — such as VetCompass — to enable automated extraction of clinical information from medical records, elucidating antimicrobial prescribing patterns and practices among veterinary practitioners and supporting the optimisation of antimicrobial stewardship.

Genomic Analysis

Whole-genome sequencing (WGS) integrated with AI is advancing genotype-based prediction of resistance phenotypes. Studies applying ML to metagenomic analyses at poultry farms and abattoirs have identified antimicrobial resistance genes (ARGs) with potential for horizontal transfer between livestock and surrounding environments. The analysis identified a core set of 233 ARGs and 186 microbial species as strong predictors of *E.coli* resistance, including clinically relevant genera *Arcobacter*, *Acinetobacter*, and *Sphingobacterium*. Notably, 145 potentially mobile ARGs were shared between chickens and farm environments. Environmental temperature and humidity were further found to correlate with ARG presence, highlighting the role of ecological conditions in shaping resistome dynamics. This study exemplifies a OH approach by integrating the animal, environmental, and food production interfaces to uncover AMR transmission pathways in livestock systems, offering a scalable metagenomic surveillance framework applicable to low- and middle- income countries (LMICs) (3).

Next-Generation Antibiotic Discovery:

AMPlify, an attentive deep learning (DL) model combining Bidirectional Long Short-Term Memory (Bi-LSTM) with multi-head scaled dot-product attention and context attention layers, has been designed to predict and discover novel antimicrobial peptides (AMPs) from genomic sources. Applied to the North American bullfrog genome, AMPlify outperformed existing tools - including AMP Scanner Vr.2, iAMP-2L, and iAMPpred - achieving accuracy of 93.71%, F1-score of 93.66%, and AUROC of 98.37%. From 101 candidate sequences, 4 novel AMPs (RaCa-1, RaCa-2, RaCa-3, RaCa-7) demonstrated in vitro activity against WHO priority pathogens, including a multidrug-resistant carbapenemase-producing *E.coli*, with MIC values as low as 1–6 μM. This study illustrates how DL can accelerate AMP discovery from natural genomic resources as an alternative to conventional antibiotics (4). Multiple additional models have de novo generated AMPs from repositories comprising hundreds of millions of sequences. ProteoGPT, a protein large language model (LLM) pre-trained on 609,216 UniProtKB/Swiss-Prot sequences, further fine-tuned into three specialized submodels - AMPSorter (classification, AUC = 0.97), BioToxiPept (cytotoxicity screening), and AMPGenix (sequence generation) - enabling high-throughput screening of over 410 million peptide sequences. Both mined and generated AMPs demonstrated potent in vitro activity against ICU-derived carbapenem-resistant Acinetobacter baumannii (CRAB) methicillin-resistant Staphylococcus aureus (MRSA), with MIC values as low as 4 μg/ml, and showed comparable or superior therapeutic efficacy to clinical antibiotics in mouse thigh infection models, with bacterial elimination rates reaching 83–87%. Critically, these AMPs exhibited substantially reduced resistance development compared to polymyxin B and vancomycin over 20 passages. This generative AI framework represents a scalable approach for next-generation antimicrobial discovery.

Theme 6

Environmental AMR Surveillance:

Antimicrobial residues in environmental matrices represent an escalating concern. AI algorithms have been developed to applied an explainable artificial intelligence (XAI) framework - combining Random Forest and XGBoost regressors with SHAP (SHapley Additive exPlanations) values - to predict AMR-attributable mortality rates across 203 countries for five priority pathogens (Acinetobacter baumannii, *Escherichia coli*, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Streptococcus pneumoniae), using 357 indicators spanning water quality, sanitation, food systems, socioeconomic conditions, and environmental pollution. Both ensemble models significantly outperformed linear regression across all pathogens, with R^2 values reaching 0.835 for K. pneumoniae and 0.742 for *E.coli*. SHAP analysis consistently identified water accessibility and sanitation indicators - including basic water access, improved sanitation, open defecation, and desalinated water - as the most influential predictors of AMR mortality, particularly in low-income countries. CO_2 emissions per capita and rainfed/irrigated crop ratios also emerged as significant environmental predictors. This study represents the first global-scale application of ML and XAI to predict and interpret AMR mortality, directly operationalizing the OH framework by linking human health outcomes to environmental and socioeconomic conditions, and offering a scalable decision-support tool for policymakers and health authorities.

Challenges and Barriers to AI Implementation

Data Quality, Fragmentation, and Standardisation: Training robust AI and ML models requires large, diverse, and well-curated datasets. In practice, microbiological and clinical data are highly fragmented and inconsistent. Within the OH network in particular, integrating human medical records with environmental and agricultural surveillance data faces significant obstacles stemming from divergences in governance frameworks, measurement standards, and data formats.

AI Transparency: Complex models such as deep neural networks - including convolutional neural networks (CNNs) and artificial neural networks (ANNs) - frequently function as "black boxes", generating high-accuracy predictions without interpretable reasoning. This opacity undermines trust among clinicians and regulatory authorities.

Ethical Considerations: Societal acceptance and professional ethics constitute substantial barriers. Evidence indicates a tension between individual and collective interests in AI-driven prescribing: individuals tend to prefer an "Individual-AI" paradigm - prioritising antibiotic prescription for rapid cure - over a "World-AI" paradigm aimed at restricting antimicrobial use to curb population-level AMR. Public resistance to AI-standardised diagnostics further underscores that technology alone cannot resolve AMR if psychological and sociological dimensions are overlooked. Additionally, health data sharing for AI development faces considerable obstacles related to patient privacy rights and the absence of clear regulatory oversight frameworks.

Infrastructural Inequities: Paradoxically, regions bearing the heaviest AMR burden - including parts of Africa and Asia - often lack the digital infrastructure, high-performance computing capacity, and specialised expertise required to develop and sustain AI-based solutions. Without equitable investment and international technology transfer, AI risks exacerbating existing global health inequities.

Discussion

The escalating AMR crisis represents one of the gravest threats to global public health and food security, demanding a systematic, cross-sectoral response - as embodied by the OH model - to address complex transmission dynamics at the human-animal-environment interface. Against this backdrop, AI has emerged as a set of transformative tools with substantial potential to reshape AMR surveillance, diagnostics, and stewardship. Among the most significant opportunities is AI's capacity to process massive, heterogeneous datasets from multiple sectors, enabling the establishment of biological surveillance systems with real-time early warning capabilities. AI is also revolutionising diagnostic pathways through the analysis of mass spectrometry data and genomic sequences to rapidly identify drug-resistant pathogens, supporting antimicrobial stewardship (AMS) programmes in formulating evidence-based treatment regimens and reducing the overuse of broad-spectrum antimicrobials. DL and generative AI further serve as powerful catalysts in novel drug discovery, particularly in the identification of next-generation antimicrobial peptides.

Despite this substantial promise, practical integration of AI into OH-based AMR management continues to face considerable challenges. Data quality and standardisation constitute the most critical barrier, followed by the opacity of complex DL algorithms, which impedes the interpretability of machine-generated decisions. A persistent concern is the pronounced disparity in digital infrastructure, financial resources, and technical

Theme 6

expertise between nations. Data collection for AI model development is also accompanied by unresolved ethical dilemmas concerning patient privacy and the absence of comprehensive legal frameworks. To fully realise the potential of AI in AMR prevention and control, future efforts must emphasize developing open, explainable AI models (XAI) and fostering robust interdisciplinary collaboration among data scientists, microbiologists, veterinarians, and policymakers to establish transparent regulatory frameworks that ensure effective AI deployment within a global OH vision.

In recent years, the Vietnamese government has adopted a series of policies to accelerate digital transformation, with the strategic aim of positioning AI as a priority technology sector. In January 2021, the gorvernment issued the National Strategy for Research, Development, and Application of Artificial Intelligence to 2030, targeting Vietnam's emergence as an AI innovation hub within ASEAN by 2030. Subsequently, the Law on Artificial Intelligence entered into force on 1 March 2026 - the first standalone AI legislation enacted by a Southeast Asian country. Comprising 35 articles and designed around a "govern to enable development" principle, the law seeks to balance risk management with the promotion of innovation, in alignment with international norms. Additionally, Vietnam has also recognized the threat posed by AMR. Vietnam's Ministry of Health developed the National Action Plan on Combating Antimicrobial Resistance 2013–2020 (NAPCA), structured around six strategic pillars: policy and management, public education and communication, technical capacity strengthening, healthcare workforce training, financing, and international research cooperation.

Notwithstanding these advances, the development of AI infrastructure specifically for AMR control - and more broadly for managing shared health risks at the human-animal-environment interface in Vietnam - remains insufficiently prioritised. At the time of this review's preparation, only a single study conducted in Vietnam and meeting the defined inclusion criteria was identifiable on Google Scholar (2). This critical research gap underscores the urgent need for decisive, coordinated strategies that leverage digital technologies for OH-based AMR control. Priority measures should include the establishment of a national, multisectoral AMR surveillance database integrating data from health, agricultural, and environmental sectors. Guided by the AI Law, the government should issue standards for secure data sharing and create dedicated scientific funding mechanisms for interdisciplinary AI and OH research. Relevant authorities should also promote the deployment of AI-assisted clinical decision support systems across both human and veterinary medicine to optimise prescribing, limit prophylactic antibiotic overuse, and leverage smart digital platforms to enhance public awareness of biosafety risks and the hazards of unsupervised antimicrobial use.

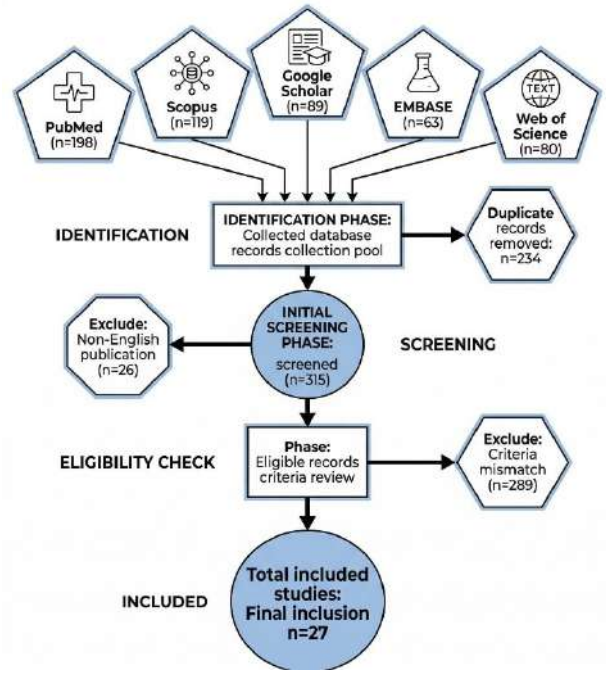


Figure 1. Flow diagram of the literature search process.

Keywords: Artificial Intelligence, Antimicrobial Resistance, One Health, Surveillance.

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Healthy herds, hidden risk: genomic antimicrobial resistance profile of commensal *E. coli* in cattle in Great Britain

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Introduction

Beef cattle farming has a crucial role in the British agricultural economy, with a production value of £4.1 billion (1). The use of genomic as a tool for antimicrobial resistance (AMR) surveillance ensures the monitoring trends of antimicrobial resistance genes (ARG) in livestock, enabling a high-resolution characterization of how it disseminates across distinct evolutionary foodborne bacteria lineages (2). Currently, national genomic ARG monitoring baselines in target bacteria isolated from healthy cattle is missing (3).

Methods

Evolving of the Pathogen Surveillance in Agriculture, Food and Environment (PATH-SAFE) programme (4), we cultured 350 commensal *Escherichia coli* isolates from caecal contents of healthy beef cattle at slaughter across Great Britain for eight months (2023–2024), using non selective and extended-spectrum cephalosporin (ESC) selective media. A subset of 200 commensal *E.coli* plus all ESC-resistant isolates (97) recovered from the 350 cultivated non-selective and ESC selective media, respectively, were whole-genome sequenced by illumina. Resistance profiles were assessed with AMRFinderPlus (5) and *E.coli* lineages were identified by sequence types (ST) assigned using MLST (6). A maximum likelihood tree was constructed from the core-genome alignment of 297 sequences parsnp and visualized with iTol. Single nucleotide polymorphisms (snp) calling was estimated by snippy, and the distance od snps calculated by snp-dist. Plasmid replicon types were identified using Plasmidfinder tool.

Preliminary results

Among all isolates, ARGs against 12 antibacterial classes with 63 distinct resistance profiles were established. Besides beta-lactams, present in 97 isolates, ARG against quinolones (67), tetracycline (36) and aminoglycosides (31) were most frequently found. From the 97 ESC-resistant isolates, at least one ESC gene was found in all ESC-resistant *E.coli*, showing the high concordance between phenotypic test and genotypic founds. Extended-spectrum beta lactamases (ESBL) represented 69% (67/97), all harboured a blaCTX-M genes, whereas 27% (26/97) were phenotypically AmpC, where point mutation C_42T was main resistance mechanism detected (20/97). Genotypically multidrug resistance was detected in 45% of ESC-resistant and in 3% of indicator *E.coli* (7/200). ST58 and ST10 accounted for 16% (49) and 5% (16) of isolates, respectively. The closest pairwise distance was 12 SNPs (1). IncFIA and IncFIB were the most frequently harboured plasmid replicon types.

Discussion

Genomic surveillance provides early detection of emerging ARG variants and AMR lineages, supporting effective monitoring and control strategies (7). In our dataset, ARGs were identified across multiple *E.coli* lineages, strongly indicating horizontal gene transfer mediated by mobile genetic elements (MGEs). A cluster of 35 isolates in two sister-clades, belonging to ST58 but separated by more than 12 SNPs, were identified. This level

Theme 6

Theme 6

of diversity suggests that the lineage has been established and evolving within the population for a considerable period. ST58 carrying ARGs has been reported in environmental sources, food producing animals, and humans (8). As a next step, we aim to characterise in depth the MGEs involved in the ARGs detected, supported by ongoing long read sequencing, to better understanding targets of monitoring.

Conclusion

Genomic analysis offers powerful insights into AMR dynamics across target bacterial species, providing strong application for targeted AMR monitoring.

Keywords: Whole-genome sequencing, Genomic surveillance, Genomic insight, Livestock, extended-spectrum cephalosporin.

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Monitoring of antimicrobial resistance in the interface between domestic animals, wildlife, and the environment

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Background and Objectives

The establishment of the Quadripartite partnership in March 2022, has reaffirmed the importance of the environmental sector in One Health [1]. The Quadripartite considers One Health as the main approach for addressing complex health challenges such as antimicrobial resistance (AMR). In its latest call to action, the Quadripartite urged stakeholders to focus on a number of priority actions, among which to strengthen and sustain prevention of health threats at source, in order to reduce the risk of zoonotic spillover. The Quadripartite's One Health Joint Plan of Action extensively addresses the possible spillover of AMR between food-producing animals, humans and the environment, and recognizes the role of the interface between domestic animals and wildlife in the emergence of zoonotic epidemics [1].

Denmark is internationally recognized for a long-lasting successful intersectoral collaboration for the monitoring of AMR in animals, food and humans – the DANMAP program. In a recent evaluation of its One Health scope, DANMAP scored lowest in the target of coverage/transdisciplinary, due to the lack of representation of the environmental sector in its program [2]. The monitoring of AMR in the environment is crucial to understand the dynamics of AMR dissemination outside of clinical, veterinary and farm-to-fork settings [3]. It can serve both the purposes of assessing the dissemination of already resistant bacteria, and of studying how the environment acts as a source of new AMR hazards [3]

Theme 6

Research on the environmental monitoring of AMR of anthropogenic origin is in its infancy, with the majority of the existing studies having focused on farm waste or wastewater. However, wildlife is known to have a role in the spread of AMR and has been increasingly hypothesized as a useful marker for environmental pollution with antimicrobial resistance [4].

Hypothesis

Terrestrial animals participate in the spread of resistance between food producing animals and the surrounding ecosystem. Mussels are successful bioindicators for environmental spread of AMR from the terrestrial to the aquatic environment. *E.coli* can be used as indicator for future environmental surveillance of AMR.

Methods

Faecal samples were collected from septic tanks from pig farms selected within a 5 km radius of the Limfjord straight in western Denmark. Faecal content from wildlife and whole mussels were collected from the surrounding area. *E.coli* was isolated from all samples on selective media (MacConkey) and DNA was isolated followed by whole genome sequencing and phenotypic testing (broth microdilution). All samples had geolocation. Phylogenetic analysis will be performed to investigate the genomic relationship between the *E.coli* isolates, and the pathway of AMR environmental spread will be modelled utilizing GIS software.

Results

Preliminary results will be available at the conference.

Keywords: One Health surveillance, antimicrobial resistance (AMR), environmental surveillance, wildlife–livestock interface, *Escherichia coli* (*E.coli*).

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Poster presentations

Antimicrobial Resistance in Food-Producing Animals Across Seven Provinces of Cambodia: Findings from Livestock Farm Surveillance

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Background

Theme 6

Antimicrobial resistance (AMR) in food-producing animals is an important One Health and food safety concern. Data on bacterial contamination and AMR in Cambodian livestock production remain limited.

Methods

The study investigated commercial chicken and pig farms across seven provinces (Kampong Cham, Prey Veng, and Pursat, Battambang, Siem Reap, Kampong Chhnang, and Kampong Speu). A total of 840 samples from 140 farms, including animal, boot/floor, environment, feed tank, and water samples, were analysed. *Escherichia coli* and *Salmonella* spp. were isolated using standard microbiological methods, and antimicrobial susceptibility testing was performed using broth microdilution.

Results

E. coli was detected in 470/840 samples (56.0%), demonstrating widespread contamination across livestock environments. Prevalence was consistent between provinces, with 55.8% (201/360) in Kampong Cham, Prey Veng, and Pursat and 56.0% (269/480) in the remaining provinces. *Salmonella* spp. was detected in 75/840 samples (8.9%), with substantial provincial variation. The highest prevalence was reported in Prey Veng (24.2%), followed by Kampong Chhnang (9.2%). In the four-province study, boot swabs and cloacal/rectal swabs showed the highest *E. coli* contamination (100% positivity), while boot swabs had the highest *Salmonella* spp. contamination detection (18.8%).

AMR analysis revealed substantial *E. coli* resistance to ampicillin (63.6%) and trimethoprim sulfamethoxazole (36.4%), as well as additional resistance to gentamicin, ciprofloxacin, and colistin. *Salmonella* spp. marked resistance to several antimicrobials, although resistance patterns varied across provinces.

Conclusion

Seven Cambodian provinces demonstrate persistent widespread *E. coli* contamination and substantial AMR, with considerable geographical variation in *Salmonella* spp. occurrence and resistance profiles. The results suggest strengthening farm biosecurity and sanitation, responsible antimicrobial use, laboratory capacity, and integrated, continuous AMR surveillance across livestock production systems.

Keywords: Antimicrobial resistance, *Salmonella* spp.; *E. coli*; food-producing animals; poultry; pigs; livestock farms, Cambodia.

Theme 7

Theme 7: Surveillance in livestock and food production systems and value chains

Oral presentations

Opportunities and limitations of avian influenza surveillance data harmonization for outbreak forecasting in Vietnam

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Summary

Avian influenza is spreading globally, affecting the poultry industry and wildlife biodiversity. Vietnam has been recognised as a hotspot for highly pathogenic avian influenza (HPAI), experiencing recurrent outbreaks since its first detection in late 2003 (Gutiérrez et al., 2009). Understanding the spatiotemporal structure of outbreaks is essential for effective surveillance and control.

This study evaluated structural differences in HPAI outbreak records reported by two international surveillance systems, WAHIS and EMPRES-i, in Vietnam from 2006 to 2022. We assessed how reporting structure and data processing influence spatiotemporal cluster detection and identified hotspots that persisted across analytical parameter settings.

Following harmonisation, deduplication, and spatial validation, clustering was analysed using the SaTScan space–time permutation model under multiple spatial (10–100 km) and temporal (30–90 days) windows. Sensitivity to window choice was examined within each dataset, and cross-dataset comparison used predefined spatial and temporal matching criteria.

EMPRES consistently detected more clusters with smaller radii and shorter durations, whereas WAHIS identified fewer but broader and longer-lasting clusters. Persistent hotspots were concentrated in northern Vietnam, particularly the Red River Delta, with secondary foci in the Mekong Delta. These differences primarily reflect surveillance structure rather than underlying incidence. Rather than privileging one dataset over the other, their complementary strengths suggest that integration may provide broader insight when supported by rigorous harmonisation and sensitivity analysis. In particular, datasets with higher reporting density may be more sensitive to localised clustering, whereas more aggregated reporting structures may provide greater stability for regional or temporal trend analysis.

Methods

2.1 Data Sources

The WAHIS dataset was obtained from the World Organisation for Animal Health (WOAH) SharePoint platform (infur 20250623) and is hereafter referred to as the WAHIS It comprised 749 records of highly pathogenic avian influenza (HPAI) outbreaks reported between 2006 and 2022, each containing 63 variables.

The second dataset was obtained from the public interface EMPRES-i of the Food and Agriculture Organisation of the United Nations (FAO) and is hereafter referred to as the EMPRES. This dataset initially included 3,336 outbreak records (16 variables) spanning 2006-2022, covering both HPAI and low-pathogenic avian influenza (LPAI). After restricting the dataset to HPAI outbreaks only, 1,513 records were retained for analysis.

Each row in both datasets was assumed to represent a single outbreak event. Variables related to outbreak timing, geographic location, and key epidemiological characteristics were selected for subsequent analysis.

Theme 7

2.2 Data Quality Assessment

Data wrangling and harmonisation were conducted in R (version 4.5.1). Variable names were standardised across years, and Ha Tay province, merged into Ha Noi in 2008, was recoded as Ha Noi to ensure temporal consistency.

Exploratory analysis assessed data completeness and duplicate records. In EMPRES, 2.7% of outbreak start dates were missing and were imputed using report dates where appropriate. De-duplication procedures differed due to reporting structure. WAHIS was deduplicated using outbreak ID, start date, coordinates, location name, and province. EMPRES, which frequently recorded multiple entries for the same event, was deduplicated based on observation date, locality, province, and coordinates.

Spatial validation was conducted by overlaying outbreak coordinates with provincial boundaries from the Global Administrative Areas database (GADM v4.1). Records falling outside their reported province were flagged, and distances to administrative boundaries were calculated. Coordinates within 5 km of the assigned boundary were retained. Larger discrepancies were investigated through commune-level matching and external verification via local news outlets, and corrected coordinates were reassigned to commune centroids where necessary.

Outbreak duration was calculated for WAHIS records using available start and end dates to characterise temporal patterns.

2.3 Clustering Assessment

Spatiotemporal clustering was assessed using SaTScan (version 10.1) (Kulldorff et al., 2005) with the space–time permutation model. This model detects space–time interaction without requiring population-at-risk denominators, evaluating whether cases are more concentrated in space and time than expected given the dataset's marginal spatial and temporal distributions.

Sequential Monte Carlo inference was applied to improve computational efficiency. Clustering was evaluated across multiple spatial (10, 50, and 100 km) and temporal (30, 60, and 90 days) window settings to assess scale sensitivity, yielding 9 parameter combinations per dataset. Clusters were compared across settings and between datasets using the number of significant clusters ($p \leq 0.05$), cluster radius, duration, observed case counts and test statistics, and spatial and temporal displacement between matched clusters.

Cluster agreement across parameter settings and between datasets was assessed using predefined spatial and temporal overlap criteria. Two clusters were considered matched if the centroid distance was less than or equal to 0.5 times the sum of their radii and if the temporal overlap proportion exceeded 70% of the union of their time intervals. Cluster persistence was defined as the proportion of parameter settings in which a matched cluster was detected. Clusters appearing in five or more settings (>50%) were classified as persistent signals.

Results

3.1 Data Quality

Data validation revealed structural inconsistencies in the WAHIS dataset, including approximately 5% duplicate events, primarily concentrated between December 2020 and February 2022, and 20% spatially mismatched records. Additionally, approximately 0.7% of outbreak coordinates were positioned outside the national boundary or in coastal waters. Spatial validation of WAHIS outbreak coordinates revealed substantial geolocation inconsistencies with reported administrative limits. A substantial proportion of records (17.6%; N = 125) were located 30–200 km outside their reported provincial boundary, with extreme outliers exceeding 300 km and reaching up to 1,000 km. The locality descriptions were heterogeneous and inconsistently defined, often referring to different political-geographic units, including communes, villages, streets, or informal place names. This variation substantially complicated automated geocoding and likely contributed to the misplacement of coordinates. However, cross-verification with contemporaneous outbreak reports published in online news sources enabled manual validation and correction of many affected records (8.5%, N = 61), highlighting the potential added value of triangulating surveillance data with publicly available outbreak reporting and opportunities to enhance internal troubleshooting steps in surveillance systems.

In contrast, EMPRES records showed consistent geolocation but included approximately 8% duplicate entries, mostly due to multi-species reporting. These findings indicate systematic geocoding errors in the database and highlight the need for spatial validation and correction prior to spatiotemporal modelling.

Theme 7

After de-duplication and harmonisation, 712 outbreak records were retained from the WAHIS dataset and 1,271 from the EMPRES dataset, covering the period 2006–2022. In the WAHIS dataset, the median outbreak duration was 25 days (mean 26.1 days; SD 8.0), and duration remained relatively stable over time. Most outbreaks were resolved within 3–4 weeks, consistent with established containment, culling, and quarantine procedures for highly pathogenic avian influenza. Prolonged outbreaks were uncommon, with a maximum recorded duration of 131 days, and likely reflect reporting delays or administrative closure processes rather than sustained farm-level transmission. Overall, the temporal stability of outbreak duration suggests a relatively consistent outbreak management cycle throughout the study period, despite marked fluctuations in outbreak incidence.

Notably, across 17 years of surveillance data, only one HPAI record involving a wild or non-domestic animal was identified in each dataset. In WAHIS, this record involved a non-avian animal, a captive civet, while in EMPRES the single non-poultry record corresponded to a farmed swift. No confirmed outbreaks in free-ranging wild birds were recorded in either dataset during the study period. This absence of wild bird records likely reflects limited wildlife surveillance and reporting rather than the true absence of infection.

3.2 Cluster Detection

Space–time permutation analysis identified marked differences in clustering structure between the EMPRES and WAHIS datasets across parameter settings. EMPRES consistently detected a higher number of significant clusters (40–55 across window combinations) compared with WAHIS (14–18), with clusters in EMPRES characterised by smaller median radii and shorter durations. Increasing spatial and temporal window sizes resulted in fewer but larger and longer clusters in both datasets, consistent with the merging of local outbreak signals into broader regional waves.

Persistent space–time clusters (detected in > 50% of 9 parameter settings) exhibited clear geographic structuring across Vietnam. Robust cluster centres were predominantly located in northern Vietnam, particularly within the Red River Delta and adjacent northeastern provinces, where multiple persistent signals were detected across both the EMPRES and WAHIS datasets. Additional stable clusters were identified in southern Vietnam, notably within the Mekong Delta region, although these were fewer and more spatially dispersed. Several persistent centres were also observed along the North Central Coast, forming a corridor of recurrent outbreak activity extending south from the Red River Delta. In contrast, the Central Highlands and much of the South Central Coast showed comparatively limited persistence, with only isolated recurrent cluster centres detected.

Notably, several northern hotspot areas were detected consistently in both datasets, suggesting recurrent amplification zones rather than parameter-dependent artefacts. However, slight spatial displacement between the EMPRES and WAHIS cluster centres within the same regions was observed, consistent with differences in geocoding precision or outbreak-aggregation. The spatial concentration of persistent clusters in northern Vietnam and parts of the Mekong Delta broadly corresponds to provinces with higher poultry density, suggesting that structural production intensity may contribute to recurrent outbreak patterns. Although poultry density was not formally incorporated into the clustering model, this alignment supports the plausibility of identified hotspots and indicates that integrating independent production data could help refine surveillance prioritisation. Areas with substantial poultry populations but limited persistent clustering may warrant closer examination to determine whether reduced detection reflects genuinely lower risk or potential surveillance gaps.

Discussion

4.1 Implications for Risk Modelling and Policy

The results have important implications for downstream modelling and decision-making. At fine spatial scales, such as 10 to 30 km, cluster detection proved highly sensitive to reporting granularity and coordinate precision. Fine-scale risk models that do not account for these structural differences may overestimate localised hotspots or interpret reporting artefacts as meaningful transmission dynamics.

In contrast, clustering using broader spatial windows of 50 to 100 km appeared less sensitive to coordinate variability and reporting granularity (Loth et al., 2021). However, given Vietnam's elongated and geographically narrow structure, larger spatial windows may also aggregate epidemiologically distinct areas, and results at these scales should therefore be interpreted cautiously. Persistent hotspots were consistently identified in northern Vietnam, particularly within the Red River Delta, and to a lesser extent in the Mekong Delta (Artois et al., 2016). These regions remained detectable across multiple analytical configurations and across datasets, suggesting structurally stable outbreak-prone areas rather than parameter-dependent artefacts.

Theme 7

The persistence framework applied in this study provides a practical approach to distinguishing robust signals from window-sensitive detections. Evaluating cluster stability across multiple spatial and temporal scales improves confidence in hotspot identification and strengthens the evidence base for targeted surveillance reinforcement and control strategies.

These findings highlight the importance of harmonised reporting standards and transparent metadata documentation in international surveillance systems. Clear outbreak definitions, consistent date attribution, and explicit reporting of geocoding precision would enhance cross-dataset comparability and improve the reliability of integrated analyses. Sensitivity analysis should therefore be considered an essential component of multi-source surveillance integration to ensure that modelling outputs reflect stable epidemiological patterns rather than artefacts of data architecture.

4.2 Surveillance System Limitations and Structural Differences

This comparative analysis indicates that differences in the spatiotemporal clustering patterns detected from WAHIS versus EMPRES data are largely attributable to structural characteristics of the surveillance systems rather than to underlying epidemiological differences. Several important limitations were identified.

First, duplicate inflation was evident, particularly in EMPRES, where outbreaks were sometimes recorded separately by affected species. Without rigorous harmonisation and deduplication, such reporting practices can artificially increase cluster counts and fragment outbreak signals. Second, inconsistencies in date attribution, including differences between outbreak onset and reporting dates, introduced temporal uncertainty that may shift cluster boundaries and influence measures of time overlap across datasets. Lastly, inconsistent and heterogeneous locality descriptors increase verification difficulty and constrain effective cross-dataset integration.

Spatial precision variability emerged as a major source of divergence. Outbreaks were geocoded at heterogeneous administrative levels, ranging from commune-level coordinates to district or provincial centroids. This variation influenced cluster radius, spatial displacement, and stability under smaller spatial windows. At fine scales, minor coordinate discrepancies substantially altered overlap assessments, whereas broader windows reduced sensitivity to geocoding heterogeneity. Differences in outbreak definition, particularly whether multi-species events were recorded as single or multiple outbreaks, further contributed to variation in cluster frequency and duration.

An additional limitation concerns the under-representation of wild bird surveillance data. Both WAHIS and EMPRES primarily capture reported outbreaks in domestic poultry, with relatively sparse and inconsistent reporting from wildlife surveillance systems. Given the recognised role of wild birds in maintaining and disseminating avian influenza viruses across regions, the detected clusters in this study predominantly reflect patterns within domestic production systems rather than full ecological transmission dynamics (Jindal et al., 2025). The absence of harmonised wildlife data limits interpretation at the wild–domestic interface and may underestimate pathways of introduction linked to migratory flyways. Incorporating structured wildlife surveillance data would improve ecological interpretation and strengthen One Health integration.

Together, these findings demonstrate that surveillance data structure directly shapes spatiotemporal inference.

Conclusion

Integrating multi-source avian influenza surveillance data provides valuable opportunities to strengthen outbreak detection and risk assessment. However, this study demonstrates that differences in reporting structure, geocoding precision, and outbreak definition substantially influence spatiotemporal cluster outputs. Rigorous data quality assessment, including harmonisation, deduplication, and spatial validation, is therefore essential before conducting integrated analyses or translating results into policy recommendations.

Our findings highlight the need for greater standardisation of outbreak definitions, date attribution practices, and geospatial reporting across surveillance systems. Without such standardisation, analytical outputs may reflect structural artefacts rather than epidemiological reality. By incorporating sensitivity analysis and persistence assessment, more robust hotspot identification can be achieved, supporting evidence-based surveillance prioritisation.

Theme 7

Overall, these results reinforce the importance of transparent, integration surveillance frameworks to enable reliable One Health data integration. Strengthening interoperability and metadata documentation will enhance the utility of integrated surveillance systems in Southeast Asia.

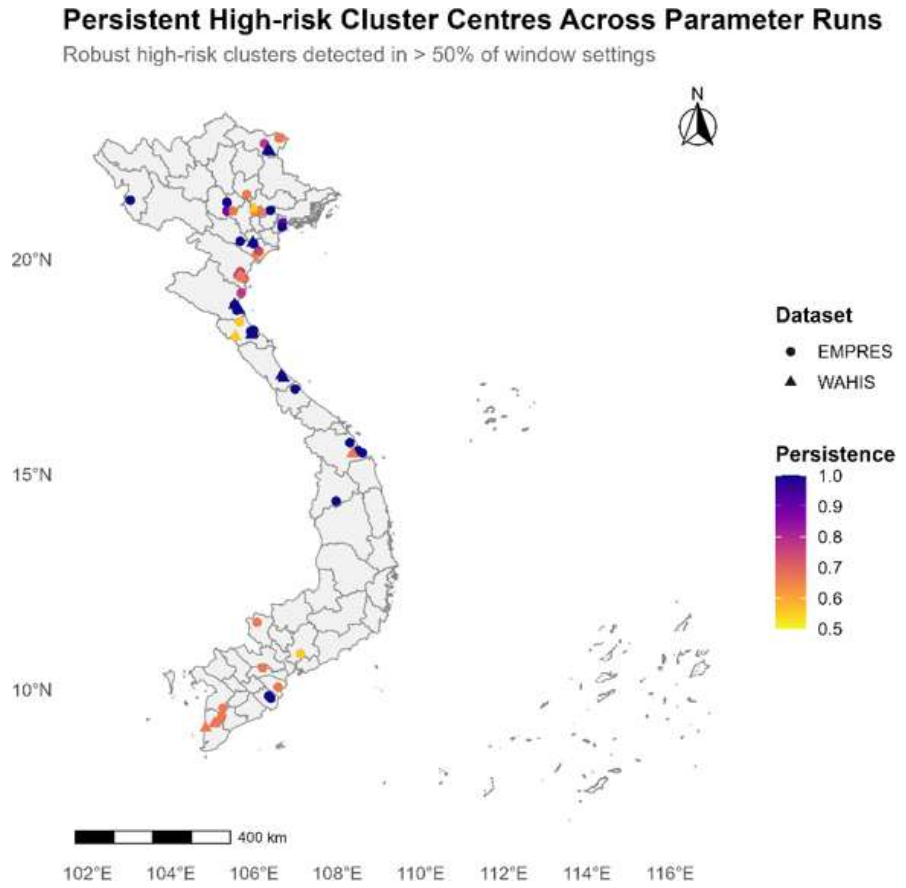


Figure 1: Spatial distribution of persistent space–time cluster centres identified across seven parameter settings in a comparative analysis of HPAI surveillance datasets in Vietnam, 2006–2022

Keywords: Panzootics, Surveillance integration, Data curation, Space-time clustering, Vietnam.

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Theme 7

A Generic Surveillance Framework for Assessing Illegal Meat Introduction Risk

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Summary

Illegal meat introduction poses unrecognised risks of disease introduction, a topic of shared concern among many countries. This work identifies the main pathways of entry of illegal meat and develops a model framework to assess the risk of illegal meat introduction. Air and land passengers were identified as two of the most relevant pathways of illegal meat introduction in the European area. Scenario analysis using synthetic data revealed up to a 2.9-fold variation in risk depending on traveller compliance, regardless of the border inspection sensitivity. Increasing inspection coverage from 0% to 100% produced a moderate reduction in overall risk with a 0.77-fold decrease under an inspection method with average detection sensitivity (Se=0.5), and high traveller non-compliance scenario (p_{carry} =0.5). Surveillance interventions tailored to a given epidemiological and trade reality could substantially reduce the risk of disease introduction from illegal meat. This framework model can be applied to countries where such data are available to help design targeted surveillance programs for specific disease and operational resources. Arrival data of travellers to relevant airports and ports, seizure data from border inspections and expert opinion can be used to parametrize tailored risk levels of illegal meat introduction into a specific area and subsequent disease introduction.

Introduction

The risk of introducing new and emerging diseases through illegal meat smuggling has been a longstanding concern for many countries. African Swine Fever (ASF) is one of these diseases that has increasingly come under the spotlight, as its spread poses significant economic and biosecurity threats to the global swine industry. There have been several instances where long geographic jumps of this disease have been reported in wild boar populations, which cannot be explained by natural animal moves (Dixon et al., 2019). This was the case for Belgium in 2018(Linden et al.), Sweden in 2023 (Chenais et al., 2024), and, most notably, with the introduction into the island of Sardinia (Dei Giudici et al.). The possibility of illegal movement of animals or animal products have been hypothesized as the most plausible cause for the introduction of ASF (Wooldridge et al., 2006). With globalization and the increased movement of people and goods, this concern has only grown in scale.

For the purpose of this work, illegal meat refers to products carried by individuals who have intentionally or unintentionally evaded established entry procedures by not being declared to authorities and that are in contravention of the personal concessions permitted. Illegal meat is considered one of the highest risk pathways for disease introduction due to its potential to harbour multiple pathogens and the absence of sanitary inspection. Nevertheless, the risks associated with these illicit animal products remain poorly defined, largely because limited data exists on their volume, origin, and pathogen load. Passenger baggage is one of the routes of introduction due to the low frequency of routine inspections conducted at borders. This is of particular concern in areas where freedom-of-movement agreements are in place, such as the Schengen scheme operating across many European countries (Costard et al., 2013).

When considering the risk of introduction of infectious diseases via trade, there is a tendency to focus on legal commercial routes. It is well understood that routes that circumvent legal procedures, such as veterinary inspections and health certificates in the exporting country, pose a risk. However, such routes are inherently hard to quantify to any degree of accuracy due to the lack of concrete available data regarding point of origin, point of entry and volumes of products. In this project we set out to put together a generic framework to illustrate the effects of inspection rates and sensitivity as a key component of surveillance modelling. This sets the path for a subsequent quantitative risk assessment to estimate the risk of illegal meat introduction posed by a specific route of concern and determine the feasibility of parameterising for any geographic area and surveillance setting.

The United Kingdom constitutes an interesting case study in that, despite being an island, it has a major land-based route of entry for both passenger and cargo via the port of Dover. As one of the country's busiest points of entry, Dover handles more than one third of the UK's goods traded with the EU (Port of Dover, 2024), making it a key gateway for international trade and, consequently, an important location for border control activities. Border control inspections across the UK have reported an upward trend in illegal meat seizures in the recent year. At

Theme 7

Dover specifically, the Dover Port Health Authority recorded a notable peak in early September 2025, with 10 tonnes of illegal meat seized in just two weeks (Dover, 2025). While this figure reflects intensified enforcement at that a particular port, it also illustrates the scale of the wider illegal meat challenge faced across the national border system. The risk associated with the introduction of illegal meat remains ever present and is influenced by the volume of passenger and consignment movements, which can place considerable pressure on border control resources.

Methods

Model Framework

Through literature review and discussion with experts in the field, we put together a framework consisting of six key routes of introduction of illegal meat (Figure 1, left). These routes covered different modes of transport (air, sea, road, rail) and purpose (commercial and personal). A detailed workflow that combines available data, both public and private, sets a generic framework to estimate the overall risk of disease introduction via illegal meat (Figure 1, right). Entry probability assessment of illegal meat is conducted prior to checks at customs or border inspection posts. Thus, all the confiscated products stopped or seized at border inspections together with the estimated products that have bypassed such controls are considered as an introduction event. The model does not consider the subsequent consequences nor exposure to the product given incursion. The model is coded in the R software package version 4.5.2 (R Core Team, 2025).

Figure 1. Overview of main pathways of introduction for illegal meat (left). To the right, overview of the final risk assessment framework to estimate the risk of disease introduction through illegal meat. Suggested data sources required to parametrize each step are provided in the text next to each blue box, with the equivalent parameter in the model shaded in grey. Highlighted in red is the step related to the work presented.

The number of undetected illegal meat introductions per inspection coverage c, $Undetected_{t,c}$, was given by Equation 1, $Undetected_c = p_{carry} * (1-c*Se)$ [1], where p_{carry} is the probability of illegal meat being carried, and Se, the likelihood that illegal meat is detected by a check if it is present. As such, (1-c*Se) represents the probability that illegal meat escapes detection. We assumed randomly allocated inspections, as opposed to risk-based. In the estimation of absolute disease introduction via illegal meat applied to a specific case scenario, the proposed Equation 2 can be used: $Undetected_{c,r} = \lambda * p_{carry} * p_{contam} * (1-c*Se)$ [2], where λ corresponds to traffic level, quantified as number of travellers or the volume of traded goods, according to the specific route r, and p_{contam} is the probability that carried meat is contaminated with a hazard of interest (e.g., ASFv).

Parameterisation

To ensure the framework is generic and applicable across diverse border control contexts, we developed a scale free, dimensionless model where risk depends only on behavioural and inspection parameters rather than absolute traffic volumes. We explored risk across combinations of different inspection coverage rates (0%, 1%, 10%, 15%, 30%, and 100%), detection sensitivities (0.3, 0.5, and 0.7), and the probability that travellers carry illegal meat (0.1, 0.25, and 0.5). This approach avoids dependency on operationally sensitive traffic data while revealing general behavioural and surveillance dynamics relevant to a wide range of ports and jurisdictions.

Seizure data collected by enforcement bodies and port health authorities was used to estimate the quantity of illegal meat that is introduced in the country throughout the year. Data included number of seizures, weight of the seized products, date and seizing port, checks without seizures and total staff time performing inspections, which allowed to parametrize c, Se and p_{carry}. Given their sensitive nature, these data are not presented in this work.

The probability of carrying an illegal product, p_{carry}, when set to 0.5, simulates a hypothetical worst-case scenario where compliance with legislation is low and assumes one in two visitors or consignments contain illegal meat. Conversely, a value of 0.1 suggests high compliance with existing restrictions and a lower risk of illicit goods being introduced. Detection sensitivity (Se) reflects the fact that detections are imperfect, even at high inspection rates. The chosen values aim to represent different inspection techniques, such as visual inspection, X-ray screening, and sniffing dogs. Operational intelligence from border inspection teams can inform the selection and calibration of these parameters according to higher-risk areas or seasonal risk peaks.

Results

Theme 7

Passenger baggage was highlighted as the biggest contributor to the risk of hazard introduction through illegal imports (expert opinion). The scenario analysis comparing different detection sensitivities and compliance levels reveals that traveller compliance is a key factor to significantly reduce risk. Across inspection sensitivity scenarios, risk decreased non linearly with inspection coverage.

For the traveller cluster with the poorest compliance with the rules (i.e. p_{carry}=0.5) with medium to low detection sensitivity methods, even the highest of inspection rates are insufficient to drop the risk of illegal meat introduction below 20%. This highlights that enforcement of inspections alone is not enough to reduce the risk. A combination of measures is required to further reduce the risk to low values, i.e. 10% or lower, which includes raising awareness among travellers to increase compliance with law (i.e., reduce p_{carry}), targeting inspections, use of more sensitive inspection methods (increase Se), such as detection dogs.

Discussion

Estimating the volume of illegal meat introduction into a country is highly dependent on the resources available for border inspections. By definition, these resources cannot detect all illicit products, and the absence of seizures does not equate to an absence of risk. In this study, we evaluated effect of inspection rates performed at different intensities and using different sensitivity strategies.

This analysis showcases a generalisable, dimensionless model that visualizes the effect of inspection risk relationships across different surveillance scenarios. Further, the risk function can be tailored to actual arrival values (λ) of an airport or port of interest, risk levels (probability of specific areas where disease is present), and passenger compliance (p_{carry}) to give absolute figures for risk introduction of a disease, such as ASF, via illegal meat. This approach can also be applied to compare risk across different ports of entry, seasons, or transport modalities (e.g. passenger versus cargo).

Illegal meat introduction is shaped by a complex set of behavioural and socioeconomic factors, including lack of awareness of biosecurity risks, cultural food carrying practices, and demand for traditional or medicinal animal products. A comprehensive analysis integrating social behavioural components would strengthen risk assessments and support the design of more effective communication and intervention strategies.

Sanitary and phytosanitary (SPS) inspection levels have increased at selected border points in Great Britain in response to elevated risks associated with ongoing disease outbreaks in Europe and beyond. Within the UK's current border biosecurity framework, the Border Target Operating Model (BTOM), the Department for Environment, Food and Rural Affairs (Defra) determines inspection rates based on the risk categorisation assigned to each commodity and country of origin. The BTOM has been operationalised in recent responses to outbreaks of Foot and Mouth Disease (FMD) and African Swine Fever (ASF) across the continent (House of Commons, 2026). Identifying high-priority surveillance areas, such as those highlighted in this work, can support the targeted allocation of limited inspection resources toward port practices or characteristics that pose the greatest risk. The traffic volume at the port of entry can also play a decisive role in the overall risk of introduction, especially if effective inspection rates cannot be guaranteed.

Future research

The data currently available will enable to assess the risk of disease introduction into Great Britain via illegal meat carried by air and land travellers, applicable to diseases preset in travellers' countries of origin. In collaboration with other European partner Institutes, future work will apply this model to actual traffic data and incorporate European wide passenger flows, including major hotspots linked to long distance land and air travel. This would enable estimation of the risk of ASF entry and spread across the European Union.

Seizure data explored in this work (not shown) reflects resource availability and targeted interventions at the time of collection. A key limitation is that these data represent a temporal snapshot from a specific surveillance operation. Because illegal imports fluctuate throughout the year, the analysis may either overestimate or underestimate annual risk. For example, if the spot checks occurred during a period when visitors were more likely to carry food products, annual extrapolation would lead to overestimation. Conversely, if inspections took place during a low traffic period, estimates would underestimate the true scale of illegal meat introduction. Without year round enhanced inspection, it is not possible to determine where within this spectrum the snapshot lies. The analysis further assumes that these trends remain stable across successive years.

Inspection coverage is also partial: only a fraction of entries are inspected, typically at random, and therefore inspections are unable to provide a comprehensive picture of the full range of illegal items crossing the border.

Theme 7

We assume the proportion of seized items is representative of the total influx of traffic, although this assumption introduces additional uncertainty. Nevertheless, inspections in this dataset were performed across the entire week, including weekends, meaning the estimates are not affected by weekday bias.

In order to better understand how many illegal meat items pass borders undetected, it would be ideal to introduce a correction factor derived from the identification of illegal meat products already circulating within national food outlets. Such findings could provide an external validation layer for border seizure based estimates and help quantify the proportion of items that evade detection. Integrating this type of downstream surveillance, whether through market inspections, retail audits, or targeted sampling, would strengthen the capacity to approximate the true burden of illegal meat introduction and reduce uncertainty in model outputs.

Conclusion

Illegal meat poses a considerable risk of disease introduction, with passenger baggage and traveller compliance to rules as the highest risk contributors to meat smuggling. Despite the inherent challenges and uncertainties associated with estimating illegal meat introduction volumes, the present work provides a general framework to estimate the risk of hazard introduction applicable to different border posts when seizure data is available. Seizure data is often considered a sensitive topic that involves many different actors, which hinders data availability and consistency. Standardizing and centralizing these data would improve estimates and contribute to an improved intelligence, enhanced trust with trading partners and overall health assurance for animal and human populations. Effective inspection planning requires quantifying how different coverage levels translate into probability based risk bands across port operational practices, as well as by identifying data inputs that have the greatest impact on decision uncertainty.

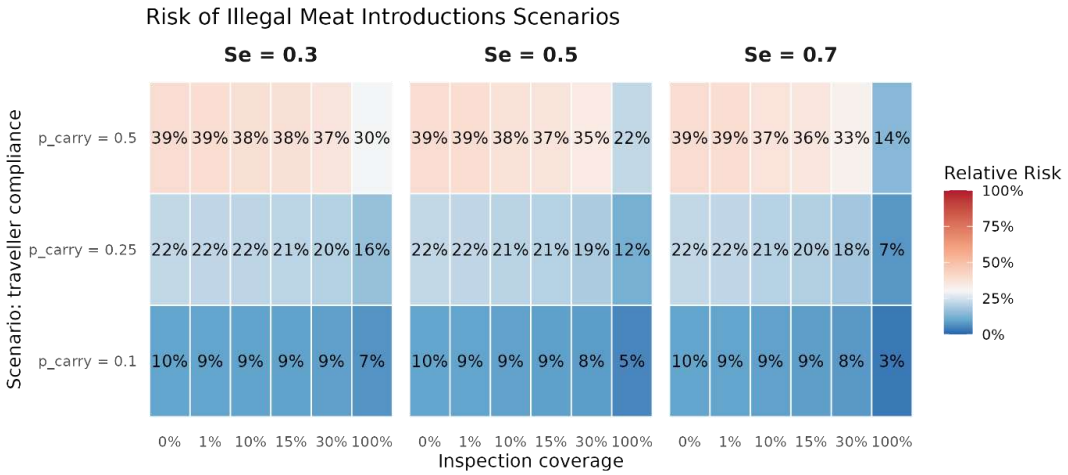


Figure 2. Relative probability of illegal meat introduction for different inspection intensities and traffic level of the port of entry. Se: detection sensitivity; p_{carry}: probability of carrying illegal meat.

Keywords: surveillance modeling, international trade, illegal meat, Border biosecurity, Inspection strategies.

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Surveillance for farm-to-farm wind dispersion during outbreaks of highly pathogenic avian influenza in southeastern Australia: from integrated research to decision-making

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Summary

Although spatio-temporal clustering of outbreaks of highly pathogenic avian influenza has been consistently observed, there is little agreement as to the exact transmission mechanism. This in turn creates challenges in developing and implementing efficient surveillance. Building on advances in atmospheric dispersion modelling, a structured, modular approach ("SPREAD-HPAI") was developed which should enable veterinary authorities to define the epidemiological and atmospheric conditions under which farm-to-farm wind dispersion (FFWD) occurs. However, a challenge is the lack of fundamental research on which to base model parameters, and to overcome this we present a framework which serves to both identify research priorities and to assemble the interdisciplinary team needed to resolve the uncertainties.

Introduction

Outbreaks of highly pathogenic avian influenza (HPAI) in Australian commercial poultry have a unique virology, all being caused by distinct lineages of H7 strains [2]. These strains have been shown to circulate in the low pathogenic form in wild ducks in Australia with sporadic spillovers to commercial poultry [3]. Previously these spillovers were sporadic and confined to only one or two infected premises (IPs). However, in recent years these outbreaks have increased in frequency and seriousness, particularly with respect to farm-to-farm spread within defined spatio-temporal clusters.

The exact pathway of transmission of the HPAI viruses between farms is uncertain, as the secondarily infected premises (IPs) have generally had in place high standards of biosecurity. There is evidence, albeit somewhat

Theme 7

anecdotal, from field investigations of outbreaks in Europe and North America of the role of windborne fine dust aerosols as a transmission pathway [4]. However, confirming farm-to-farm wind dispersion (FFWD) has proved challenging using conventional field sampling [5], which indicates the need for novel approaches. Herein, we describe the development of a holistic approach which combines field epidemiology, laboratory investigative experiments and integrated epidemiological-environmental modelling with the goal of arriving at outbreak surveillance system to inform farms at risk of aerosol transmission and to inform infected premise (IP) management to minimise risk of onward transmission.

Methods

The development of a FFWD surveillance system for HPAI outbreaks is an evolving series of projects which has as its origin the investigation of an outbreak of HPAI H7N7 in southern Victoria in July/August 2020. This outbreak involved 3 IPs, with the virus being detected in IP2 and IP3 within three weeks of that in the index IP. All three IPs had a high standard of biosecurity and whilst the pathway of infection of IP3 is uncertain, integrated environmental and epidemiological modelling provided evidence that a plausible pathway of infection of IP2 was FFWD, with the latter conclusion supported by a network analysis of full viral genomes collected during the outbreak [1].

Further outbreaks of HPAI occurred in both Victoria and New South Wales in 2024, during which there was a general consensus between both the industry and veterinary authorities that FFWD might have been responsible for transmission to some of the secondary IPs. This led the industry, via its research funding body, Australian Eggs, to request an investigation into aerosol spread during destruction and disposal on HPAI-infected farms in an outbreak response. Industry is now funding integrated studies to quantify the emission of fine dust aerosols from sheds at end-of-production (field study) and the viability of HPAI virus in shed litter substrates under different environmental conditions (laboratory study) to improve understanding of factors that prolong virus viability within layer sheds.

The findings of these studies will subsequently be integrated in the epidemiological-environmental modelling framework SPREAD-HPAI to investigate the epidemiological and atmospheric conditions which favour farm-to-farm wind dispersion (FFWD).

Results

At the outset of the investigation of the farm-to-farm transmission of H7N7 HPAI in Victoria in 2020 outbreak, a literature review revealed that there was little consensus amongst virologists on whether aerosol transmission of avian influenza virus might occur over inter-farm distances of 1-10 km. Nevertheless, there was a broad agreement in the aerobiological community that a suitable approach for investigating windborne dispersion of pathogens was to define three sequential stages, viz. “emission”, “transport” and “deposition” [6]. This approach was built into an integrated field and genomic epidemiology system to investigate farm-to-farm transmission of foot-and-mouth disease virus (FMDV), which we had formalised into a software application SPREAD (System for Preparedness and Response to Emergency Animal Disease) [7]. SPREAD-FMD provided an exemplar to develop SPREAD-HPAI. Given the urgency to resolve the role of FFWD in the transmission of HPAI during outbreaks in Australia, initial investigations with SPREAD-HPAI involved a global sensitivity analysis to guide research priorities, which identified the potential impact of culling operations on the production of fine dust (Figure 1a).

Now, our studies are underway, with field sampling that has quantified the production of fine dust (PM10 and PM2.5) during routine culling of layer hens and litter disposal at the end of production (Figure 2), activities which approximate the impact of depopulation, disposal and decontamination during the management of a HPAI outbreak. The associated laboratory study is studying the impact of environmental conditions - principally temperature and humidity - on the viability of avian influenza viruses on litter substrates.

Discussion

During the past 50 years, considerable progress has been made in developing efficient surveillance systems for production animal diseases [8]. However, there remain disease scenarios which continue to be problematic. Most obvious is where there is the lack of a sensitive diagnostic test for diseases with long incubation periods, but a second challenging problem arises where the transmission pathway is variable and/or uncertain. With regards to the specific example of HPAI this uncertainty is well illustrated from a recent investigation of H5N1 2.3.4.4b outbreaks during 2022-23 in British Columbia, wherein integrated field and viral genomic epidemiological investigations were not able to assign the transmission pathway for the majority of the 127 infected commercial premises [9]. Rather, for 82 of the IPs, the pathway was assigned to be “local spread” which

Theme 7

was defined as occurring if a secondary IP was genetically and spatially connected but no epidemiological links were identified. The exact transmission pathway for local spread could not be further defined, and although windborne spread was listed as one of these mechanisms, this was not specifically assessed due to limitations in available weather data and microclimates in the Fraser Valley, the principal affected site.

In the case of the relatively small H7N7 HPAI cluster in 2020, initial investigation encountered the same problem of not having weather data at a high spatio-temporal resolution, but this was resolved by engaging with climatologists and pollutant dispersion modellers. Combining weather data with a high-resolution atmospheric dispersion model, enabled hourly simulations at a very high spatial resolution. The results from this dispersion modelling were instructive showing that potential transmission of virus by FFWD might occur for only one or two hours in a day. By contrast, investigation limited to averaged daily wind directions - as has been used by comparable investigations [10]- would have incorrectly concluded that FFWD was unlikely.

Having demonstrated that FFWD was plausible, the next step was to determine if it was the probable pathway. Undertaking a sensitivity analysis of the SPREAD-HPAI output demonstrated the overriding importance of the concentration of contaminated dust into downwind farms. This requires that we develop a model for fine dust emission from poultry sheds which also accounts for the viability of the virus on the surfaces from which the fine dust is produced. We are now achieving this by the combined expertise of a team of domain specialists, viz. aerobiologists familiar with dust sampling and virologists experienced with the culture of avian influenza viruses, along with experts in poultry health, epidemiology and biosecurity who have strong industry linkages.

At this stage (April 2026), the field and laboratory work is still too preliminary to make definitive conclusions. However, what is recognised by both the industry and the funding bodies is the benefit of using a modelling framework to define the most important research gap and to specifically assemble interdisciplinary teams of domain specialists who can apply their knowledge and expertise to enable field and laboratory studies. This experience suggests that this might be a useful and generalisable approach for complex surveillance and disease control problems (Figure 1b).

Acknowledgements

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Theme 7

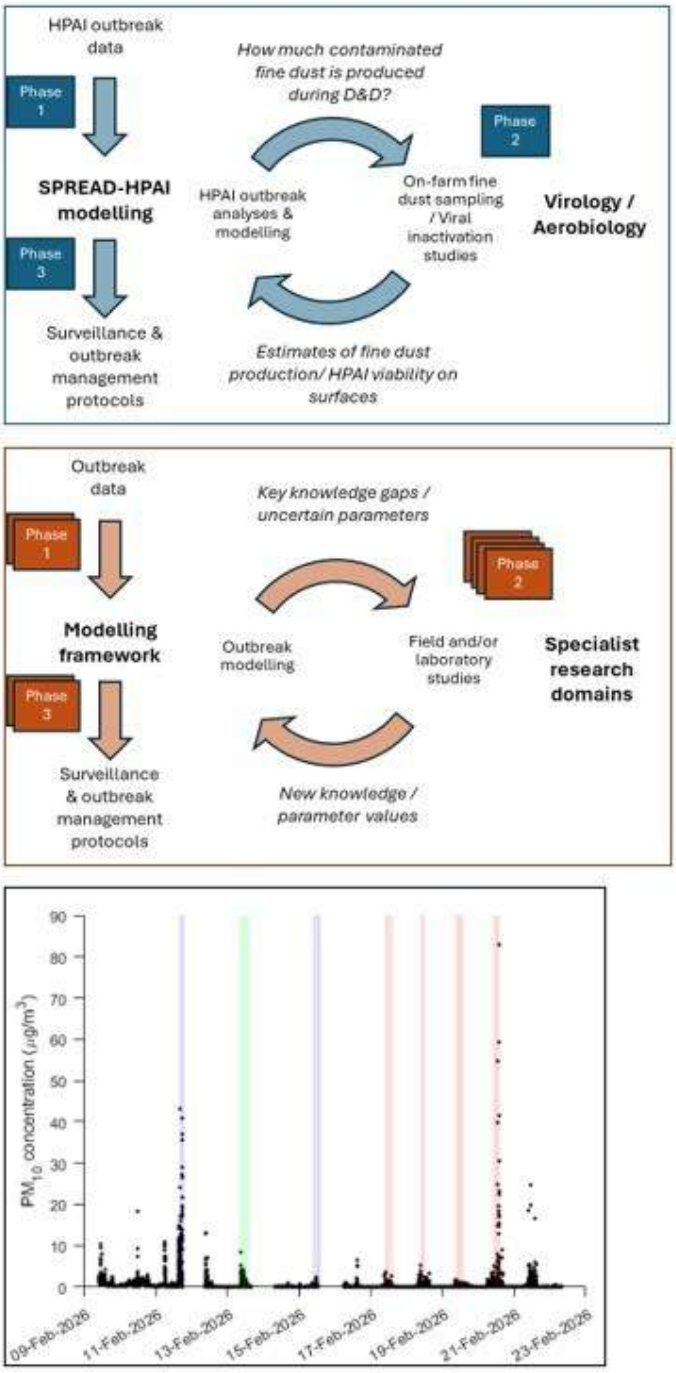


Figure 1a. Schematic of the research path for developing an integrated research framework and enhanced surveillance for managing farm-to-farm wind dispersion of contaminated dust aerosols in commercial layer flocks. Figure 1b. Generalised framework for developing an integrated research surveillance system. This generalised framework may go through a number of iterations which, with increasing knowledge, can lead to a "virtuous cycle". Figure 2. Field sampling of fine dust (PM10) from a commercial layer shed during routine end-of-lay depopulation and decontamination. Blue are cull periods, green is dry cleaning and red is manure removal.

Keywords: Farm-to-farm windborne dispersion, Highly pathogenic avian influenza, Integrated surveillance system.

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The impact of the age structure in Dutch dairy herds on surveillance indicators

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Summary

Understanding how demographic structures influence routinely monitored indicators is essential for accurate interpretation of cattle health surveillance outputs. Using near census data from the Dutch Cattle Health Surveillance System (CHSS), this study quantified how dam age contributes to variation in key surveillance indicators, including perinatal, postnatal and pre weaned calf mortality, as well as twin births. More than 2.4 million dairy cows were evaluated (2019–2023), and multivariable mixed effects logistic regression models were applied across dam age categories (<3 years, 3–5 years, 6–8 years, >8 years) while accounting for herd level and temporal factors. Younger (<3 years) and older (>6 years) dams showed elevated odds of perinatal mortality compared with the reference category, and young cows also exhibited higher postnatal mortality risk. Twin births followed a clear age dependent pattern, peaking in mid aged cows before declining in the oldest group. Dam age demonstrated the strongest association with each surveillance indicator relative to other herd level factors. These results show that shifts in herd age structure - such as those driven by longevity strategies - can meaningfully influence national surveillance trends. Incorporating dam age structure into the design, interpretation and communication of operational monitoring systems is therefore essential to avoid misinterpretation of demographic variation as emerging health problems. This surveillance informed understanding supports more accurate signal detection and more reliable policy and management decisions within the dairy sector.

Introduction

Routine animal health surveillance systems in dairy production are primarily designed to monitor key health and performance indicators over time. These systems enable the continuous assessment of population-level outcomes, such as calf mortality and reproductive performance, and support the identification of trends, shifts, and emerging risk patterns within herds.

Effective monitoring requires understanding how structural changes in the population influence observed indicators. Animal health can change for multiple reasons, including emerging diseases, management or sectoral developments, and demographic shifts such as ageing of the herd. In recent years, increased dairy cow longevity has altered herd age structure. Consequently, trends in monitored indicators may reflect not only true health or management changes, but also demographic composition. Distinguishing between these causes is essential for correct interpretation of surveillance outcomes. Dam age can potentially explain observed variation

Theme 7

in several routinely monitored indicators. Young cows, particularly primiparous heifers, have an increased risk of dystocia due to incomplete skeletal development, contributing to higher perinatal mortality (1, 2). At the other end of the age spectrum, older cows experience age-related declines in reproductive efficiency and increased susceptibility to metabolic disorders, which may affect calf survival (3). In addition, the probability of twin pregnancies increases with age and production level due to higher rates of double ovulation (4). Twin births are associated with a range of adverse outcomes, including dystocia, retained placenta, metabolic disease, reduced fertility, and increased culling (5), and are therefore relevant to monitor alongside mortality indicators.

Despite the routine availability of these indicators, limited insight exists into how variation in dam age contributes to observed patterns in monitoring data at population level. In particular, the combined effect of age structure on both calf mortality and twinning remains insufficiently quantified, while accounting for herd-level and temporal variation. Improved understanding of these relationships is necessary to correctly interpret monitored trends and to identify meaningful deviations from expected patterns. This study aims to quantify how dam age contributes to variation in routinely monitored indicators within a national cattle health surveillance system. Specifically, the study:

- Quantifies associations between dam age and perinatal, postnatal, and pre-weaned calf mortality, as well as twin births, using large-scale monitoring data;
- Evaluates how differences in herd age structure influence observed patterns in these indicators over time;
- Supports improved interpretation of monitoring outputs by identifying age-related baseline patterns and risk profiles.

Material and methods

Study population

Data originated from the Dutch Cattle Health Surveillance System (CHSS), which includes near census information from approximately 98% of Dutch dairy herds. Records from the first quarter of 2019 to the fourth quarter of 2023 were analysed, comprising data of on average 2.43 million female cattle per quarter.

Definitions

Dam age was recorded quarterly. Mortality and twinning outcomes were defined as:

- Perinatal mortality: death before the moment of ear tagging i.e. late abortions, stillborn or death within 3 days after birth since it is mandatory by law to tag newborn calves within a maximum of 3 days after birth.
- Postnatal calf mortality (0–14 days): liveborn calf received an ear tag but died ≤14 days.
- Pre-weaned calf mortality (15–56 days): death between 15 and 56 days.
- Twin births: >1 calf per calving.

Data cleaning and processing

Encrypted raw data from different data sources (including data on cattle movement registrations, milk production, herd health statuses and veterinary registration of antimicrobial deliveries) were imported into SAS 9.4 for validation and processing. Records were checked for biological plausibility, internal consistency, and completeness; implausible values were set to missing. All datasets were merged into a single analytical file structured at the cow quarter level. Each cow received one record per quarter, regardless of whether a calving occurred. For descriptive analysis, proportions of calvings resulting in each outcome were calculated for each dam age category (year) per quarter of the year within the analysed period. Standard errors were included and visualised in plots to reflect precision.

Model structure and statistical analysis

To evaluate associations between dam age and each outcome, multivariable mixed effects logistic regression models were fitted using Stata 17. Dam age was the primary variable of interest and was categorised as: <3 years, 3-5 years, 6-8 years, or >8 years. These categories reflect biologically meaningful stages of the productive lifespan and ensured adequate sample sizes. For each quarter, calving events were identified and outcomes assigned sequentially:

- If a calf was born, it could either be alive or dead during the perinatal stage
- If a calf was ear-tagged, it could subsequently live until 15 days old or die during the postnatal period
- If a calf entered the pre-weaned stage, it could either die during this period or live and enter the weaned period at 56 days old.
- If a calving took place, it was evaluated whether more than 1 calf was born, indicating a twin birth.

Theme 7

Each model included a random cow-level and herd-level variable, and included other explanatory variables such as herd size, milk production level, region, season and trend in time. Because of computational constraints in handling 48 million records per outcome, each model was fitted using random subsamples of up to 5 million cow quarter records. Each model was repeated three times. Results were considered stable and robust when ORs and CIs were nearly identical across runs.

Results

The proportion of older cows (>8 years) increased from 3.3% in Q4 2019 to 4.6% in Q4 2023. Perinatal calf was highest in dams <3 years (10.1%), lowest in 3–5 year-old dams (4.3-4.7%) and increased again in older age groups (5.3-7.4% in cows >8 years). Postnatal calf mortality (≤14 days) and pre-weaned calf mortality (15–56 days) were similarly highest in <3 year dams and declined and stabilized gradually in older cattle. Twin births were at their lowest in cows <3 years (around 0.5%), peaked at 6–8 years (~4.1%) before declining in >8 year dams (around 3% in cows ≥13 years) (Figure 1).

Multivariable results

The multivariable models showed that dam age was strongly associated with calf mortality and twin births. A dam younger than 3 years was associated with higher odds of perinatal calf mortality compared with the reference category (OR = 2.30; 95% CI: 2.24–2.35). Calves with dams aged 6–8 years also had increased odds of perinatal mortality (OR = 1.19; 95% CI: 1.16–1.22), as did calves with dams over 8 years old (OR = 1.54; 95% CI: 1.47–1.61). Across all explanatory variables included in the model, dam age showed the strongest association with perinatal calf mortality.

For postnatal calf mortality, associations with dam age were also observed. Young ear tagged calves (≤14 days old) with dams younger than 3 years had increased odds of mortality (OR = 1.10; 95% CI: 1.06–1.14), whereas calves with dams aged 6–8 years had lower odds (OR = 0.96; 95% CI: 0.93–1.00). Calves with dams >8 years were associated with higher odds for calf mortality (OR = 1.07; 95% CI: 1.00–1.14), however this association was not significant (P=0.06). The model for pre-weaned calf mortality did not converge. As a result, no adjusted effect estimates are reported for this outcome.

Dam age was also strongly associated with the occurrence of twin births. Cows <3 years had lower odds to give birth to more than one calf (OR = 0.19; 95% CI: 0.18–0.20), whereas cows aged 6–8 years (OR = 1.33; 95% CI: 1.29–1.37) and >8 years (OR = 1.27; 95% CI: 1.20–1.35) had higher odds of twin births compared to cows 3-5 years. These age-related effects were stronger than those observed for other explanatory variables in the model.

Discussion

This study demonstrates that dam age is a major determinant of variation in routinely monitored indicators such as calf mortality and twin births. The observed associations show that herd demographic composition substantially influences the levels of these indicators. This has direct implications for how monitoring results are interpreted within animal health surveillance systems.

Monitoring systems are designed to identify unusual changes or emerging problems over time. However, indicator levels are not only influenced by health events or management factors, but also by structural characteristics of the herd. The results show that dam age is one of these structural characteristics. Differences in age distribution between herds, or gradual shifts in age structure over time, can therefore influence observed mortality and twinning rates independently of new or emerging disease issues. Moreover, age structure is also essential when comparing populations, as differences in calf mortality between herds or regions may partly reflect demographic composition rather than true differences in health status.

The elevated perinatal mortality observed in young cows (<3 years) is consistent with known risks related to dystocia and reduced neonatal vitality in primiparous heifers (1, 2). In monitoring practice, herds with a relatively high proportion of young animals may show persistently higher perinatal mortality compared with herds with a higher proportion of mature cows. Without considering age composition, such differences could be misinterpreted as deteriorating herd performance.

Theme 7

In older cows, increased perinatal mortality likely reflects age-related physiological changes, including greater susceptibility to metabolic disorders (3). At the same time, the absence of a strong progressive increase in mortality suggests that increasing longevity does not automatically lead to marked increases in monitored calf losses. The clear age-dependent pattern in twin births further illustrates how demographic composition influences monitoring results. Because twin pregnancies are associated with adverse health and performance outcomes (4, 5), rising twinning rates may attract attention within surveillance systems. However, the findings indicate that such increases may partly reflect a higher proportion of older cows rather than new reproductive problems. Interpreting twinning rates in relation to age structure can therefore improve the accuracy of monitoring conclusions.

Several limitations should be considered. Misclassification of dam age due to quarterly recording may have slightly weakened observed associations. Moreover, age was the only cow-level factor in the models while other variables were on herd-level. In addition, breeding strategies, such as the use of beef semen in older cows, may influence calf outcomes and interact with age effects.

Overall, this study shows that demographic structure, and dam age in particular, is essential for correctly interpreting routinely monitored calf mortality and twin births. Incorporating age distribution into monitoring frameworks can improve the detection of meaningful changes while reducing the risk of false alarms, thereby strengthening the effectiveness of animal health surveillance systems.

Conclusion

Integrating dam age into routine monitoring frameworks is essential to correctly interpret variation in calf mortality and twin births. This improves the performance of surveillance systems by reducing misinterpretation and supporting more reliable identification of true health signals

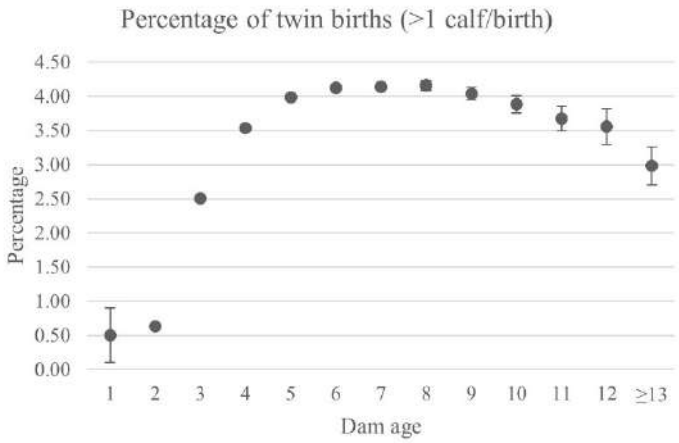


Figure 1. Percentage of twin births (at least two calves born per birth) per age group of dams (varying between one and ≥13 years old).

Keywords: Dam age, Calf mortality, Twin births.

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Theme 7

Impact of post slaughter broiler meat treatments on human disease risk from *Campylobacter* contaminated meals

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SUMMARY

Campylobacter is a major cause of foodborne gastroenteritis worldwide, with poultry meat as the primary human exposure route. This study quantified how two post slaughter meat treatments—slurry ice carcass cooling and high oxygen modified atmosphere packaging (MAP O_2 with ≈ 80% O_2 and 20% CO_2)— can affect human *campylobacteriosis* risk from broiler meals in Denmark. Here, MAP O_2 is commonly used to extend product´s shelf life, whereas slurry-ice is not yet applied extensively, but appears promising for faster carcass chilling. Recent field studies indicated that both treatments reduce *Campylobacter* concentrations (colony forming units per gram, cfu/g). We used 2024 Danish surveillance data from four slaughterhouses (SA–SD), consisting of leg skin (LS) concentrations from 1,296 flocks. These data were integrated into the quantitative microbial risk assessment (QMRA) model from the Danish Action Plan for *Campylobacter*. Human average risk per meal was estimated for both monthly and annual surveillance periods. Next, the relative risk (RR) was defined as the ratio between scenario specific risk estimates and the baseline mean risk from 2019–2021. Six scenarios were evaluated: a reference scenario (without considering any meat treatment) and five mitigation scenarios using slurry ice, MAP O_2, or their combination. Treatment specific reductions in concentrations, when changing from the reference to a mitigation scenario, were taken from recent Danish research. Next, two Generalized Estimating Equation (GEE) models, were used to assess statistically significant effects on concentrations and related apparent flock prevalence (AP), which affected the risk estimates. Slurry-ice produced a 7% reduction in the overall annual RR, while MAP O_2 caused much larger effects across seasons and slaughterhouses, lowering the annual RR by 67–84%. GEE analyses confirmed significant pairwise interactions of season, slaughterhouse, and scenario, with MAP O_2 giving the strongest AP and concentration reductions during summer, especially at higher risk slaughterhouses. Overall, MAP O_2 emerges as an effective post slaughter risk mitigation measure.

1. INTRODUCTION

Campylobacter spp. infections remain a major cause of foodborne bacterial gastroenteritis worldwide. Poultry meat is consistently identified as the leading source of consumers exposure, largely due to contamination during slaughter and processing [1]. Faecal leakage and cross contamination (e.g. through contaminated equipment) can spread the pathogen onto carcasses. Although chilling can reduce bacterial survival, *Campylobacter* may persist on fresh poultry products and be transferred to consumers through improper handling and/or insufficient cooking.

Denmark operates a comprehensive surveillance and risk assessment system under the National Action Plan for *Campylobacter* [2]. Central to this system is a quantitative microbial risk assessment (QMRA) model from Nauta et al. [3], which integrates flock prevalence, carcass contamination, consumer handling, and dose–response modelling. Previous Danish work using this framework has shown that flock prevalence varies remarkably across farms, slaughterhouses, and seasons [2]. Summer months consistently display higher flock prevalence and human incidence. Within this context, recent Danish research [4, 5] investigated effects of post slaughter meat treatments—i.e. those applied before retail—on *Campylobacter* meat concentrations. Those treatments were:

a) Slurry ice spraying [5]. Currently, not systematically applied in Danish slaughterhouses.
b) Modified atmosphere packaging (MAP), with high oxygen concentrations (i.e. MAP O_2 with ≈ 80% O_2 and 20% CO_2) which is already widely implemented in Denmark for retailed poultry meat [4].

The aim of this study was to assess the effects of slurry-ice and MAP O_2 on the risk of human *campylobacteriosis* posed by a *Campylobacter*-contaminated broiler meal, according to the new science-based information from Calvo-Fernandez et al. [4, 5].

Theme 7

2. MATERIALS AND METHODS

2.1 Surveillance data

Surveillance data from 2024 were obtained from the Danish Veterinary and Food Administration. The dataset included 1,330 leg skin (LS) samples (one sample per flock) collected at the four main Danish slaughterhouses referred here as: SA, SB, SC, and SD. After data handling (i.e., keeping formatted flock-ID identifiers), 1,296 flocks were maintained. Metadata included: slaughter date, flock-ID, flock type (organic or conventional), farm-ID (CHR), slaughterhouse, and culture results (in colony forming units per gram, cfu/g). Apparent flock prevalence (AP, not corrected for test performance) was defined as the proportion of flocks with contaminated LS samples ≥10 cfu/g. Data handling, descriptive statistics and statistical analysis were carried out in the free software R (version 4.5.2).

2.2 The QMRA model

The QMRA model estimated average monthly and annual probabilities of human illness from a broiler-based meal. Next, the relative risk (RR) was estimated, to compare the 2024 (monthly and annual level) risk per serving against the average risk from the three-years period 2019–2021, representing the baseline risk within the Action Plan. The model preserves consumer behaviour and dose-response variability constant across scenarios and surveillance periods, ensuring that RR changes stem from scenario specific surveillance inputs (i.e. data-driven) [2].

2.3 Risk mitigation scenarios

Six risk assessment scenarios were investigated: a reference (ScenRef = no mitigation) and five mitigation scenarios applying slurry ice, MAP O_2 or both, based on different concentrations reduction factors. Accordingly, six scenario data tables were created (each including the 1,296 flocks with adapted concentrations) and fed independently into the QMRA model. Percentage (relative) reduction factors for *Campylobacter* concentrations (used to create the different scenarios), were set considering different meat cuts:

- ScenI (slurry-ice on LS): 10.9% cfu/g reduction [5]
- ScenII (MAP O_2 on neck skin): 84.5% [4]
- ScenIII (MAP O_2 on breast fillet): 94.2% [4]
- ScenIV (average of ScenII and ScenIII): 90.6%
- ScenV (slurry ice + MAP O_2): i.e. ScenIV reduction applied on values from ScenI

Descriptive statistics on APs and meat concentrations distributions (across positive flocks) were carried out for each scenario, quarter of the year (Q1-Q4) and slaughterhouse.

2.4 Statistical analysis

For the statistical analysis the six scenario tables used in the QMRA model, were combined into an overall analytical dataset. Next, two Generalized Estimating Equation (GEE) models were fitted: i) a binary (logistic) GEE model considering response variable: flock result = positive or negative (1,296 * 6 = 7,776 records), and 2) a linear (Gaussian) GEE model with response variable: log10(cfu/g) across positive flocks (1,856 records).

In both models, predictors included: scenario, quarter, slaughterhouse, and all their pairwise interactions. Robust standard errors and Tukey adjusted post hoc comparisons were used. Cluster structure was defined by flock ID. Assumptions of statistical models were evaluated. Sensitivity analysis was also carried out by: a) comparing the Quasi-Likelihood Information Criterion (QIC) across different working correlation structures within each GEE model, and b) investigating alternative mixed-effect models with farm-ID or within-farm stable unit variables set as random factors.

3. RESULTS

3.1 QMRA outputs

Under the 2024 reference scenario (ScenRef), the QMRA estimated an annual relative risk (RR) of 1.03, indicating a slight (+ 3%) increase of risk per meal, compared with the 2019–2021 baseline estimate. Applying slurry ice (ScenI) reduced the annual RR marginally to 0.96 (i.e. -7%). In contrast, MAP O_2 scenarios generated substantially larger reductions (67-84%): ScenII yielded an RR of 0.34, ScenIII an RR of 0.17, and ScenIV an RR of 0.24. Combining slurry-ice with MAP O_2 (ScenV, RR = 0.22) provided a minor improvement over MAP O_2 alone

Theme 7

(ScenIV). Moreover, MAP O_2 scenarios appeared capable of maintaining monthly RRs consistently below 1.0 across all months.

3.2 Outputs of descriptive statistics

In ScenRef, 418 of the 1,296 flocks tested positive (AP = 32.3%). Mitigation scenarios reduced this overall annual AP to 29.2% (ScenI), 22.8% (ScenII), 18.2% (ScenIII), 20.5% (ScenIV), and 20.3% (ScenV). In general, AP showed strong seasonal variation, with Q3 exhibiting the highest values (58.5%). Slaughterhouse SC showed the highest AP (64.9%), followed by SD (49.5%), SA (26.0%) and SB (18.7%). Organic flocks showed higher AP than conventional flocks (49.5% vs. 30.9%).

Carcass *Campylobacter* concentration across positive flocks, was higher in the ScenRef and lowered across scenarios, with seasonal (Q1 > Q2 > Q3 > Q4), slaughterhouse (SC > SB > SA > SD), and flock-type (conventional > organic) patterns.

3.3 Outputs of statistical analysis

GEE based odds ratio (OR) estimates (Figure 1) confirmed that ScenRef consistently had the highest odds of carcass-flock positivity across all slaughterhouses and quarters. All pairwise interactions were significant. Slurry-ice (ScenI) resulted in modest odds reductions compared to ScenRef, while MAP O_2 based scenarios produced large decreases. The strongest effects occurred in Q3, in all slaughterhouses, under ScenIII. Between slaughterhouses (in the same season and scenario) ORs were higher at SD (mean OR = 10.3), followed by SA (3.3), SC (2.8) and SB (2.4) (Figure 1).

The linear GEE model showed that concentration levels were strongly influenced by scenario, with ScenRef and ScenI yielding the highest predicted log10 concentrations across all quarters and slaughterhouses, with lower values under ScenII to ScenV. These reductions, however, varied substantially by season and slaughterhouse, according to the significant (pairwise) interaction terms. The largest scenario driven decline in concentration occurred at SC in Q2, where MAP O_2 reduced the predicted mean log10 cfu/g by up to −1.02 (decrease from 2.67 in ScenRef to 1.65 in ScenIII).

Diagnostic checks confirmed stability of the two GEE models estimations, realistic predicted probabilities (logistic model) and concentrations (linear model), and absence of problematic collinearity. The independence working correlation structure provided the best (lowest) QIC fit for both GEE models. Mixed effects models showed fitting issues, confirming the GEE approach as preferable for the aimed flock population average inference.

4. DISCUSSION

4.1 Main findings

This study quantitatively showed that MAP O_2 can be a highly effective post-slaughter mitigation measure for reducing *Campylobacter* concentrations, prevalence, and related human risk from broiler based meals. It consistently reduced apparent prevalence and carcass contamination across all seasons and slaughterhouses, causing 67–84% reductions in the annual RR per broiler-based serving. MAP O_2 is already widely applied in Denmark, meaning that, apart its benefits on prolonged product´s shelf life, there is a relevant concomitant *Campylobacter* risk mitigation.

For slurry ice spraying, more modest risk reductions were estimated. It is not currently implemented systematically in Danish slaughterhouses, but it appeared that this measure alone would not substantially reduce public health risk, though it may still provide marginal supplementary benefits if combined with other measures, as shown in ScenV. Moreover, it should not be excluded that in the future, greater reductions in *Campylobacter* concentrations may be achievable through slurry-ice spraying, as research continues and the specific biological mechanisms of action on *Campylobacter* through this technology, become clearer. Such a measure has been developed mainly to speed up the chilling process and to increase production capacity, i.e. to reduce the slaughter line energy costs and to optimize productivity.

The GEE models corroborated the descriptive statistic results and their related QMRA findings. Both models showed that scenario effects on prevalence and contaminations varied across quarters and slaughterhouses and were relevant especially under MAP O_2 treatment. The largest prevalence reductions occurred during Q3 (when *Campylobacter* prevalence typically peaks in Denmark), and at the highest risk slaughterhouses. Thus,

Theme 7

MAP O_2 optimization—ensuring consistent high-oxygen conditions across all product lines and flocks, particularly during summer—can yield significant overall risk-mitigation benefits.

Overall, in this study, it is shown that, integrating post-slaughter treatments with upstream interventions could produce additive risk mitigations effects along the food chain. Several mitigation measures have already been investigated in different studies, such: farm level high-biosecurity, logistic-slaughter strategies, hygiene improvements at slaughterhouses (to reduce cross-contaminations) and use of feed and water additives. The effect of feed and water additives was recently investigated in Denmark, but was not included here, because the caecal *Campylobacter* presence was measured; but not the meat concentrations which are needed to inform the QMRA model. The Danish Action Plan already emphasizes risk based and surveillance data driven approaches for decision making [2]. The findings from this work could be integrated into the continuous science-based support aimed at optimizing the comprehensive farm to fork and One Health (OH) *Campylobacter* control strategy. Follow-up cost-benefit analysis could further help driving risk-based prioritization of measures along the food chain.

4.2 Limitations of the study

Estimates of the QMRA model regarded risk of human disease per serving, and thus, eventual extrapolations in terms of national human disease incidences and their comparisons with reported public health data should be made with caution, because for that purpose, several (often uncertain) variables should be considered (e.g. proportion of the human population actually consuming broiler meat, disease underreporting factors, diagnostic tests used and their performance, etc.).

A similar caution applies if extrapolating our results to other countries. For instance, variations in MAP gas compositions and their concentrations used elsewhere may result in different per meal risks—and different mitigation effects—than those estimated here for Denmark.

The potential impact of initial (pre treatment) *Campylobacter* concentrations associated with different meat cuts was incorporated based on only two studies [4, 5], as these were conducted recently and under current meat processing practices in Denmark. However, the simulated prevalence and concentration distributions were remarkably similar between ScenII and ScenIII, despite being based on reduction factors defined for neck skin and breast fillet—cuts known to exhibit substantially different contamination levels at the slaughterhouse. Finally, it should be noted that, in this study, the two mitigation measures (or their combination) were applied simultaneously to all 1,296 flocks, in order to enable an overall comparison of their effects. In reality, however, some broiler meat produced in the country may undergo different treatments (e.g. vacuum packaging), and some cuts may also be sold directly as unpacked fresh meat (e.g. in butcheries).

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Theme 7



Figure 1. Odds ratios (ORs) for *Campylobacter*-positive flocks under the reference scenario (ScenRef) compared with mitigation scenarios (ScenI–ScenV), stratified by slaughterhouse (SA–SD) and quarter (Q1–Q4). ORs were estimated using a binomial GEE model with robust standard errors and are shown with associated 95% confidence intervals. ORs greater than 1 (dashed line) indicate that ScenRef had higher odds of carcass-flock positivity relative to the corresponding mitigation scenario. Tukey adjustments were applied to all scenario comparisons within each slaughterhouse–quarter combination.

Keywords: *Campylobacter*, QMRA, Risk mitigation, MAP, Slurry-ice.

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Theme 7

Risk-based surveillance for early detection of transboundary animal diseases at the Brazil–Bolivia border in Mato Grosso State

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Summary

The state of Mato Grosso, Brazil, shares an extensive and accessible border with the Republic of Bolivia, creating a continuous risk of introduction of transboundary animal diseases. Mato Grosso is one of the world's largest livestock-producing regions and is officially recognized as free from Foot and Mouth Disease without vaccination, free from Classical Swine Fever, and has never reported High Pathogenic Avian Influenza in commercial poultry. Maintaining this sanitary status requires surveillance strategies capable of early detection, particularly in high-risk border areas. In this context, we developed and implemented a risk-based surveillance approach for the Mato Grosso–Bolivia border region. Farms were ranked according to their probability of disease introduction using epidemiological risk factors and a proxy risk measure derived from expert-based modelling. The top 50% highest-risk farms were selected, and surveillance activities were conducted through structured field operations combined with animal health education. During the initial implementation period (February–March 2026), 384 farms were planned for surveillance, of which 337 were effectively visited. A total of 571 surveillance forms were issued, covering both prioritized farms and additional field activities. During these visits, more than 150,000 cattle and thousands of animals from other species were inspected, and animal health education was delivered to producers and animal caretakers to improve early recognition of clinical signs and timely notification to the Official Veterinary Service. This approach demonstrates that risk-based surveillance, combined with field implementation and farmer engagement, can strengthen early detection capacity in border regions under continuous risk of disease introduction. It represents a practical and scalable strategy to support the protection of the country's sanitary status at its entry point through the state of Mato Grosso.

Methods

The methodology can be found in Schettino et al. (2021) [1]; however, briefly, we used a combination of factorial design and conjoint analysis, the latter being a statistical tool widely used in marketing as an approach to evaluate decision-making preferences and the relative importance of different risk factors. This method allows the assessment of trade-offs between multiple attributes within hypothetical scenarios. Combinations of factors that contribute to the introduction of specific diseases were created, and for the border region, we selected risk factors related to the introduction of the target diseases.

Through the ordinal categorization of these factors, from lowest to highest, four experts from the Official Veterinary Service (OVS) of Mato Grosso ranked, according to their personal perception and knowledge on the subject, ten hypothetical farms, labeled from A to J (from lowest to highest risk), for the possible introduction of each target disease.

The combination of seven risk factors in eight hypothetical scenarios was created using a factorial model in IBM SPSS [2]. In addition, two combinations representing the extremes of risk were included: combination A (score 1) and combination J (score 10), corresponding to the lowest and highest risk, respectively.

After this grading, an ordinal logistic regression was performed to estimate the weight of each risk factor (regression coefficient) on the probability of disease introduction, according to expert knowledge. Using the coefficients of each risk factor in the model, we categorized farms located within 50 km of the Mato Grosso–Bolivia border according to the presence or absence of these factors, applying an additive model. This allowed us to generate a proxy risk for farms in the border region, supporting the implementation of risk-based surveillance based on the highest estimated risks. The farm database was obtained from the computerized system of the Official Veterinary Service (OVS) of the State of Mato Grosso based on data from January 2026.

Risk factors for each target disease:

Foot and Mouth Disease (FMD)

The risk factors considered in the epidemiological risk analysis model were: cattle density; location in relation to the border line (up to 15 km) or within the border region (up to 50 km); high inflow of cattle; presence of multiple

Theme 7

species susceptible to FMD; whether the farm is binational; presence of an international gate; and road density, which facilitates animal movement.

Classical and African Swine Fever (CSF and ASF)
The risk factors considered were: pig density; presence of free-ranging feral pigs; subsistence pig production systems; swill feeding; location within the border region (up to 50 km); road density; and human population density, as these factors are related to the movement of people and the transport of potentially infected animals and animal products.

Avian Influenza and Newcastle Disease
The risk factors considered were: domestic poultry density; proximity to migratory bird sites; farms with multiple poultry species (e.g., ducks, also chickens, guinea fowl, turkeys); location within the border region (up to 50 km); proximity to water bodies; road density; and human population density.

The output of this risk analysis was a list of farms for each target disease, from which we selected the top 50% (median) highest-risk farms for Foot and Mouth Disease, Avian Influenza, and swine fevers.

The list of farms to be visited was provided to official veterinarians who work in 10-day shifts in the region, rotating over time. Farm selection has already been randomized through the end of 2026, and for subsequent years, new analyses will be performed, since risks are dynamic and may change over time. As a result, farms may increase or decrease in risk, making this risk analysis model dynamic and more sensitive for detecting disease introduction.

This methodology was implemented starting in February 2026, with four teams (each composed of one official veterinarian and one veterinary assistant) per 10-day shift. Each team received a list of 16 farms where they were required to conduct surveillance activities in four regions along the Mato Grosso–Bolivia border, known as 'Corixinha', 'Las Petas', 'Ponta do Aterro', and 'Marphil'.

At the farms, official veterinarians perform not only active surveillance but also mainly animal health education for producers and animal caretakers, teaching them how to identify clinical signs and lesions of these transboundary animal diseases and also emphasizing the importance of timely notification to the Official Veterinary Service (OVS) when they notice something unusual in their animals.

Results

Figure 1 shows the farms assigned for surveillance activities during the initial phase of implementation (February–March 2026). The Bolivian departments bordering Mato Grosso (San Ignacio de Velasco, San Rafael, and San Matías) are highlighted in orange. The colored dots represent farms assigned to each region: Marphil is shown in pink, Ponta do Aterro in dark orange, Las Petas in blue, and Corixinha in grey.

After ranking farms according to their risk (using the median to select the top 50% highest-risk farms), a database of 3,134 farms was generated. For the selection of 16 farms per team, per region, through the end of 2026, a proximity-based random selection was performed using the RStudio data analysis software [3]. A maximum distance of 100 km (straight-line distance) was defined between one randomly selected farm (seed) and the remaining fifteen farms. After this process, a total of 2,048 farms were selected. Each list is made available through a dashboard in Microsoft Power BI, facilitating access to farm names and geographic coordinates and optimizing field location. This approach ensured logistical feasibility while maintaining spatial representativeness of high-risk farms.

During the initial implementation period, 384 farms were planned for surveillance activities based on risk prioritization in the four regions along the Mato Grosso–Bolivia border. Of these, 337 farms were effectively visited, while 47 were not completed.
Execution varied across regions, with 81.2% of planned farms visited in Corixinha and Las Petas, 93.8% in Ponta do Aterro, and 94.8% in Marphil.

A total of 571 surveillance forms (FVV) were issued during the study period, covering both risk-based selected farms and additional surveillance activities conducted as part of routine field operations, such as animal movement inspections.
During these activities, 150,244 cattle, 4,350 sheep, 2,464 pigs, 144 poultry, and 47 goats were inspected. Clinical examination was performed on 12,670 poultry, 1,443 cattle, 28 pigs, and 4 sheep.

Theme 7

Animal health education was incorporated into all field activities and was delivered during these surveillance visits, focusing on improving the recognition of clinical signs of transboundary animal diseases and reinforcing timely notification to the Official Veterinary Service.

Discussion

Risk-based surveillance is increasingly used as a strategy to optimize limited resources in animal health systems, especially in large territories with heterogeneous risk profiles. By prioritizing farms with a higher probability of disease introduction, surveillance efforts can be more efficiently allocated without compromising coverage.

The integration of passive surveillance through farmer engagement is a key component of early detection systems. In remote and border areas, where continuous official presence is limited, the ability of farmers to recognize and report suspicious events becomes essential for a timely response. The combination of targeted active surveillance and strengthened passive surveillance contributes to a more sensitive and responsive system, particularly in regions under constant risk of disease introduction.

The implementation of this approach in the Mato Grosso–Bolivia border region showed that it is feasible under field conditions. The prioritization of farms based on epidemiological risk factors allowed a structured allocation of surveillance activities, which is particularly important in extensive and logistically challenging regions.

Mato Grosso has a long and accessible international border with Bolivia. Although Bolivia has a similar sanitary status to Brazil regarding Foot and Mouth Disease (free without vaccination), it is not free from Classical Swine Fever. In addition, as this involves two different national veterinary services, it is not possible to ensure that a disease outbreak would be detected and contained on the Bolivian side before spreading into Mato Grosso. Therefore, the border region should be considered an area of increased risk for disease introduction.

The proportion of planned farms effectively visited (337 out of 384) indicates a high level of operational execution, although differences among regions were observed. Lower execution in some areas was mainly associated with logistical constraints, such as long travel distances, poor road conditions, and limited accessibility. These factors highlight the importance of considering operational feasibility when designing surveillance strategies in border regions.

The number of surveillance forms issued (571 FVV) exceeded the number of farms selected through the risk-based approach, reflecting the integration of targeted surveillance with routine field activities. Although these additional activities were not part of the initial prioritization, they contributed to strengthening the overall surveillance system and increasing the likelihood of detecting unusual events.

An important aspect of this approach was the incorporation of animal health education into surveillance activities. By engaging producers and animal caretakers during farm visits, the strategy aimed to improve recognition of clinical signs and reinforce timely notification to the Official Veterinary Service. This is particularly relevant in areas where access is limited and continuous monitoring is challenging.

The large number of animals inspected during the study period demonstrates the capacity of the system to achieve substantial epidemiological coverage, particularly for diseases of major economic importance such as Foot-and-Mouth Disease, Classical and African Swine Fever, and Avian Influenza.

Overall, this experience shows that combining risk-based surveillance with field implementation and farmer engagement can be a practical and scalable strategy for strengthening animal health systems in border regions. Continuous updating of risk factors and periodic reassessment of prioritized farms will be essential to maintain system sensitivity over time.

Conclusion

This epidemiological model focuses on the introduction of diseases rather than their spread. Identifying farms with a higher probability of infection based on the presence of risk factors, and directing surveillance efforts accordingly, contributes to increasing the sensitivity of the surveillance system by strengthening passive surveillance. This approach represents an important advance for the surveillance of transboundary animal diseases and enhances protection of the country's sanitary status at its 'entry point' through the state of Mato Grosso.

Theme 7

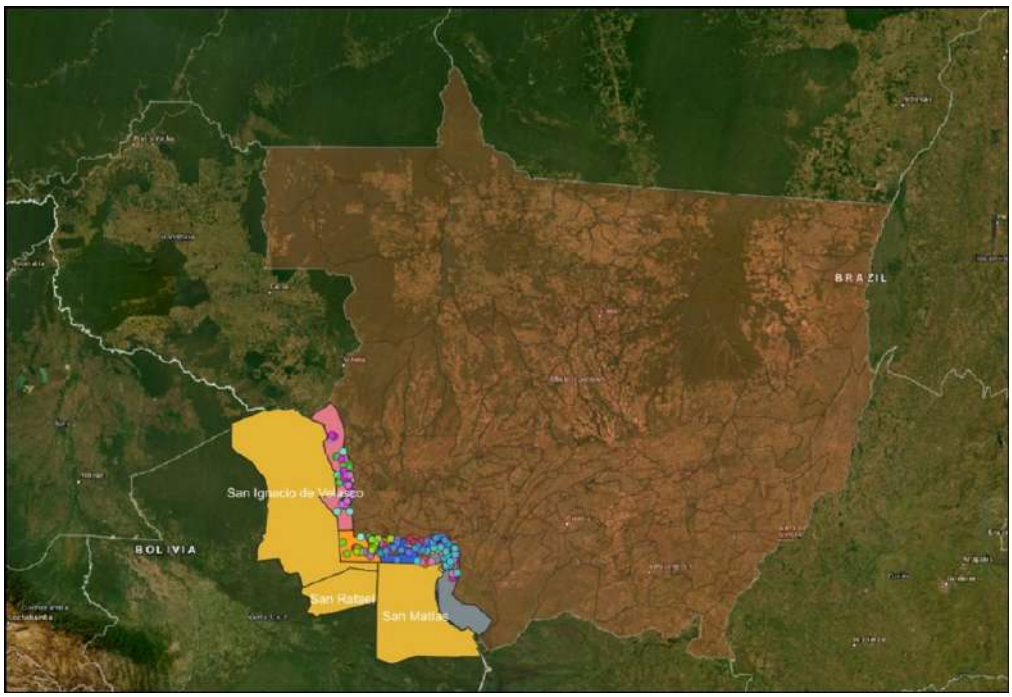


Figure 1. Map of the Mato Grosso–Bolivia border showing farms assigned from shift 1 (02/01/2026–02/10/2026) to shift 6 (03/20/2026–03/31/2026), and the regional divisions used to optimize field surveillance activities.

Keywords: Risk Assessment, Risk-based Surveillance, Transboundary Animal Diseases, Ordinal Logistic Regression, Official Veterinary Service.

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Case story presentations

Evidence of a novel orthobunyavirus from the Simbu serogroup in New South Wales, Australia, from 2012

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Summary

Orthobunyaviruses from the Simbu serogroup are arthropod-borne viruses that can cause congenital malformations and neurological disease in ruminants, leading to significant economic losses. In Australia, the National Arbovirus Monitoring Program (NAMP) conducts surveillance for veterinary-important arboviruses, including testing of a sentinel cattle herd network across the country. In 2017, a novel orthobunyavirus from the Simbu serogroup (K902) was isolated from sentinel cattle in northern New South Wales (NSW), Australia. This virus had not previously been detected in Australia, raising concerns about its emergence. To establish the timeline for the introduction of K902 into NSW, a two-stage survey of archived sera from sentinel cattle was

Theme 7

carried out: first, a targeted presence survey; and, if no antibodies were found, testing was expanded to evaluate freedom using a design prevalence of 2.5% with 95% confidence. Evidence of K902 transmission could be detected in NSW since 2012. The serosurvey of archived NAMP samples from 2000 to 2011 also confirmed no evidence of K902 before 2012. This supports the absence of K902 transmission during the decade preceding its first detection in the NSW sentinel herd network. The undetected transmission of K902 for five years prior to its initial isolation underscores the importance of long term surveillance systems for the detection of emerging arboviruses. These surveillance systems, together with an extensive sample archive, provide valuable opportunities and resources for the characterisation of novel and previously unidentified veterinary important arboviruses.

Introduction

Several orthobunyaviruses in the Simbu serogroup are emerging and re-emerging teratogenic viruses that can severely impact livestock industries. Schmallenberg virus (*Orthobunyavirus schmallenbergense*) emerged in Europe in 2011-2012, resulting in widespread outbreaks of congenital malformations in cattle, sheep, and goats [1]. In addition to Schmallenberg virus, five other viruses in this serogroup have been recognised to cause congenital malformations or neurological disease in livestock [2]. Akabane (*Orthobunyavirus akabaneense*), Aino (*Orthobunyavirus ainoense*), Shuni (*Orthobunyavirus shuniense*), Peaton (*Orthobunyavirus peachesterense*) and Shamonda (*Orthobunyavirus schmallenbergense*) viruses have all been associated with disease in ruminants.

Surveillance for these veterinary-important arboviruses is critical to maintaining international trade in livestock and animal products [3]. To monitor virus transmission, surveillance programs employ strategies such as light trapping of insect vectors and sentinel herd surveillance [4]. Longitudinal testing through sentinel herd surveillance can detect the timing of infection within defined regions and timeframes. Across Australia, Akabane virus has been monitored using longitudinal sampling of naïve sentinel cattle herds since the 1980s [4]. Since 1993, the sentinel herd network has been formalised nationally, and the transmission patterns of important veterinary arboviruses have been monitored by the National Arbovirus Monitoring Program (NAMP) [4].

In 2017, an orthobunyavirus from the Simbu serogroup (K902) was isolated from cattle in a sentinel herd in northern NSW. The isolation of K902 prompted a critical question: How long has this virus been present in NSW?

Materials and Methods

New South Wales sentinel herds and sample collection

Across NSW, the NAMP recruits approximately 30–40 sentinel cattle herds annually over a 10 month period from October to July, corresponding with seasonal arbovirus vector activity [4]. Each herd comprises at least ten property born cattle, typically around six months of age at initial sampling in October [4]. Herds are strategically selected across the state to define the Bluetongue virus transmission zone, with blood samples collected monthly to quarterly, depending on location and risk [5]. Following collection, clotted blood samples were transported to the NSW Department of Primary Industries and Regional Development (NSW DPIRD) Virology Laboratory. Serum was separated by centrifugation (3000 × g for 5 min at 4 °C), stored at 4 °C prior to testing, and archived at −20 °C for long term storage [6].

Stage 1: Targeted survey for K902 antibodies in archived samples from 2005-2018

The samples from the archived collection were selected based on the following criteria to maximise the likelihood of detecting antibodies against an unknown orthobunyavirus from the Simbu serogroup: 1) Samples were from animals within a NSW sentinel herd where seroconversion was observed in at least one animal during the monitoring period using a Simbu serogroup-reactive ELISA; 2) The sample was collected on the final collection date of the monitoring period for the sentinel herd; and 3) The samples have 'unexplained' antibodies against an orthobunyavirus in the Simbu serogroup, testing positive in the group-reactive ELISA and negative for the known endemic viruses in this serogroup by virus neutralisation test (Akabane, Aino, Douglas, Peaton, and Tinaroo).

Stage 2: Demonstration of the absence of transmission of K902

The freedom survey was also completed on the archived samples from the NSW sentinel herds. The required sample size was calculated as 102 samples in each monitoring period to achieve 95% confidence at a design prevalence of 2.5% [7].

Theme 7

Virus neutralisation test for K902 antibodies

Detection of K902 antibodies was performed using a virus neutralisation test (VNT) following a standard protocol [8]. Briefly, serum samples were heat inactivated at 56 °C for 30 min and incubated with a working stock of K902 (1.8–2.5 $\log_{10}$ $TCID_{50}$ per 50 µL) at 37 °C for 1 h prior to the addition of HmLu 1 cells. Plates were incubated at 37 °C for 120 hours and subsequently examined for cytopathic effect.

Results

The targeted survey indicates that K902 was present in the NSW sentinel herd network from 2012 to 2018 (Table 1). From 2005 to 2018, 362 (82.4%) of the selected samples were available for testing from the sentinel archive. From 2012 to 2018, K902 antibodies were detected in a mean proportion of 70.2% of tested samples per monitoring period (range: 22.2-85.4). No antibodies were detected in targeted samples collected between 2005 and 2012. Consistent with this finding, no K902 antibodies were detected by VNT in 1,409 samples collected between 2000 and 2011 as part of the freedom survey (Table 2).

Discussion

This study used archived sentinel herd sera to establish a serological timeline for the introduction of a novel orthobunyavirus, K902, into NSW. No serological evidence of K902 infection was detected from 2000 to 2011. The freedom survey followed parts of the study design previously used for Schmallenberg virus, with a prevalence threshold of 2.5% [9]. Although the number of samples required to fully meet this survey design could not be tested for 2011, the samples available were sufficient to support the absence of K902 in NSW sentinel herds at a prevalence of ≥3% with 95% confidence.

Overall findings supported the absence of K902 transmission prior to 2012. However, this interpretation must also consider the two inconclusive reactors identified in 2000 and 2001 (Table 2). These inconclusive samples detected early in the study period are most plausibly explained by serological cross reactivity with other endemic Simbu serogroup viruses, reflecting the limitations of VNT interpretation in regions where multiple orthobunyaviruses co circulate [6, 10].

Testing targeted samples with a higher likelihood of demonstrating antibodies against an unknown orthobunyavirus enabled efficient detection once K902 was present, consistent with the risk based design of the NSW sentinel herd network, in which herds are selected from locations optimised for arbovirus surveillance [4-6]. While the seroprevalence of K902 cannot be estimated from this study, these results provide the first serological evidence of a novel orthobunyavirus from the Simbu serogroup circulating in Australia from 2012. Continued detections from 2012 indicate several years of undetected K902 transmission prior to virus isolation in 2017. These findings highlight the challenges of identifying newly introduced orthobunyaviruses from the Simbu serogroup in the absence of reported disease and reinforce the importance of long term surveillance systems for detecting emerging arboviruses.

Theme 7

Year	No. of eligible samples	No. tested in the VNT	VNT results			
			Positive	Inconclusive	Negative	No result
2005	7	7	0	0	7	0
2006	29	21	0	0	21	0
2007	38	29	0	0	29	0
2008*	0	0				
2009	57	46	0	0	46	0
2010	24	22	0	0	22	0
2011	13	12	0	0	12	0
2012	37	9	7	2	0	0
2013	55	48	41	6	1	0
2014	35	34	20	6	7	1
2015	20	18	10	2	5	1
2016	32	27	6	5	14	2
2017	46	43	22	7	11	3
2018	46	46	15	9	14	8
Total	439	362	121	37	200	15

* For this detection survey, samples from the monitoring period ending in 2008 could not be included because VNT results were unavailable to identify eligible samples.

Table 1. Results from the virus neutralization tests (VNT) for antibodies against K902 as part of the detection using targeted samples from sentinel herds in New South Wales during each monitoring period (2005 – 2018).

Year	No. of eligible samples	No. tested in the VNT	VNT results			
			Positive	Inconclusive	Negative	No result
2000	196	120	0	1	119	0
2001	274	117	0	1	116	0
2002	237	119	0	0	119	0
2003	312	111	0	0	111	0
2004	259	113	0	0	112	1
2005	247	121	0	0	121	0
2006	216	136	0	0	131	5
2007	251	121	0	0	113	8
2008	273	111	0	0	111	0
2009	347	108	0	0	92	16
2010	393	135	0	0	112	23
2011	381	97	0	0	97	0
Total	3386	1409	0	2	1354	53

Table 2. Results from the virus neutralization tests (VNT) for antibodies against K902 as part of the freedom survey to demonstrate the absence of this virus at a design threshold of ≥2.5% prevalence with 95% confidence using archived samples from sentinel herds in New South Wales during each monitoring period (2005 – 2011).

Keywords: Arbovirus surveillance, Disease freedom, Orthobunyavirus, Serosurvey, Simbu serogroup.

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Short oral presentations

Evaluation of the surveillance system for Avian Influenza and Newcastle Disease Virus in Ghana

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Summary

This project evaluated the surveillance system for Avian Influenza (AI) and Newcastle Disease virus (ND) in poultry in Ghana. APHA staff collected data from surveillance stakeholders at all levels of the surveillance system. At the lower-levels of the system this included poultry workers (farmers, market sellers, transporters and slaughter facility workers), district veterinary officers (DVOs) and animal health professionals (AHPs). Local contractors visited 24 selected districts to meet participants and carry out questionnaires. The data was analysed and used to inform conclusions and recommendations for surveillance system improvements. This paper focuses on disease reporting and response behaviour by these groups. The recommendations included: providing more education to poultry workers on the clinical signs of AI and ND and the risk of disease transmission; prioritising access to means of transport and equipment for veterinary professionals; considering widening the remit of compensation paid following outbreaks of AI; ensuring that poultry workers know how to contact a veterinary professional when none are present in the village; and clarifying the routes of reporting for transporters.

Introduction

The most effective and sustainable way to protect against biothreats from natural, deliberate or accidental origin include strengthening existing systems for surveillance, early on-farm detection and rapid response, and good biosafety and biosecurity practices[1]. This project focused on the evaluation of the surveillance system for AI and ND in poultry in Ghana. AI and ND are endemic in Ghana. Both diseases can lead to high mortality in poultry and can have significant economic consequences for farmers and others who work with poultry. Both AI[2]and ND[3] can be transmitted from wild birds to poultry via direct contact, faeces, and contaminated feed, water and equipment. ND is an important differential diagnostic for AI, as the two diseases have very similar clinical signs. The aim of the project was to identify and analyse surveillance processes related to these pathogens to highlight areas for improvement. This paper focuses on disease reporting and response behaviours by poultry workers, AHPs and DVOs.

Materials and methods

SERVAL framework

The surveillance system was evaluated using the SERVAL framework[4], a standardised framework to characterise a surveillance system and highlight its strengths and weaknesses. Using the framework guidance, 12 surveillance system attributes were selected for assessment, based on the objectives of the surveillance system (early detection, case finding of infected animals, and identification of changes in the population at risk). The results presented here correspond to the attributes of Sensitivity, Impact and Representativeness. The

Theme 7

techniques that would be used to assess each attribute were determined, as well as the data and information required to carry out the assessment.

Field data collection

The APHA team worked with a sub-contractor based in Ghana, The Ghana Poultry Network (GAPNET), who carried out field-based data collection from individuals working directly within the poultry industry (farmers, market sellers, transporters and slaughter facility workers), AHPs who work directly with animals at the village level, and DVOs who are responsible for overseeing the AHPs and veterinary activities undertaken in their district.

The APHA team prepared seven questionnaires, each tailored to a stakeholder group. The questionnaires were prepared in Qualtrics online, an online platform for surveys. Paper questionnaires were also produced for use where internet connection was not available.

The GAPNET team travelled to 24 selected districts to meet participants and carry out the questionnaires in person. The 24 selected districts consisted of eight randomly selected districts in each of the three epidemiological zones in the country (the Northern, Middle and Southern zones). Within each selected district, two villages were visited (48 villages in total).

Planned participant numbers were determined based on the available time and resources to complete the field work, with a focus on collecting data from farmers and AHPs. Four farmers were to be interviewed in each village (192 in total). One market seller and one slaughter facility worker were to be interviewed per district (24 of each in total), and three transporters were to be interviewed per epi zone (nine in total). Seven AHPs were to be interviewed per district (168 in total) in addition to the DVO (24 in total).

The APHA team visited Accra in July 2024 to train the GAPNET team and pilot the questionnaires. The main field data collection took place during July and August 2024.

Theme 7

Questionnaire data cleaning and analysis

Data cleaning and analysis were carried out using Excel, Stata and R software. Frequency tables were produced and summary statistics were generated. The results of the data analysis were used to evaluate each of the selected SERVAL attributes and inform our overall conclusions and recommendations for surveillance improvement.

Results

Participant numbers

Of 441 planned questionnaires, 328 were carried out in total. The vast majority of the shortfall was within the AHP category, due to lower numbers of these professionals being employed in the selected districts than anticipated. Questionnaires were completed by 178 farmers, 22 market sellers, 17 slaughter facility workers, 19 transporters, 70 AHPs and 22 DVOs.

Disease reporting and response behaviour

Over 30% of farmers, who had previously noticed signs of disease consistent with AI or ND in their birds, said they did not report the issue to a veterinary professional the last time it occurred (Table 1A). Higher percentages of market sellers, transporters and slaughter facility workers said the same, though sample sizes for these groups were low.

AHPs reported that they do not always visit the premises to investigate after being notified of a suspected case of disease. AHPs also indicated that they are unlikely to take samples for laboratory testing when they do suspect AI or ND during a visit, with the median response indicating they would do this 1-10% of the time for suspected cases on farms, though they were more likely to take samples for suspected cases at markets and larger abattoirs or slaughterhouses (Table 1B).

When asked about suspected cases of disease in wild birds, of 43 farmers who said they had previously noticed signs of disease in wild birds, only 12 (27.9%) said they reported the issue to a veterinary professional. In addition, only 55.4% of farmers (98/177) said they believe that diseases in wild birds can affect the health of their poultry birds, with even lower percentages seen for the other poultry worker groups.

Key issues impacting reporting, identified by poultry workers, included concerns regarding financial losses that could result from control measures being put in place in the event of confirmed disease and a lack of compensation. In addition, a lack of visible/accessible AHPs in the area was identified as an issue by all poultry worker groups, but was a particular issue for transporters. Veterinary staff also identified concerns around financial losses and a lack of compensation as factors limiting reporting by poultry workers, as well as a lack of awareness of the risk of disease transmission.

AHPs identified factors limiting their ability to respond to notifications of suspected disease as staffing shortages, a lack of available transportation, and a lack of basic equipment including sample collection kits and rapid testing kits.

Farmers were asked what actions they took the last time they experienced disease consistent with AI/ND in their flock. Over 60% of farmers said they separated the sick birds from the healthy-looking birds and over 80% tried to treat the sick birds. In addition, over 80% of participants said they disposed of the dead birds by burying them, while a small number (3.8%) disposed of them by burning them, both considered appropriate methods of disposal. Some participants reported actions that could increase the risk of disease transmission. For dead birds, these included disposing of them by throwing them away (10.8%), consuming them at home (4.4%), feeding them to other animals (1.3%) or selling the carcasses as meat (1.3%). For sick birds, these included killing them and consuming them at home (10.1%), feeding them to other animals (0.6%) or selling the carcasses as meat (1.9%), selling the live sick birds (2.5%), and not doing anything with them (5.1%). For healthy-looking birds, nearly a quarter of participants said they did not do anything with them (24.1%), while some said they sold them (15.8%), slaughtered them and sold them as meat (3.2%), or slaughtered them for home consumption (10.1%). Only around a third of participants reported putting movement restrictions in place or carrying out enhanced cleaning and disinfection, and only around 5% implemented restrictions on sales, all of which are key biosecurity measures recommended to prevent the spread of disease.

Discussion

Theme 7

Some clear recurring themes were seen across stakeholder groups, helping to identify the key areas that should be prioritised for improvement.

Financial concerns

Poultry workers cited financial concerns as one of the main factors limiting reporting. Currently, in the event of a confirmed case of AI, compensation is paid to the farmer if the disease is confirmed to be highly pathogenic AI (HPAI), with the amount based on a percentage of the slaughter value of the birds. Expanding the remit of compensation so that it is paid for all cases of AI, compensating the full value of the birds, and compensating other financial losses arising from the outbreak, may improve the willingness of farmers to report. For confirmed cases of ND, where the policy is for the affected flock to be vaccinated, subsidising these vaccinations may help. However, if this is not possible due to financial constraints, then targeting areas where financial support would have the greatest impact should be identified and prioritised for any funding that is available.

Education

Veterinary professionals said that they think a lack of awareness of the risk of disease transmission limits reporting by poultry workers. This was reflected by reports of actions that could increase the risk of disease transmission being taken by farmers the last time they experienced disease in their flock consistent with AI/ND, and a lack of awareness that disease in wild birds presents a risk to their birds. A key recommendation is to provide education to poultry workers on the risks of disease transmission, as well as ensuring they are aware of the clinical signs of AI and ND.

Veterinary staffing shortages

Veterinary professionals noted that staffing shortages impact their ability to respond to notifications of disease. This was also reflected in the responses from poultry workers, with many noting a lack of visible or accessible veterinary staff in their area. If it is not possible to increase staffing levels, then it is important to ensure that all poultry workers are aware of who they should contact to report an issue, and how to contact them. Transporters in particular noted difficulties accessing veterinary professionals and several suggested that a phone app to report issues would help. Clarifying the routes of reporting for transporters may help to improve levels of reporting from this group.

Lack of transportation for veterinary staff

Responses from veterinary professionals indicated that a lack of means of transport is a significant issue impacting their ability to carry out their roles. Improving access to transportation should be considered a key area to prioritise for funding. Options for improving the situation include providing vehicles, providing vehicle/fuel allowances, and providing funds for hiring drivers or use of other public transport.

Lack of diagnostic equipment

An area to prioritise for funding is the provision of diagnostic equipment including sample collection kits and rapid testing kits. Veterinary professionals noted that there is a shortage of these items, limiting their ability to accurately diagnose cases of disease. This is of particular importance due to the need for differential diagnosis between AI and ND through testing, given that the two diseases have similar clinical signs.

Conclusion

This project helped to identify a number of areas that should be prioritised for improvement to enhance the sensitivity and overall effectiveness of the AI and ND surveillance system in Ghana. Improvements could lead to better control and monitoring of disease risks within the country, and a reduction in the risk of disease transmission. Strengthening surveillance of AI and ND in Ghana could also provide regional and global benefits to biosecurity, by reducing the risk and consequences of disease transmission whether natural, accidental or deliberate to other countries, including the UK with which Ghana has strong ties for trade, people movement and bird migration.

Theme 7

Acknowledgements

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A) Questions asked to poultry workers					
	Farmers	Market sellers	Transporters	Slaughter facility workers	
No. who had ever noticed signs of disease in their birds consistent with AI or ND	158/175 (90.3%)	20/22 (90.9%)	4/19 (21.1%)	2/17 (11.8%)	
No. who reported the issue to a veterinary professional the last time it occurred	107/158 (67.7%)	7/20 (35.0%)	2/4 (50.0%)	0/2 (0.0%)	
No. who said a veterinary professional visited to investigate	91/107 (85.0%)	7/7 (100.0%)	2/2 (100.0%)	-	
B) Questions asked to AHPs					
	Farms	Markets	Transporters	Abattoirs or slaughterhouses	Other slaughter facilities
How often do you visit the premises after being notified of a suspected case of disease? (Median probability[a])	61-70% of the time	51-60% of the time	41-50% of the time	61-70% of the time	51-60% of the time
If you suspect AI or ND during the visit, how often do you take samples for laboratory testing? (Median probability[a])	1-10% of the time	31-40% of the time	1-10% of the time	51-60% of the time	0% of the time

[a]For both questions, participants were asked to select a category (0-10% of the time, 11-20% of the time, etc).

Table 1. Responses from poultry workers and AHPs to questions on disease reporting and response behaviour

Keywords: Avian Influenza, Newcastle Disease, Surveillance system evaluation, Ghana.

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Surveillance of Avian Influenza in Vaccinated Poultry: A Systematic Review of Strategies and Implementation Challenges

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Background:

Highly Pathogenic Avian Influenza (HPAI) is one of the most significant transboundary animal diseases worldwide affecting poultry, with far-reaching consequences for animal health, trade, food security, and public health (1). Repeated incursions of HPAI in the recent years, have led to unprecedented outbreaks across Europe,

Theme 7

prompting renewed consideration of vaccination as a complementary preventive and control measure alongside enhanced biosecurity, movement restrictions, and stamping-out (2). While vaccination has the potential to reduce clinical disease, mortality, and viral shedding (3), its implementation introduces important surveillance complexities that must be addressed to ensure early detection of virus circulation and to maintain confidence in disease freedom claims (4).

One of the principal challenges of surveillance in vaccinated populations is the reduction of clinical signs and mortality without completely preventing infection, thereby increasing the risk of subclinical or silent virus circulation (5). Therefore, surveillance systems must remain sufficiently sensitive to detect infection at low-prevalence and potential viral evolution within vaccinated flocks.

In the European Union, ongoing policy discussions on avian influenza vaccination emphasize the need for robust surveillance systems capable of demonstrating absence of virus circulation, providing epidemiological evidence for control measures, and supporting safe trade (5). Several countries outside Europe, particularly in Asia, Africa, and Latin America, have longstanding experience with vaccination programmes and have developed diverse surveillance approaches tailored to vaccinated poultry populations (3). Despite this, there has been limited synthesis of how surveillance is structured in vaccinated settings. Gaps in the implementation of diagnostic approaches, as well as operational, epidemiological, and regulatory challenges remain.

The objective of this work is to describe the surveillance strategies having been in use for vaccinated poultry, and summarize reported challenges in its implementation.

Methods:

A systematic review was conducted following PRISMA guidelines. Comprehensive searches were performed across major bibliographic databases and relevant grey literature sources to identify studies describing avian influenza surveillance in vaccinated poultry populations. Eligible records include observational studies, surveillance reports and policy documents detailing surveillance objectives, sampling strategies, diagnostic tools, and implementation challenges. Screening is currently at the full-text stage. Data extraction focuses on surveillance structure, active and passive components integration, diagnostic methodologies, and reported constraints related to sensitivity, specificity, logistics, cost, and trade implications.

Insights:

Initial screening suggests considerable heterogeneity in surveillance approaches across different regions. Serological monitoring combined with confirmatory virological testing appears central to most systems, often supported by molecular diagnostics. Frequently reported challenges include interpretation of serological results in vaccinated populations, ensuring adequate sampling coverage, maintaining laboratory capacity, managing data integration, and addressing stakeholder and trade concerns.

Expected Contribution:

By synthesizing global experience, this review will provide an overview of surveillance strategies applicable to vaccinated poultry systems and identify key factors limiting surveillance efficacy. These findings are intended to inform policymakers and authorities in designing surveillance systems. These systems should ensure early detection, transparency, and sustained confidence in avian influenza control programmes in the context of vaccination.

Keywords: Highly Pathogenic Avian Influenza (HPAI), surveillance, vaccination, systematic review.

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Theme 7

The business case for foot and mouth disease elimination in Nusa Tenggara Barat, Indonesia

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Summary:

After a long absence, foot and mouth disease (FMD) re-emerged in Indonesia in 2022 and, at the time of writing, the disease is endemic. In this study, we provide an economic evaluation of FMD elimination in the province of Nusa Tenggara Barat. Costs were estimated for commercial beef farms, smallholder farms and the provincial veterinary services. The costs of the FMD elimination programmes for three different timelines were estimated and the benefit-cost ratio (BCR) for FMD elimination for each timeline calculated. Provincial veterinary service costs (including delivery of vaccination programs) accounted for most of the financial losses attributable to FMD. Financial losses for commercial beef and smallholder farms were similar. The BCR for FMD elimination was below one for all three elimination timelines which is expected for countries or zones without established export markets.

Introduction:

Foot-and-mouth disease is considered one of the most economically important diseases of livestock globally. Despite relatively low mortality rates in adult animals, the economic impact of the disease in countries where the disease is not endemic is significant due to the loss of export markets. In countries where FMD is endemic loses arise from frequent recurrence, high rates of morbidity and relatively high rates of mortality in young stock which impairs herd replacement management (Knight-Jones and Rushton, 2013). Considering non-endemic countries and endemic countries as a single group, the main financial impact of FMD arises from production losses, the implementation of control measures such as vaccination or stamping out, and restrictions on international trade of animals and animal products (James and Rushton, 2002; Knight-Jones and Rushton, 2013).

On 6 May 2022 Indonesia notified the World Organisation for Animal Health that FMD serotype O had been confirmed in East Java and Aceh before which the country had been free from the disease without vaccination since 1986. The Government of Indonesia has executed guidelines to control and eliminate FMD where the main control tools consist of vaccination and zoning. Mass vaccination of cattle started in October 2022. Given that Indonesia is an archipelago, elimination of FMD at the individual island level is thought to be achievable in the short to medium term. Progressive island-by-island FMD elimination is expected to lead to national disease freedom. However, for countries such as Indonesia where there are no established export markets for dairy or beef products, the financial incentives for: (1) reducing the probability of FMD incursions; and (2) controlling and eliminating disease if entry does occur are not as great as for countries with established export markets.

In the past, decisions related to FMD control and elimination were often made without comprehensive analysis of economic losses or costs involved (James and Ellis, 1978). In the endemic situation the recurring nature of the disease and its ability to negatively impact on herd reproductive performance and replacement management, in addition to production performance has sustained negative effects on herd profitability. For FMD control and elimination programs to be successful, particularly when they may extend over many years, it is essential for stakeholders (herd managers and those managing animal health at the provincial level) to have a good understanding of the likely benefits and costs arising from proposed control and elimination programs.

The aim of the study was to estimate the benefits and costs arising from FMD elimination in Nusa Tenggara Barat, Indonesia. These analyses are expected to provide stakeholders (farmer groups and provincial authorities) with realistic expectations related to the amount of financial benefit arising from elimination and, perhaps more importantly, the amount of time required for that benefit to be returned. The methodological approach and cost estimates used in this study might also be used for benefit-cost analyses of FMD elimination in other provinces of Indonesia.

Theme 7

Materials and methods:

The geographic area of interest for this study was the province of Nusa Tenggara Barat (NTB) province, Indonesia. In NTB cattle and small ruminant production are significant contributors to the local economy. The archipelagic nature of the province provides geographic advantages for implementing disease control strategies. The study focused exclusively on the cattle population for the economic analysis of FMD control. The emphasis on cattle was because, in NTB, cattle were identified as the predominant species affected by FMD, with cattle farms accounting for over 90% of the total number of farms affected compared to those with other FMD-susceptible species (Rehman et al., 2025). The costs for FMD control were categorised into two main types: farm-level costs and costs for provincial veterinary services. Due to variations in farm structures, production type and FMD management practices, farms were divided into two categories for the calculation of costs and benefits: (1) commercial beef farms (10 to ≥ 100 adult cattle); and (2) smallholder farms (comprised of between 1 and 9 adult cattle). A literature review was conducted to gather information about past economic models of FMD control in different parts of the world. Following a review of the current FMD situation in NTB, an NTB-specific analysis was defined. The input data were collected from literature review, expert opinion and publicly available medication and product costs.

Separate calculations were performed for commercial and smallholder cattle farms. In commercial and smallholder farms, direct costs of FMD included losses from mortality (LMT), reduced milk production (LRMP), reduced weight gain (LRWG), abortion (LA). Indirect costs included costs for treatments (CTRT), the costs associated with culling and replacement (LRP), movement controls (CMC), and biosecurity measures (CBS). Provincial veterinary service costs included those associated with vaccination, surveillance, movement restrictions, public awareness campaigns and implementation of enhanced biosecurity measures. All the costs were calculated in Indonesia rupiah (IDR, million).

Costs were estimated at the individual farm level. For NTB the number of calves, heifers, cows and bulls on 10,000 commercial beef farms and 200,000 smallholder farms were simulated based on the Badan Pusat Statistik Indonesia data (BPS, 2023). For commercial beef farms the most likely number of adult cattle per farm was 15 (minimum 10, maximum 120). For smallholder farms the most likely number of adult cattle per farm was 2 (minimum 1, maximum 9). Since there are no commercial dairy farms in Nusa Tenggara Barat, this category was excluded from our calculations. The economic analysis was conducted using two models: (1) a total economic cost model; and (2) a benefit-cost analysis (BCA) model. FMD elimination was assumed to take several years so the expected number of incident FMD positive farms per year was calculated using the exponential decay function (Serway et al., 1989) for the first five years. After five years the number of incident FMD positive farms per year was set to follow a low frequency, undulating pattern (Kumpai and Modnak, 2025):
$\mu(t)=\mu 0\ e^{-\lambda t}$ Equation 1
$\mu(t)=\mu 0\ e^{-\lambda t}[1+A \cos 2\pi t/T]$ Equation 2

Where:
$\mu 0$ = The number of FMD positive farms in year 0.
λ = The long-term decline rate.
A = Amplitude.
T = Time period (year).

Three timelines were selected (2035, 2040 and 2045) and the total cost of elimination for each timeline calculated. Future costs were converted to present value of costs and present value of benefits:
PVB= ∑_(t=1)^nBt/(1+i)^t Equation 3
PVC= ∑_(t=1)^nCt/(1+i)^t Equation 4

Where:
n = The total number of program years.
Ct = Program costs in year .
Bt = Program benefits in year .
i = Discount rate, as a decimal fraction.

Results:

The average cost of FMD for a commercial beef farm was 15.6 (minimum 6.54, maximum 69.1) million IDR per year with a yearly farm level FMD incidence risk of 10%. Most of the annual cost was due to biosecurity

Theme 7

measures followed by animal mortality. The average cost for a smallholder farm was 1.41 (minimum 0.31, maximum 9.68) million IDR per year. Similar to commercial beef farms, most of the annual cost was due to biosecurity measures followed by animal mortality.

The total cost of the elimination programme for the province was around 162,153 million IDR per year with 83% of the total provincial cost due to vaccination at 90% population coverage. Movement restrictions accounted for 7.5% of the total provincial cost per year. The estimated costs of FMD elimination by 2035 for commercial beef farms, smallholder farms and the provincial authority were 31,417 million IDR, 57,770 million IDR and 1,849,972 million IDR, respectively. If the year of elimination success was extended to 2040 the estimated costs for commercial beef farms, smallholder farms and the provincial authority were 36,100 million IDR, 66,379 million IDR and 2,420,610 million IDR, respectively. When the elimination was achieved by 2045, the costs for commercial beef farms, smallholder farms and the provincial authority were 37,746, 68,542 and 4,348,150 IDR million, respectively. The benefit-cost ratio for FMD elimination reduced as the time taken to eliminate disease increased.

Discussion:

Economic analyses are an essential component to support decision making around whether or not to eliminate disease from a given area. Several studies have evaluated the economic impact of foot-and-mouth disease (FMD) control measures in different regions of the world (Randolph et al., 2002; Hasler et al., 2021). In this study, most of the costs for FMD elimination were carried by the provincial veterinary authority (for vaccination and enforcement of movement restrictions). In terms of losses on individual farms, the per cattle costs were similar for both commercial beef and smallholder farms. However, another study showed that the impact were higher in small holder farms in Tanzania compared to larger production systems (Hasler et al., 2021). For elimination years set to 2035, 2040 and 2045 BCRs were below 1 which is expected in areas with no established export markets. In countries with established export markets, the costs can be even higher, but the return on investment is positive. So, eliminating FMD would result in positive economic returns once trade restrictions were lifted. In a farm-level economic evaluation in South Vietnam, prevention and control of FMD had a positive BCR (Truong et al., 2018). Similarly, in Ethiopia, a benefit-cost analysis of different FMD control strategies returned positive outcomes. The BCR for FMD elimination in NTB was close to 1 for all three elimination scenarios and since cattle from NTB are exported in different provinces of Indonesia, freedom from FMD might produce positive outcome in the future.

Conclusion:

In endemic countries without established export markets, such as Indonesia, control strategies must be carefully planned to maximise program benefits. While immediate economic returns are not profitable in NTB, there is substantial potential for FMD elimination to become economically favourable under improved control efficiency and favourable market conditions.

Elimination year	Total (IDR million)		Present value (IDR million)		BCR
	Costs	Benefits	Costs	Benefits	
2035	1,944,793	1,631,105	1,704,052	1,449,324	0.851
2040	3,112,749	2,601,979	2,523,635	2,133,305	0.845
2045	4,454,437	3,604,745	3,334,759	2,731,681	0.819

Table 1. Benefit-cost estimates for FMD elimination by 2035, 2040 and 2045 in Nusa Tenggara Barat, Indonesia

Keywords: Foot-and-mouth disease, benefit cost ratio, cattle, ecomony.

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Insights from Questionnaire-Based Assessment of Farm Management Weaknesses during a Haemorrhagic Septicemia Outbreak in Prachin Buri, Thailand

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Summary

Surveillance systems in livestock and food production systems play a critical role not only in detecting disease outbreaks but also in identifying underlying risk factors embedded within farm management and biosecurity practices. This study evaluates the characteristic of animal health and farm management during an outbreak of haemorrhagic septicemia (HS) in Prachin Buri province, Thailand, with a particular focus on how questionnaire-based surveillance can reveal weaknesses in farm management that contribute to disease risk.

The investigation combined passive and active surveillance, laboratory confirmation, and structured questionnaires to assess animal health practices and farm-level biosecurity. While laboratory results confirmed *Pasteurella multocida* serotype B:2 as the causative agent, the questionnaire findings revealed substantial gaps in vaccination coverage, quarantine implementation, hygiene practices, and water management. These deficiencies represent critical vulnerabilities that may facilitate pathogen introduction, amplification, and transmission within livestock systems.

Although statistical analysis did not identify significant associations between individual risk factors and disease occurrence, the overall pattern of weak farm management and low biosecurity strongly suggests a conducive environment for HS outbreaks. The findings highlight the importance of integrating farm management assessments into surveillance systems to support disease prevention, improve livestock productivity, and strengthen food safety across value chains.

Introduction

Theme 7

Haemorrhagic septicemia (HS) is a highly fatal bacterial disease of cattle and buffalo caused by *Pasteurella multocida*, particularly serotypes B:2 and E:2, and is widely distributed in tropical regions of Asia, Africa, and the Middle East (1,2). The disease is characterized by rapid onset, septicemia, respiratory distress, and high mortality, often approaching 100% in untreated cases (2). Transmission occurs primarily through inhalation or ingestion of contaminated feed and water, as well as direct contact with infected or carrier animals (1).

Farm management and biosecurity play a critical role in the epidemiology of HS, as the disease is strongly associated with stress conditions, poor nutrition, inadequate vaccination, and environmental factors such as high humidity and rainfall (3). In endemic regions, a proportion of healthy animals may act as carriers, shedding the pathogen during periods of stress and contributing to disease spread (3). Biosecurity measures, including quarantine of new animals, sanitation practices, control of water and feed sources, and restriction of animal movement, are essential to prevent pathogen introduction and transmission. Similarly, proper animal health management, including vaccination, deworming, and record-keeping, plays a vital role in maintaining herd immunity and reducing disease susceptibility. Therefore, inadequate farm management and weak biosecurity systems significantly increase the risk of outbreaks.

In many smallholder and semi-intensive livestock systems, these practices are inconsistently applied due to limited resources, lack of awareness, or insufficient veterinary support. As a result, surveillance systems must not only detect disease events but also evaluate farm-level practices to identify systemic weaknesses that increase outbreak risk.

This study examines an HS outbreak investigation in Prachin Buri province, Thailand, with a specific focus on how questionnaire-based assessments, can identify weaknesses in farm management and biosecurity. The findings provide insights into how improving these practices can reduce the risk of HS and other infectious diseases, thereby enhancing the resilience of livestock production systems and safeguarding the food value chain.

Methods

The study was conducted as an outbreak investigation using a combination of passive and active surveillance. Passive surveillance was initiated following notification of abnormal buffalo deaths, while active surveillance was implemented to assess disease spread and identify risk factors in surrounding farms within a 5 km radius, focusing on cattle and buffalo farms in Nadee and Thung Po subdistricts, Prachin Buri province, during September to October 2024.

A structured questionnaire was developed to systematically assess farm management and biosecurity practices. The questionnaire covered four key areas, including general farm characteristics, active case detection, animal health management, and farm management practices. Particular emphasis was placed on evaluating biosecurity measures such as quarantine of new animals, sanitation and disinfection practices, water and feed management, housing systems, and vector control. The questionnaire also assessed animal health management practices, including vaccination, deworming, and record-keeping. A total of 29 farms participated in the survey, representing 93.55% of farms within the study area.

Data were collected through farmer structural and unstructural interviews, laboratory information management system, and field observations. Laboratory confirmation of HS was performed using bacterial culture and PCR methods.

Descriptive analysis was conducted to summarize farm practices and identify common weaknesses, while logistic regression was used to explore associations between risk factors and disease occurrence.

Results

Haemorrhagic septicemia was confirmed in a buffalo farm, with two laboratory-confirmed cases and three additional suspected cases. Active surveillance identified 15 suspected cases in cattle from nearby farms, although all recovered following treatment.

The questionnaire findings revealed widespread deficiencies in farm management practices that are directly relevant to HS risk. Vaccination coverage was inconsistent across farms, with several farms lacking prior HS vaccination despite its availability. Even among vaccinated farms, booster schedules were often not followed,

Theme 7

reducing the effectiveness of immunization programs. Quarantine practices were notably absent, as farms introducing new animals did not implement isolation periods before mixing them with existing herds. This represents a significant biosecurity gap, as asymptomatic carriers of *P. multocida* can introduce infection into susceptible populations. Water management practices were identified as a critical weakness, as most farms relied on untreated natural water sources such as canals. The lack of water treatment increases the risk of pathogen transmission, particularly in environments where contamination from other animals or environmental sources may occur. Sanitation and hygiene practices were also insufficient, as although some farms reported cleaning animal pens, the use of disinfectants was uncommon. Cleaning frequency varied and was often based on visible dirt rather than a preventive schedule, reducing its effectiveness in controlling pathogens.

In addition, farm biosecurity measures were generally weak, with limited control over animal movement, minimal restriction of visitors, and lack of dedicated equipment for different animal groups. These conditions increase the likelihood of disease introduction and spread within and between farms.

Animal health management practices were similarly inadequate. Deworming programs were inconsistently applied, and only a small number of farms treated all animals systematically. Poor parasite control may contribute to reduced immunity and increased susceptibility to infections such as HS. Record-keeping was also limited, with many farmers lacking documentation of vaccination history, disease events, and treatments. This lack of data reduces the effectiveness of surveillance systems and hinders evidence-based decision-making.

Although, no statistically significant associations were identified between specific risk factors and disease occurrence. However, the overall pattern of poor farm management and low biosecurity suggests that these factors collectively contribute to increased disease risk.

Discussion

The findings of this study support the widely recognized relationship between poor farm management, low biosecurity, and increased risk of HS outbreaks. Disease occurrence is not solely dependent on the presence of the pathogen but is strongly influenced by management-related factors such as animal health status, environmental stress, and husbandry practices (3). In particular, stressors such as poor nutrition, overcrowding, and adverse weather conditions can trigger the transition from asymptomatic carriage to clinical disease (3).

One of the most important observations is the widespread lack of effective biosecurity measures across farms, including hygiene practices, disinfection, and controlled access to farms, creates an environment that facilitates pathogen persistence and transmission. The absence of quarantine for newly introduced animals represents a major vulnerability, as it allows potential carriers of *P. multocida* to enter the herd without detection. Similarly, inadequate sanitation and lack of disinfectant use create an where pathogens can persist and spread. Biosecurity principles emphasize that prevention of disease introduction is more effective and cost-efficient than treatment after an outbreak has occurred (4)

Water management emerged as a particularly important risk factor, as untreated water sources can serve as reservoirs for pathogens. This is of particular concern because *P. multocida* can survive for extended periods in moist environments, and contaminated water can act as a source of infection (1). Additionally, environmental conditions such as high humidity and rainfall have been shown to facilitate disease transmission and increase outbreak frequency (2). Contamination of water sources may play a significant role in disease transmission, especially when combined with high animal density and environmental stress.

Inadequate vaccination practices also emerged as a major concern. Although vaccination is considered the most effective preventive measure against HS, inconsistent application and failure to maintain protective immunity can leave animals susceptible to infection (5). Studies have shown that immunity from certain vaccines may be short-lived if booster schedules are not properly followed, further emphasizing the importance of adherence to vaccination protocols (5).

The role of animal health management is also critical, as poor nutritional status, parasitic infections, and lack of preventive care can weaken the immune system and increase susceptibility to HS. The absence of proper record-keeping further compounds these issues by limiting the ability of farmers and veterinary services to monitor and respond to health problems.

While statistical analysis did not demonstrate significant associations between individual risk factors and disease occurrence, the overall pattern of findings strongly indicates that poor farm management and low

Theme 7

biosecurity act synergistically to increase susceptibility to HS outbreaks. This highlights a key limitation of relying solely on quantitative analysis and underscores the importance of descriptive and field-based surveillance approaches in understanding disease dynamics.

From a surveillance perspective, the use of questionnaires proved to be highly valuable in identifying these weaknesses. While statistical analysis did not yield significant associations, the descriptive findings provide strong evidence that poor farm management and low biosecurity are key contributors to disease risk.

These findings have important implications for livestock production systems and food value chains. Weaknesses at the farm level can compromise not only animal health but also food safety and trade, as diseased animals may enter the production chain if surveillance and control measures are insufficient.

Therefore, strengthening farm management and biosecurity should be a central component of surveillance systems. This includes promoting vaccination, improving hygiene and sanitation, ensuring safe water and feed, implementing quarantine measures, and enhancing farmer awareness and training.

Conclusion

This study demonstrates that surveillance systems in livestock production are not only essential for detecting and confirming disease outbreaks but also serve as critical tools for identifying underlying weaknesses in farm management and biosecurity that contribute to disease risk. Through the integration of passive and active surveillance with questionnaire-based assessments, the investigation of haemorrhagic septicemia (HS) in Prachin Buri province provided valuable insights into the conditions that facilitate the occurrence and spread of infectious diseases in cattle and buffalo farms.

Although laboratory findings confirmed the presence of *Pasteurella multocida* serotype B:2 as the causative agent, the broader significance of this study lies in the identification of systemic management gaps across farms. The absence of consistent vaccination practices, lack of quarantine for newly introduced animals, inadequate sanitation and disinfection, and reliance on untreated water sources collectively represent critical biosecurity weaknesses. These factors create an environment that not only allows the introduction of pathogens but also supports their persistence and transmission within and between farms.

From a broader perspective, the findings emphasize that improving farm management and biosecurity is fundamental to strengthening livestock production systems and safeguarding food value chains. Weaknesses at the farm level can have downstream impacts on animal health, productivity, food safety, and trade, particularly in regions where smallholder and semi-intensive farming systems predominate.

In conclusion, strengthening farm management and biosecurity must be prioritized as central components of disease prevention strategies for haemorrhagic septicemia and other infectious diseases. By addressing these fundamental issues, surveillance systems can move beyond reactive responses to become proactive tools for improving animal health, ensuring food safety, and enhancing the resilience of livestock production systems.

Keywords: Biosecurity, Farm management, Animal Health Management, Surveillance, Haemorrhagic Septicemia.

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Differential Diagnosis of Nodular Skin Lesion in Bali Cattle: A Surveillance Case Study from Keerom District, Papua Province, Indonesia

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Summary

This study details a clinical field investigation of nodular skin lesions in Bali cattle in Keerom District, Papua Province, Indonesia, conducted in January 2025 to differentiate endemic conditions from high-priority diseases like Lumpy Skin Disease (LSD) and Foot and Mouth Disease (FMD). Using an active case-finding approach and laboratory analysis at DIC Jayapura, the investigation focused on a closed herd where 33.3% of animals exhibited firm multifocal nodules. Despite physical similarities to LSD, the affected cattle remained systemically stable, and diagnostic testing—including RT-PCR and ELISA—was negative for LSDV and FMDV, while microscopic evaluation confirmed a *Demodex* sp. infestation. These findings highlight the importance of diagnostic precision in strategic border regions to prevent economic alarm and ensure evidence-based biosecurity protocols.

Introductions

Nodular skin lesions are critical for differentiating endemic conditions from National Strategic Contagious Diseases (PHMS) such as Lumpy Skin Disease (LSD) and Foot and Mouth Disease (FMD). While LSD typically presents with generalized nodules (0.5–5 cm) that undergo central necrosis, and FMD is characterized by oral and pedal vesicles, bovine demodicosis manifests as firm, localized nodules associated with the hair follicles (1, 2, 3). These *Demodex* sp. nodules, predominantly found on the head, neck, and shoulders, serve as key clinical indicators for distinguishing this parasitic infestation from highly contagious viral pathogens (4).

Bovine demodicosis is a widely distributed parasitic disease with prevalence rates ranging from 4.9% in Ethiopia to 43.5% in Russia (4, 5). In Indonesia, this condition has been documented in Bali cattle (*Bos javanicus*) across various regions, including reports from Badung District, Bali Province, in 2014 and more recently in Gowa District, South Sulawesi Province, in 2023, where one in three cattle was found infested (1, 6). The recurring presence of this parasite across the archipelago underscores the necessity for continuous monitoring and its inclusion as a primary differential diagnosis for nodular skin diseases.

Geographically, Keerom District is a strategic border region that serves as a critical point for national animal health surveillance. Amidst the widespread outbreaks of Lumpy Skin Disease (LSD) and Foot and Mouth Disease (FMD) across Indonesia, Keerom District position as a cross-border gateway increases the risk of introducing transboundary animal diseases. The tropical climate, characterized by high humidity and abundant insect vectors, creates an ideal ecosystem for mechanical virus transmission, which can be clinically difficult to distinguish from endemic diseases such as demodicosis (2, 3). The emergence of nodular skin lesions in this border area demands high vigilance and accurate differential diagnosis to prevent significant economic impacts and safeguard the national animal health status. Consequently, precise clinical and laboratory evaluation of these manifestations is essential for implementing appropriate biosecurity and therapeutic protocols.

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Theme 7

Methods

The investigation was conducted in Wulukubun Village, Skanto Subdistrict, Keerom District, Papua Province, Indonesia, from December 1, 2024 to January 31, 2025. To verify the case in cattle, an active case-finding approach using a defined case definition was applied. Cases were classified as suspected or confirmed. A suspected case was defined as cattle with Multiple nodules with or without folliculitis and furunculosis of skin lesion in the face, neck and shoulders, occurring in Wulukubun Village between December 1, 2024 and January 31, 2025. A confirmed case was defined as a suspected case with laboratory confirmation through ectoparasite identification.

To describe the case characteristics, field data were gathered through direct clinical observations of the animals and farm conditions conducted on the visited farms and Face-to-face structured interviews with the cattle farmer. An investigation form used that captured details such as farmer's name and location, timeline, incidence, affected animals and clinical signs, and potential risk factors.

Animal samples were collected from a farm managing six Bali cattle (Bos javanicus), two of which exhibited clinical manifestations. Sampling procedures included the collection of whole blood with EDTA, serum, nasopharyngeal swabs, and skin scrapings from the nodular lesions. Diagnostic tests were performed at the DIC Jayapura, comprising molecular detection using Real-Time PCR (RT-PCR) for Foot-and-Mouth Disease Virus (FMDV) from two nasopharyngeal swabs, and Lumpy Skin Disease Virus (LSDV) from two whole blood samples and one skin scraping. Serological analysis for LSD antibody detection was performed on two serum samples using ELISA. For ectoparasite identification, two skin scrapings were obtained from each symptomatic animal; processed with 10% Potassium Hydroxide (KOH), and the samples were placed on glass slides for direct microscopic examination. Data were analysed using descriptive and simple analytical methods to characterize the clinical presentation and correlate field findings with laboratory confirmatory results.

Results

Descriptive Finding

The cutaneous condition progressed over a two-month period prior to the formal investigation. The index case, identified by the farmer on December 1, 2024, initially presented with minor cutaneous discoloration. A secondary case occurred on January 1, 2025, suggesting a slow and progressive intra-herd transmission. On January 14, 2025, the incident was officially reported to the Keerom District animal health officer at Keerom District Agricultural Office, prompting an initial administration of multivitamin therapy and formal notification to the DIC Jayapura. The comprehensive veterinary investigation and diagnostic sampling were subsequently conducted on January 15, 2025.

The investigation was localized to a smallholder farm in Wulukubun Village, Skanto Subdistrict, Keerom District, Papua Province, Indonesia. This region is characterized by high tropical humidity and a significant population of biting insects. The facility functioned as a closed-herd system; the affected cattle were born and raised on-site with no history of movement or introduction of new animals from outside Wulukubun Village for the duration of their lives. The spatial risk was confined to a single communal enclosure where all six cattle were housed, facilitating close physical contact.

Physical examination of the six Bali cattle (Bos javanicus) revealed that two of six cattles (33.3% of the herd) exhibited multifocal cutaneous nodules. The index case is a 2-year-old female cattle, and the secondary case is a male cattle aged under 1 year. The lesions were primarily localized on the facial region, neck, and abdomen. These nodules were characterized by a firm consistency upon palpation (induration) and lacked the central depression typical of necrotic LSD lesions.

The diameter of the nodule lesions varied significantly, ranging from 2 cm to 8 cm. Cutaneous nodules in the secondary case were less severe than those in the index case, with lesion sizes characterizing a 'dollar plaque' appearance. Chronic progression was evident, with the index case showing extensive skin thickening and localized alopecia (hair loss) around the nodular sites. Despite the severity of the cutaneous manifestations, both affected cattle remained systemic-physiologically stable, maintaining a normal rectal temperature, consistent appetite, and active behavioural patterns. No mucosal lesions or lymph node enlargements were observed during the clinical workup.

Theme 7

Laboratory and Diagnostic Findings

The diagnostic results from the DIC Jayapura provided definitive evidence for the exclusion of transboundary viral pathogens (FMDV and LSDV) and the confirmation of parasitic infestation (*Demodex* sp. mite) shown in Table 1.

Nucleic acid extraction from whole blood with EDTA, nasopharyngeal swabs, and skin scrapings yielded negative results for the *Capripoxvirus* (LSDV) genome via RT-PCR. Furthermore, all samples tested negative for Foot-and-Mouth Disease Virus (FMDV), effectively ruling out primary differential diagnoses of national strategic concern. Complementing the molecular results, ELISA for LSD antibody detection was also negative, indicating a no of prior exposure or immune response to the *Capripoxvirus* in the sampled cattle.

Figure 3. *Demodex* sp. adult mite isolated from skin scrapings, observed under light microscopy (400x magnification)

Microscopic examination of deep skin scrapings, processed with 10% Potassium Hydroxide (KOH), revealed a high density of *Demodex* sp. mites across various life stages, including adults and nymphs. The presence of these mites within the hair follicles was highly consistent with the chronic nodular dermatitis observed during the field investigation.

Action Taken

Immediate medical intervention was implemented on January 14, 2025, through the administration of Ivermectin to eradicate the *Demodex* sp. infestation, with a follow-up dose scheduled for January 28, 2025. In addition to antiparasitic therapy, the farmer was provided with disinfectants and anthelmintics to enhance overall stall hygiene and herd health. The investigation team also conducted Communication, Information, and Education (CIE) sessions focusing on biosecurity protocols and the clinical recognition of National Strategic Contagious Diseases (PHMS). As a precautionary measure against intra-herd transmission, the owner was instructed to maintain the isolation of symptomatic animals while awaiting definitive laboratory confirmation.

Discussion

The clinical manifestation of multifocal cutaneous nodules in Bali cattle often presents a diagnostic challenge, particularly in distinguishing between endemic parasitic infestations and high-priority transboundary viral diseases. In this case, the large nodular lesions initially necessitated a thorough differential diagnosis involving Foot-and-Mouth Disease (FMD) and Lumpy Skin Disease (LSD).

The clinical investigation in Wulukubun Village underscores the critical importance of differential diagnosis in managing nodular skin diseases in border regions. Although the initial physical presentation raised concerns regarding Lumpy Skin Disease (LSD), the laboratory results effectively ruled out *Capripoxvirus* and FMDV, confirming a case of bovine demodicosis. The 33.3% herd prevalence observed in this smallholder farm is significantly higher than the general prevalence of 4.9% reported in broader cross-sectional studies (4), likely due to the closed-herd communal housing system which facilitated prolonged physical contact between the index and secondary cases.

The progression of lesions over two months reflects the chronic nature of *Demodex* sp. infestations. The localized distribution on the face, neck, and abdomen as primary predilection sites in Bali cattle (1). Furthermore, the variation in nodule diameter (2–8 cm) and the "dollar plaque" appearance in the secondary case are consistent with the morphological descriptions of demodicosis, which often starts as small circumscribed papules before progressing into larger, indurated nodules as the mites multiply within the hair follicles (1).

A key diagnostic differentiator in this case was the systemic stability of the affected cattle. Unlike LSD, which typically presents with high fever, lymphadenopathy, and "sit-fast" necrotic cores (2), the cattle in Keerom maintained normal appetite and rectal temperatures. This lack of systemic involvement, despite extensive skin thickening and alopecia, is highly characteristic of demodicosis. The statistically significant variation in infestation sites reported in literature—specifically the high prevalence in the shoulder and neck regions (4)—further supports the field observations where lesions were concentrated in the anterior portion of the animal's body.

Theme 7

The environmental conditions in Keerom, characterized by high tropical humidity and biting insects, may have acted as predisposing factors. While the laboratory results confirmed *Demodex* sp. as the primary etiologic agent, the role of mechanical vectors or environmental stress in exacerbating cutaneous manifestations in Bali cattle warrants further longitudinal surveillance. These findings demonstrate that even in high-risk zones for transboundary diseases, endemic parasitic conditions like demodicosis can manifest with high clinical severity, necessitating robust laboratory-backed surveillance to prevent unnecessary economic alarm.

The therapeutic use of Ivermectin on January 14, 2025, followed by a booster on January 28, was essential to interrupt the *Demodex* sp. life cycle (1). Beyond clinical recovery, providing CIE on National Strategic Contagious Diseases (PHMS) is a vital surveillance component in the Keerom border region. As emphasized by WOAH (2, 3), rapid clinical differentiation and strict biosecurity, including isolation, are crucial to safeguard against transboundary pathogens like LSD and FMD.

Conclusion

Nodular skin lesions observed in Bali cattle in Wulukubun Village, Skanto Subdistrict, Keerom District, Papua Province, Indonesia, were attributed to infestation by *Demodex* spp. Affected animals exhibited clinical signs characterized by extensive skin thickening and localized alopecia surrounding the nodular lesions, particularly on the facial region, neck, and abdomen.

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The authors express their gratitude to the DIC Jayapura for the laboratory facilities and diagnostic expertise provided during this study. We also thank the Keerom District Agricultural Office for their vital role in field reporting and case management. Special appreciation is extended to cattle farmer in Wulukubun Village for his cooperation during the field study, as well as the technical staff who contributed to the surveillance efforts in this border region.

Diagnostic Tests	Sample Type	Result
RT-PCR FMDV	nasopharyngeal swab	Negative (2/2)
RT-PCR LSDV	whole blood with EDTA	Negative (2/2)
	skin scraping	Negative (1/1)
ELISA LSD antibody detection	serum	Seronegative (2/2)
Ectoparasite identification	skin scraping	Positive *Demodex sp.* (2/2)

Table 1. Diagnostic Tests Results on Cattle Samples in Wulukubun Village, Skanto Subdistrict, Keerom District, Papua Province, 2025

Keywords: *Demodex* sp., Papua, Cattle, Nodule, LSD.

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Theme 7

Poster presentations

Surveillance capacity and value-chain integration of cattle slaughterhouses in Thailand: implications for risk-based bovine tuberculosis monitoring

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Disease monitoring relies on slaughterhouses to identify zoonotic and production-limiting infections such as bovine tuberculosis at the crossroads of animal health and food safety. In low- and middle-income settings, slaughterhouse surveillance remains one of the most feasible forms of passive surveillance, yet its implementation varies substantially according to local operational realities. In Thailand, national evidence on facility-level surveillance readiness remains limited despite the important role of slaughterhouses in disease detection and reporting. This study evaluated surveillance capacity and value-chain integration among cattle slaughterhouses in Thailand and identified system-level patterns relevant to risk-based bovine tuberculosis surveillance.

A national cross-sectional study was conducted between January and June 2024 in 90 cattle slaughterhouses selected from 462 officially registered facilities using stratified sampling by region and operational scale. Surveillance performance was assessed using a Surveillance Capacity Index (SCI), constructed from four domains: standard operating procedure compliance, documentation quality, reporting channels, and traceability infrastructure. Value-chain integration was measured using a Value Chain Integration Score (VCIS), reflecting supplier diversity, service-user access, and customer diversity. Comparative analyses were performed by operational scale, ownership type, and region.

Across all facilities, the mean SCI was 0.52 ± 0.22 and the mean VCIS was 0.67 ± 0.26. Small-scale slaughterhouses showed the highest surveillance capacity (SCI 0.55 ± 0.23) and the strongest value-chain integration (VCIS 0.76 ± 0.19), while large-scale facilities had the lowest integration (VCIS 0.22 ± 0.21). Private facilities demonstrated significantly stronger surveillance-related performance than public facilities in both SCI and VCIS. Marked regional variation was also observed, with lower surveillance readiness in some regions compared with others. These findings suggest that surveillance readiness is not uniformly distributed across the Thai slaughterhouse network and that structural characteristics influence implementation capacity.

This study provides national-level evidence that slaughterhouse surveillance capacity in Thailand is heterogeneous rather than standardized in practice. A uniform compliance model is therefore unlikely to be optimal. Instead, bovine tuberculosis surveillance policy should move toward a risk-based and context-sensitive approach aligned with operational scale, ownership structure, and value-chain position. Strengthening surveillance in slaughterhouses should focus not only on technical requirements, but also on system design that reflects how facilities actually function within livestock production and marketing networks.

Keywords: bovine tuberculosis, slaughterhouse surveillance, surveillance capacity, value-chain integration, Thailand.

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Avian Influenza bio-surveillance in Nepal: Status, opportunities and challenges

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Avian influenza is a highly infectious disease of poultry with significant socio-economic impacts but also equally important public health threat due to its zoonotic potential. Nepal faced its first outbreak of highly pathogenic avian influenza (HPAI) H5N1 in 2009, and more than 400 outbreaks have been confirmed since then causing huge financial losses to the poultry industry. Apart from HPAI, low pathogenic avian influenza (LPAI), especially the H9N2, circulation in the country has posed serious economic threat to the poultry industry. Surveillance of poultry population on a regular basis helps to monitor the virus and can be controlled before it spreads to the population level. The Food and Agriculture Organization of the UN is supporting the Central Veterinary Laboratory in conducting the avian influenza active bio-surveillance from avian influenza high-risk districts. The objective of this study is to present the findings of the avian influenza bio-surveillance conducted between 2019 to 2025 and discuss the opportunities and challenges of avian influenza bio-surveillance in Nepal. Samples were collected during December 2019- March 2020 (8 districts), September- October 2024 (16 districts) and February- April 2025 (16 districts). In total, 2708 swabs and environmental samples were collected from live markets, slaughter places, poultry and pig farms and wild-bird interfaces. The collected samples were tested by using Real Time Reverse Transcriptase Polymerase Chain Reaction (rRT PCR) for M-gene first followed by further testing of positive samples for subtype H5, H9, H7, N1, N6, N8, N9 and N2 at the Central Veterinary Laboratory, Kathmandu. Results indicated that 434 out of 2708 samples tested (16.02%) were positive for LPAI H9N2 with variability across the years (22.8% during 2019-2020; 7.38% in 2024 and 14.3% in 2025) while none of the samples tested positive for HPAI. Among LPAI H9N2 positive samples, there were substantial variations observed by districts, species and sample types. These bio-surveillance program has provided an opportunity to track the circulation of the avian influenza virus in poultry and pig population of high-risk districts of Nepal and has contributed to build a sustained capacity for conducting surveillance and testing of avian influenza virus for early detection and warning. Challenges include failure of surveillance to detect the HPAI virus, limited spatial coverage (only 16 out of 77 districts of Nepal) and limited participation of large-scale poultry farmers in the surveillance. Another challenge is the lack of gene sequencing capacity to track the changes in the virus over the years. In summary, avian influenza active bio-surveillance program in Nepal has provided evidence of different avian influenza virus circulating in the poultry and pig population in a real time basis and will provide valuable information in formulating control policies and developing early warning system in the country in the future. A combination of active and passive surveillance will be needed to detect both HPAI and LPAI virus circulating in the country. We recommend continuing the avian influenza bio-surveillance program expanding spatial and temporal coverage and building gene sequencing capacity to track the rea changes in the circulating virus.

Keywords: Bird Flu, LPAI, HPAI, Surveillance, Zoonotic disease.

Theme 7

African Swine Fever in Mindanao, Philippines: From Farm to Market—Prevalence, Risk Factors, Farmer Perspectives and Financial Losses

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This cross-sectional survey, conducted from 2020 to 2023, investigated the epidemiology of African Swine Fever (ASF) in Mindanao, Philippines. The study aimed to estimate ASF prevalence among smallholder pigs and abattoir-slaughtered pigs, detect ASF virus in pork products, identify risk factors, assess the knowledge, attitudes, and practices (KAP) of smallholder pig farmers, and quantify direct financial losses. Nearly 5,000 pigs from diverse villages and abattoirs were randomly sampled for blood, while 420 pork products (chorizo, longganisa, lumpia, and pork cuts) were collected from local markets. Serum samples were tested using ELISA for ASF antibodies, and blood and pork products were tested for viral DNA. More than 1,500 pig owners were interviewed using validated questionnaires to evaluate KAP. Results revealed low seroprevalence: 0.6% (20/3,158) in smallholder pigs and 0.1% (2/1,538) in abattoir pigs. In contrast, 5.2% (22/420) of pork products were contaminated, indicating ongoing risks in the food chain. Ten major risk factors were identified, including proximity of piggeries, absence of footbaths, swill feeding, contact with animals, and improper disposal of dead pigs. Farmers demonstrated average knowledge, favourable attitudes, and moderate practices, suggesting partial awareness but gaps in implementation. Financial losses were significant, averaging nearly US$1 million per surveyed province, demonstrating the burden of ASF on local livelihoods and the economy. In conclusion, ASF prevalence in pigs is low, but contamination in pork products persists, and farmer KAP gaps and high financial losses emphasize the urgent need for more awareness campaigns, stronger biosecurity, improved surveillance, and livelihood support to reduce risks and losses.

Keywords: African swine fever (ASF), epidemiology, pork product contamination, risk factors, Philippines.

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Seroprevalence and subclinical hemato-biochemical impact of bovine viral diarrhea virus in slaughtered cattle in Bukidnon, Philippines

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Summary

Bovine Viral Diarrhea Virus (BVDV) is a significant global pathogen, affecting respiratory and reproductive tracts, causing profound economic losses through reduced reproductive efficiency and increased morbidity (1, 2). While the virus is documented in the Philippines, data on its seroprevalence and physiologic impact in Bukidnon, a major Philippine cattle-producing region which accounts for 12.0% of national livestock production, remains scarce (3, 4). This study aimed to address this critical gap by determining the seroprevalence of BVDV among slaughtered cattle in Bukidnon and analysing associated hemato-biochemical and physiological factors (4, 5).

Methods

Between March and April 2025, blood samples were collected from 275 cattle at four selected slaughterhouses in Bukidnon. Screening was performed using a commercial BVDV Antibody Rapid Test Kit. For 63 seropositive and 63 seronegative cattle, hematological analysis was conducted using an IDEXX VetAutoread Analyzer, and serum biochemical profiling was performed with a Healgen Automatic Biochemistry Analyzer. Statistical comparisons utilized the Mann- Whitney U test for continuous profiles and Chi-square or Fisher's Exact tests for categorical indicators.

Results

The seroprevalence of BVDV-Ab was 22.91% with significant spatial clustering observed; cattle from southern municipalities were 2.48 times more likely to be seropositive ($p < 0.002$). Seropositive cattle exhibited significantly higher median monocyte percentages (7.6% vs. 5.45%, $p = 0.009$) and LDH levels (903.0 U/L vs. 855.5 U/L, $p = 0.010$). Conversely, hemoglobin (10.3 g/dL vs. 11.0 g/dL, $p = 0.003$) and hematocrit (31.8% vs. 33.8%, $p = 0.006$) were significantly lower. Above-normal rectal temperature was strongly associated with seropositivity (OR = 3.73, $p < 0.001$) (13).

Discussion

The findings suggest that BVDV is endemic and continuously circulating among Bukidnon cattle. Significant monocytosis aligns with findings by Avci et al. (2014) likely reflecting chronic antigenic stimulation or immune dysregulation (7, 9). Lower hemoglobin and hematocrit indicate a mild, virus-associated anemia resulting from bone marrow suppression, a mechanism documented (5). Elevated LDH levels, also reported by Ghanem (2012), signify subclinical tissue disruption and metabolic stress (9). These results underscore the importance of integrating hematological profiling into routine disease surveillance to identify subclinical viral impacts (10).

Theme 7

Theme 7

Furthermore, the strong association between hyperthermia and seropositivity underscores the utility of basic physiological monitoring in identifying potentially infected animals (5).

Conclusion

This study confirms that BVDV is endemic within the slaughtered cattle population of Bukidnon, Philippines. The significant spatial clustering of seropositivity in southern municipalities, is an indication of localized hot spots demanding targeted surveillance and biosecurity interventions. The physiological profile of seropositive cattle reveals a distinct subclinical impact characterized by significant monocytosis, elevated LDH, and decreased hemoglobin and hematocrit levels, suggesting that BVDV infection leads to chronic immune dysregulation, subclinical tissue disruption, and mild viral-associated anemia. Ultimately, these results highlight the necessity of integrating hemato-biochemical profiling into routine veterinary diagnostic frameworks to detect the silent, non-cytopathic effects of BVDV. Establishing robust, region-specific monitoring programs is critical to mitigating the economic and reproductive losses associated with this pathogen in one of the Philippines' primary livestock-producing regions.

Keywords: BVDV, Seroprevalence, Bukidnon, Hemato-biochemical, Slaughterhouse surveillance.

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Epidemiology of African Swine Fever in Pork Products and Slaughtered Pigs and the Lived Experiences of Selected Stakeholders in Davao de Oro, Philippines

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African Swine Fever (ASF) is a highly fatal viral swine disease that significantly impacted the Philippines since its incursion. This project was conducted to determine the prevalence and risk factors of ASF among pork products and slaughtered pigs, and to assess the lived experiences of selected stakeholders in ASF-affected areas in the province of Davao de Oro. A total of 84 pork products were assessed for ASF viral DNA using molecular test. Additionally, 84 slaughtered pigs were tested for ASF viral DNA and antibody using conventional polymerase chain reaction (PCR) and enzyme-linked immunosorbent assay (ELISA), respectively. In-depth interviews were also conducted with 30 stakeholders, consisting of pork vendors, consumers, and meat inspectors. An overall 4.76% ASF prevalence was found in pork products, with all positive samples derived from longganisa, and prevalence rates of 3.93% and 21.4% for ASF viral DNA and antibodies in slaughtered pigs, respectively. The lived experiences survey revealed five critical themes on ASF, including the socioeconomic impact of ASF, control and

Theme 7

preventive measures against ASF, the local government unit's actions against the disease, viral transmission, and common misconceptions about ASF. While stakeholders demonstrated awareness of the disease and its mitigation strategies, there is a critical need for continued information dissemination and education to reinforce biosecurity practices. This study highlights the low yet persistent presence of ASF in pork products and slaughtered pigs, posing significant risks to the province's swine industry. Enhanced and sustained surveillance, strict biosecurity measures, and targeted educational campaigns are thus essential for controlling ASF and mitigating its socioeconomic impacts.

Keywords: African swine fever, Pork products, Pigs, Lived experiences, Epidemiology.

Epidemiological and molecular characteristics of HPAI viruses (H5Nx) in selected live bird markets in Lao PDR, 2022-2023

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Abstract

Epidemiological and molecular characteristics of HPAI viruses (H5Nx) in selected live bird markets in Lao PDR, 2022-2023
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Introduction

Highly pathogenic avian influenza (HPAI) viruses, particularly A(H5N1) and A(H5N6), continue to pose significant threats to animal and public health in Southeast Asia. This study aimed to investigate the epidemiological patterns and molecular characteristics of avian influenza viruses circulating in Lao People's Democratic Republic (PDR) through active surveillance in live bird markets (LBMs) from 2022 to 2023. A total of 9,360 samples from chickens, ducks, and market environments were tested using real-time RT-PCR. Results showed that 6.86% of samples were positive for influenza A and 2.63% for H5 subtypes, with H5N1 as the predominant virus. Ducks were identified as the main reservoir, with significantly higher infection rates compared to other sample sources. Increased virus detection was observed during the dry season and in 2023, indicating temporal patterns of transmission. Geographic hotspots included Luangnamtha, Salavan, and Vientiane Capital. Molecular analysis confirmed the circulation of H5N1 clade 2.3.2.1c and H5N6 clade 2.3.4.4b, consistent with regional trends. These findings highlight the need to strengthen risk-based surveillance, enhance biosecurity practices in LBMs, and maintain continuous molecular monitoring to support early detection and effective control of HPAI in Lao PDR.

Materials and Methods

Active surveillance was conducted in six LBMs across six provinces. A total of 9,360 samples, including oropharyngeal swabs from chickens, ducks and environmental samples, were collected monthly and tested using real-time RT-PCR for influenza A and H5 subtypes. Selected positive samples were sequenced for genetic characterization. Descriptive and multivariate analyses were performed to assess associations with location, season, year, and sample source.

Theme 7

Results and Discussion

Overall, 6.86% of samples were positive for influenza A, and 2.63% for H5 subtypes. H5N1 was the predominant subtype (2.34%), followed by H5N6 (0.29%). Ducks had significantly higher odds of infection compared to environmental samples (adjusted OR >4.0 for H5). Higher detection rates were observed during the dry season and in 2023. Geographic hotspots included Luangnamtha, Salavan, and Vientiane Capital. Phylogenetic analysis showed that H5N1 viruses belonged to clade 2.3.2.1c, while H5N6 viruses were classified as clade 2.3.4.4b.

Detection rates were higher in 2023 compared to 2022 and were significantly elevated during the dry season. These patterns may be associated with increased poultry trade and wild bird migration during this period. Ducks showed the highest infection rates, confirming their role as key reservoirs, while environmental contamination—particularly in drinking water—suggests potential indirect transmission within LBMs.

Multivariate analysis indicated that ducks, dry season, and year 2023 were significant risk factors for virus detection. Molecular analysis identified H5N1 clade 2.3.2.1c and H5N6 clade 2.3.4.4b, consistent with strains circulating in the region.

Keywords: Poultry, Lao PDR, Highly Pathogenic Avian influenza, in Six Live bird Markets.

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Theme 7

Understanding the spread of African Swine Fever in Nepal: Spatio-temporal analysis of early-phase outbreaks (March 2022 – July 2024)

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Summary

African swine fever (ASF), a highly contagious and often fatal viral disease affecting pigs, was first reported in Nepal on March 2022 which rapidly spread across the country. A retrospective study analysing early phase of outbreak from March 2022 to July 2024 with 43 outbreaks affecting 21 districts spanning all seven provinces was done. Bagamati province had highest number (18) of outbreaks. The outbreaks were predominantly in domestic pigs (42) with one in wild boar. Most outbreaks (77%) occurred in 2022 peaking prominently during summer months before declining in autumn and subsequent years. Outbreaks mainly affected small and medium scale farms. Spatial analysis identified a significant high-risk cluster in Sudurpaschim province covering Kailali, Kanchanpur, Doti and Dadeldhura districts. Rainfall was found to be associated with outbreak occurrence. These findings highlight seasonal peaks, geographically concentrated high-risk areas, and the urgent need for enhanced surveillance and targeted control measures to control ASF in Nepal.

Introduction

African swine fever (ASF) is a highly contagious viral disease of pigs transmitted through contact with infected pigs, their meat and products, or contaminated equipment. Pig farming plays a vital role in the livelihoods of many vulnerable ethnic communities in Nepal, making ASF a significant threat to both food security, economics, and livelihoods. ASF was first reported in Nepal on March 19, 2022, and then spread across the country. This study aimed to describe the spatiotemporal pattern of ASF outbreaks in Nepal between March 2022 to July 2024 and to generate evidence to inform the ASF control and prevention program in Nepal.

Methods

A retrospective cross-sectional analysis of reported ASF outbreaks was conducted. Temporal trends and seasonal patterns were studied, while spatial analysis was performed to identify high-risk clusters by using SaTScan (1). Associations between outbreak occurrence and environmental variables, as well as proximity to major roads, were also examined using Poisson regression.

Results

From March 2022 to July 2024, 43 outbreaks were reported from 21 districts, including 42 in domestic pigs and one outbreak in wild boar. Table 1 presents the summary statistics of farm size of domestic pig farms with African Swine Fever (ASF) outbreak in Nepal, from March 2022 to July 2024.

Most outbreaks (77%) were reported in 2022, with a pronounced peak during the summer months, followed by a decline in autumn and subsequent years. Outbreaks were reported in all seven provinces, with Bagamati province having the highest number of outbreaks (18/43). ASF affected farms across all production scales, although most occurred in small- and medium-scale holdings, with farm size varying across provinces. Spatial analysis using the spatio-temporal permutation model identified a significant cluster in Sudurpaschim province encompassing Kailali, Kanchanpur, Doti and Dadeldhura districts (Figure 1). Among the environmental variables assessed, rainfall was significantly (p value < 0.05) associated with outbreak occurrence.

Discussion

Theme 7

The study established a foundational evidence base for targeted prevention, emphasizing high-risk in summer, particularly June to July 2022 and significant clusters Sudurpaschim and Bagamati provinces Outbreaks affected farms across all scales, indicating biosecurity vulnerabilities (2, 3). This suggests the need for targeted interventions accounting for local farm sizes, management practices, and resource availability.

Seasonal peaks in summer 2022 aligned with global patterns in Europe and Asia (4, 5), potentially driven by rainfall-enhanced virus survival, mechanical transmission, and pig density. The sharp decline in 2023 and absence of reports from February to July 2024 likely reflect effective Department of Livestock Services (DLS) measures, including intensified stakeholder awareness, movement controls, and coordination (6).
Rainfall was found to be a significant environmental factor correlated with outbreaks (7), while temperature, humidity, and dew point showed no association, suggesting preparedness before/during rainy seasons in high-risk provinces.

Conclusion

This study provided foundational evidence on the spatial and temporal distribution of ASF in Nepal, identifying high-risk areas and periods for targeted intervention. The findings further underscore the need for enhanced surveillance and longitudinal studies to enhance national ASF prevention and control efforts in Nepal.

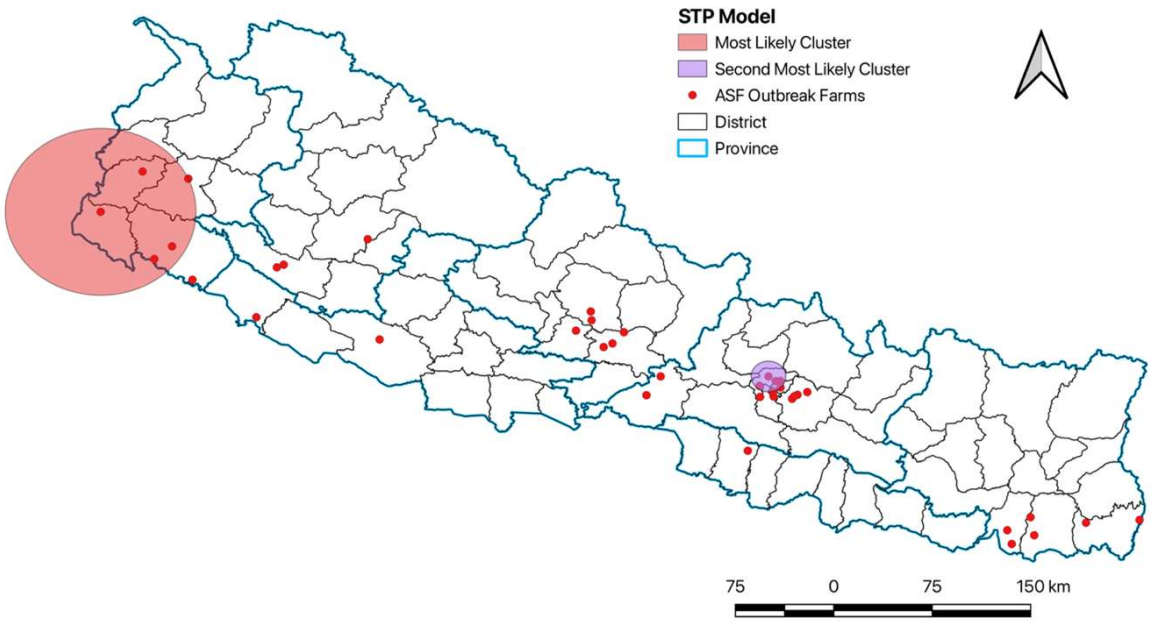


Figure 1: Spatiotemporal clusters of ASF outbreaks by Spatio-temporal Permutation Model in Nepal from March 2022 to July 2024

Keywords: ASF, Spatio-temporal patterns, cluster analysis, seasonal pattern, Nepal.

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Theme 7

Molecular Prevalence and Risk Factor Analysis of Tick-Borne Bacteria and Hemoplasmas in Beef Cattle at the Thai–Myanmar Border, Kanchanaburi Province, Thailand

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Summary

Tick-borne bacteria and hemoplasmas, including *Anaplasma* spp., *Ehrlichia* spp., *Rickettsia* spp., and *Mycoplasma* spp., cause significant morbidity and productivity losses in cattle across tropical regions. Despite their clinical relevance, data from beef cattle along cross-border regions of Thailand remain scarce. This cross-sectional study investigated the molecular prevalence and risk factors associated with these pathogens in 158 beef cattle from Thong Pha Phum, Sangkhlaburi, and cross-border cattle (CBC) imported from Myanmar, in Kanchanaburi Province, Thailand. PCR-based assays were employed to detect each pathogen. Overall, 56.9% (90/158) of cattle were positive for *Anaplasma/ Ehrlichia* spp. DNA. Among species detected, *Mycoplasma* spp. showed the highest prevalence (48.7%; 77/158), followed by *A. marginale* (17.1%; 27/158) and *Rickettsia* spp. (11.4%; 18/158). Multivariable logistic regression revealed that crossbred cattle had significantly higher odds of *Anaplasma* / *Ehrlichia* (OR=2.97; p=0.002) and *A. marginale* infections (OR=2.47; p=0.035). The presence of ectoparasites was significantly associated with *A. marginale* (OR=4.63; p=0.016) and *Mycoplasma* spp. infections (OR=6.87; p<0.001). These findings highlight the endemicity of multiple tick-borne and blood-borne bacterial pathogens in beef cattle at the Thai–Myanmar border and emphasize the importance of strengthened surveillance and tick control programs, particularly for imported cattle.

Introduction

Tick-borne pathogens (TBP) pose a major challenge to livestock health and agricultural productivity in tropical and subtropical regions, where vector tick species thrive under warm, humid environmental conditions (Jongejan & Uilenberg, 2004). Beyond protozoa, bacterial tick-borne pathogens including *Anaplasma* spp., *Ehrlichia* spp., and *Rickettsia* spp., represent a growing global concern in both veterinary and public health contexts (Parola et al., 2013). Among these, *Anaplasma marginale* is the causative agent of bovine anaplasmosis, a febrile hemolytic disease transmitted primarily by *Rhipicephalus microplus* in Southeast Asia, leading to anemia, reproductive losses, and mortality (Kocan et al., 2015). *Rickettsia* spp. are obligate intracellular bacteria of zoonotic significance that are increasingly detected in cattle and their associated ticks (Ninio et al., 2023).

Hemotropic *Mycoplasma*s (hemoplasmas), formerly classified as *Haemobartonella* spp. or eperythrozoa, are cell-wall-deficient bacteria that parasitize the erythrocyte surface of vertebrate hosts, causing hemolytic anemia and immunosuppression, particularly in immunocompromised animals (Tasker, 2022). Cattle associated hemoplasmas, including *Mycoplasma wenyonii* and *Candidatus* M. haemobos, are increasingly recognized as important subclinical pathogens in bovine populations across Asia (Aung et al., 2023).

In Thailand, most molecular studies on TBP in cattle have targeted protozoan parasites, leaving bacterial and hemoplasmal pathogens substantially under investigated, especially in beef cattle along key border areas. The Thai–Myanmar border in Kanchanaburi Province represents a critical zone of cross-border cattle trade, where animal movement may facilitate pathogen introduction and spread (Bhadury et al., 2026). To date, no study has characterized the molecular epidemiology of *Anaplasma* / *Ehrlichia* spp., *Rickettsia* spp., and *Mycoplasma* spp. in both local Thai and cross-border imported beef cattle in this region. The present study therefore aimed to determine the molecular prevalence of these pathogens and to evaluate host-related risk factors influencing infection in beef cattle at the Thai–Myanmar border.

Materials and Methods

Theme 7

Study Area, Sample Collection, and Ethical Approval

This cross-sectional study was conducted between December 2022 and January 2023 in Kanchanaburi Province, western Thailand, along the Thai–Myanmar border. A total of 158 blood samples were collected from beef cattle across three groups: Thong Pha Phum (n=50), Sangkhlaburi (n=70), and a cross-border cattle (CBC) group comprising Myanmar imported cattle held at Kanchanaburi quarantine station (n=38). Cattle with recent antiparasitic treatment or clinical illness were excluded. Approximately 2–3 mL of blood was collected aseptically from the jugular vein into EDTA-coated vacutainer tubes. All procedures were approved by the Kasetsart University Animal Care and Use Committee (Approval No: ACKU66-VET-024).

DNA Extraction and Molecular Detection

Genomic DNA was extracted from 200 µL of each blood sample using the Genomic Mini Kit (Geneaid Biotech Ltd., Taiwan) per manufacturer's protocol. Molecular detection was performed using PCR-based assays targeting: (i) a conserved region of the *Anaplasma / Ehrlichia* 16S rRNA gene for initial screening; (ii) the *A. marginale* major surface protein 5 (msp5) gene for species confirmation; (iii) *Rickettsia* spp. outer membrane protein A (ompA) gene; and (iv) a conserved region of the *Mycoplasma* 16S rRNA gene. PCR amplicons were visualized by 1.5% agarose gel electrophoresis, and representative positive samples were sequenced and compared against GenBank reference sequences using BLAST.

Statistical Analysis

Statistical analyses were performed using Stata version 15. Prevalence was calculated as the proportion of PCR-positive samples with 95% confidence intervals. Associations between infection and host-related factors (sex, breed, ectoparasite presence, age) were evaluated by chi-square test and multivariable logistic regression. Statistical significance was set at $p<0.05$.

Results

Molecular Prevalence and Geographic Distribution

Overall, 56.9% (90/158) of examined cattle were positive for *Anaplasma/ Ehrlichia*spp. DNA. Prevalence was highest in Thong Pha Phum (76.0%; 38/50), followed by Sangkhlaburi (51.4%; 36/70), and the CBC group (42.1%; 16/38) (Figure1).

Species-specific analyses revealed that *Mycoplasma* spp. was the most prevalent pathogen detected overall (48.7%; 77/158), with Sangkhlaburi recording the highest rate (65.7%), followed by Thong Pha Phum (56.0%). Strikingly, the CBC group had a markedly lower prevalence of *Mycoplasma* spp. (7.9%) but a relatively higher prevalence of *Rickettsia* spp. (18.4%) compared with local cattle (8.0–10.0%). *A. marginale* was detected in 17.1% of all cattle (27/158), with higher prevalence in Thong Pha Phum (28.0%) and Sangkhlaburi (17.1%) than in the CBC group (2.6%).

Risk Factor Analysis

Multivariable logistic regression identified significant associations between host-related factors and pathogen-specific infection. Breed was significantly associated with both *Anaplasma / Ehrlichia* spp. (OR=2.97; p=0.002) and *A. marginale* infections (OR=2.47; p=0.035), with crossbred cattle showing higher odds than local cattle. The presence of ectoparasites at the time of sampling was significantly associated with *A. marginale* (OR=4.63; p=0.016) and *Mycoplasma* spp. infections (OR=6.87; p<0.001), emphasizing the central role of tick vectors in transmission. Sex was significantly associated with *Rickettsia* spp. infection, with males exhibiting higher odds than females (OR=3.00; p=0.038), while females had significantly higher odds of *Mycoplasma* spp. infection (OR=0.24 for males vs. females; p<0.001). Age category was not significantly associated with any pathogen's infection status.

Discussion

This study provides the first molecular epidemiological data on *Anaplasma / Ehrlichia* spp., *Rickettsia* spp., and *Mycoplasma* spp. in beef cattle, including cross-border imported animals, at the Thai–Myanmar border. The overall *Anaplasma / Ehrlichia* prevalence of 56.9% indicates that haemoparasitic bacterial infections are highly endemic in this region. This is consistent with recent regional data reporting *Anaplasma* spp. prevalences of 40–

Theme 7

70% in cattle across Southeast Asian countries (Watthanadirek et al., 2021; Srionrod et al., 2022), reflecting favorable ecological conditions for *R. microplus* transmission in tropical border zones.

A. marginale was predominantly detected in local Thai cattle (Thong Pha Phum: 28.0%; Sangkhlaburi: 17.1%), while CBC cattle showed markedly lower prevalence (2.6%). This pattern likely reflects endemic establishment of *A. marginale* in local tick populations and pre-existing cattle immunity through repeated exposure. Comparable distribution patterns have been documented in a recent Vietnamese study involving cattle imported from Thailand, where locally adapted strains of *A. marginale* were molecularly characterized in resident herds (Sivakumar et al., 2018). The association of *A. marginale* infection with ectoparasite infestation (OR=4.63; p=0.016) reinforces the critical role of tick vectors in pathogen maintenance and transmission (Kocan et al., 2015).

The high overall prevalence of *Mycoplasma* spp. (48.7%), particularly in Sangkhlaburi (65.7%), is among the highest documented for bovine hemoplasmas in Southeast Asia. A recent molecular survey from Malaysia reported *Mycoplasma wenyonii* prevalences of 35–48% in cattle, attributing the high rates to dense tick burdens and semi-intensive management (Ola-Fadunsin et al., 2020). The markedly lower *Mycoplasma* spp. prevalence in the CBC group (7.9%) may reflect the shorter duration of tick exposure during quarantine transit or the different ecological origin of these animals. The ectoparasite-associated risk for hemoplasmal infection (OR=6.87; p<0.001) is consistent with evidence implicating ticks and biting flies as probable vectors of bovine hemoplasmas (Tasker, 2022; Steer et al., 2023). Additionally, the higher odds of *Mycoplasma* spp. infection in female cattle may be linked to physiological stress during lactation and parturition, which can modulate immune function and increase susceptibility to ectoparasite infestation (da Silva et al., 2013).

Rickettsia spp. were detected at an overall prevalence of 11.4%, with the CBC group showing the highest rate (18.4%). This finding has notable zoonotic implications, as several *Rickettsia* species detected in tick-infested cattle across Southeast Asia are known to be pathogenic in humans (Ninio et al., 2023; Wang et al., 2025). The significantly higher odds of *Rickettsia* spp. infection in male cattle (OR=3.00; p=0.038) may reflect differences in ranging behaviour, grazing exposure, and thus differential tick contact (Sansamur et al., 2025). The higher *Rickettsia* spp. prevalence in CBC cattle may suggest the introduction of novel *Rickettsia*l strains through transboundary cattle movement, warranting further molecular characterization of circulating genotypes.

Breed was identified as a significant risk factor for both *Anaplasma / Ehrlichia* and *A. marginale* infections, with crossbred cattle showing higher odds than local breeds. While local Thai native cattle may have developed partial breed-associated tolerance or resistance through sustained exposure to endemic tick-borne pathogens, crossbred animals, often maintained under higher input production systems with different grazing patterns that may face altered tick exposure or immune profiles (Srionrod et al., 2022). Taken together, the results emphasize the need for integrated tick management, targeted screening of imported cattle, and further investigation of pathogen diversity along this epidemiologically critical border.

Conclusion

This study provides the first molecular characterization of *Anaplasma/ Ehrlichia*spp., *A. marginale*, *Rickettsia* spp., and *Mycoplasma* spp. in beef cattle, including cross-border imported animals, at the Thai–Myanmar border. The high prevalences detected confirm endemicity of multiple bacterial tick-borne and blood-borne pathogens in this region. Ectoparasite infestation and breed emerged as the most consistent risk factors across pathogen species. The distinct infection profiles between local and cross-border cattle, particularly the elevated *Rickettsia* spp. prevalence in the CBC group, highlight the potential role of transboundary cattle movement in pathogen introduction and redistribution. These findings emphasize the urgent need for routine molecular surveillance, integrated tick control, and systematic health screening of imported cattle to safeguard livestock health and mitigate zoonotic risks in border regions.

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Theme 7

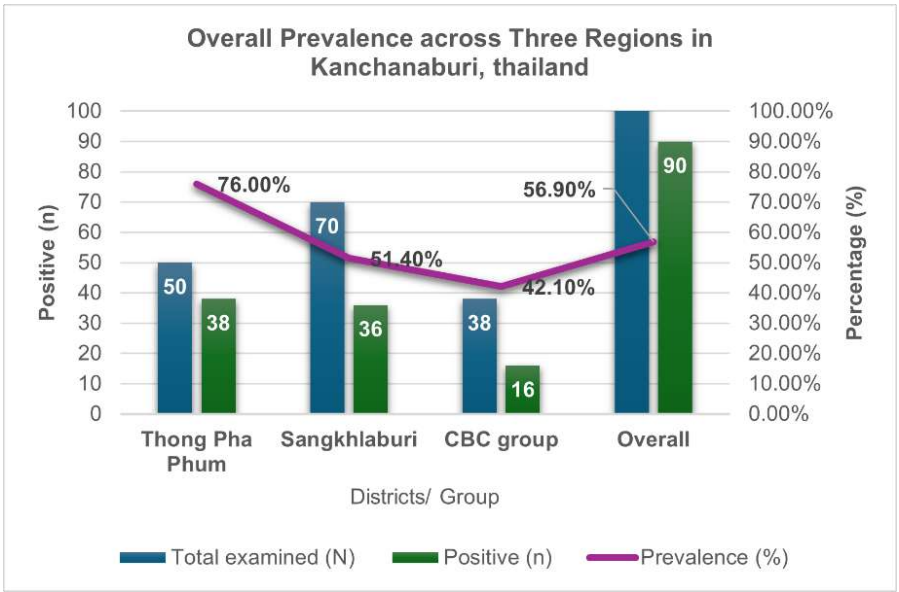


Figure 1. Overall prevalence of bacteria and hemoplasmas in beef cattle from Kanchanaburi province.

Keywords: hemoplasma, tick-borne bacteria, cross-border cattle, molecular epidemiology, Thailand.

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