



CONFERENCE PROCEEDINGS

Leveraging AI for Veterinary Public Health

ECVPH Conference & Annual General Meeting · Munich 2026

AT A GLANCE

Dates	1–4 September 2026 (Workshops 1–2 Sept · Congress & AGM 3–4 Sept)
Format	Hybrid
Location	Main Lecture Hall, Veterinary Campus LMU Munich, Oberschleißheim, Germany



Invited Speakers, Oral Presentations & Poster Abstracts





Leveraging AI for Veterinary Public Health

ECVPH Conference & AGM · Munich 2026

Table of Contents

Foreword — President of ECVPH	4
Foreword — Local Organising Committee	5
Local Organising Committee	6
Conference Programme	7
 Invited Speakers	 9
Bas van der Velden	9
Michal Majewski & Kacper Libera	10
Mareike Wenning	12
Zsuzsa Farkas	13
Peter-John (PJ) Noble	15
Sandy Carmichael	17
Iurii Savvateev & Kangwei Hou	19
Eliana Lima	21
Matthias Filter	22
Veronika Weber	24
Hila Cohen	25
 Submitted Abstracts	 26
Oral Presentations	27
Poster Pitch Session	31
Poster Presentations	42

Foreword

President of the European College of Veterinary Public Health

Dear Diplomates, Residents and guests, dear colleagues,

I'm delighted to be able to welcome so many of you to the ECVPH scientific conference and Annual General Meeting 2026 here in Munich.

The theme of the conference "Leveraging AI for Veterinary Public Health" is very appealing and particularly relevant for the current times in science, education as well as in our everyday lives.

As usual, we have invited our Residents and Diplomates to showcase their current work in VPH research and teaching. This year, we received twice as many abstracts as in previous years, which is a fantastic response. This is also a clear indication of the good health and successful work of our College!

The programme will also provide ample opportunities to connect and exchange ideas in a pleasant and inspiring environment, while catching up with old friends and meeting new colleagues.

My sincere thanks go to the local organising team for all their hard work in making this meeting possible. I wish you all a wonderful and enjoyable stay in Germany.

Yours,

Bojan Blagojevic

President of the European College of Veterinary Public Health (2024–2026)

Foreword

Local Organising Committee

Dear colleagues and friends,

It is with great pleasure — and no small amount of excitement — that we welcome you to Munich for the ECVPH Conference and Annual General Meeting 2026!

The response to this year's meeting has been truly wonderful. We are delighted to welcome around 200 participants joining us both on-site and online, to explore together how artificial intelligence is reshaping veterinary public health. The response to our call for abstracts has been just as encouraging: with 59 submissions received, this has been one of our strongest years yet, and a lovely reflection of just how much energy and creativity there is in our community right now.

Given the volume of submissions, we've decided to make a small but meaningful change to the programme this year: alongside the traditional poster display, we've introduced a dedicated Poster Pitch Session that will give ten presenters a few minutes each to pitch their work directly to the audience before the poster viewing session. We hope this engaging format sparks curiosity early and leads to even livelier conversations at the poster boards afterwards.

Alongside the scientific programme, we've put together a series of social events we're genuinely excited about. From the Residents' Social Evening and Joint Welcome Reception that kick off the week, to a Guided Tour of Munich City and our Conference Dinner at the historic Augustiner Stammhaus, we hope these moments give you plenty of opportunities to catch up with old friends, meet new colleagues, and enjoy each other's company beyond the lecture hall.

We have put a lot of care into building a programme that reflects the depth and breadth of current thinking on AI in our field, and we can't wait to see where the discussions, new connections, and shared ideas of the coming days will take us.

Last but not least — a big thanks to a wonderful team that helped make all this happen — for you!

Welcome to Munich — we hope you have a wonderful and inspiring conference!

Warm regards,

Alexandra Fetsch

On behalf of the Local Organising Committee, ECVPH Munich 2026

Local Organizing Committee



Claudia Guldemann



Silvia Klohs



Maria Wittmann



Alexandra Fetsch



Sophia Johler



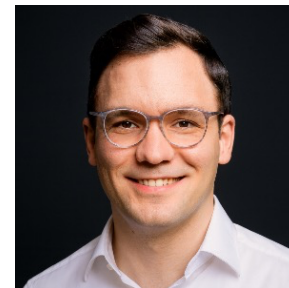
Jana Walther



Melanie
Westermann



Carola Sauter-Louis



Philipp Girt



Irene Esteban
Cuesta

Conference Programme

Organisation

Invitation

Join us at the ECVPH Conference and AGM 2026! Explore how AI advances Veterinary Public Health in the scientific program. A range of social events and networking activities will create space to inspire dialogue, encourage new collaborations, and create a stimulating conference experience for all. Looking forward to see you in Munich!

Location

Main Lecture Hall
Veterinary Campus Oberschleißheim
Sonnenstr. 18A, Oberschleißheim, Germany

Conference Dinner

Augustiner Stammhaus
Neuhauser Str. 27
80331 Munich

**Register now and check out the
webpage!**

[ECVPHMunich2026](#)

Email: ecvph2026@vetmed.lmu.de



Workshops

Pre-Conference Workshops

Location: Schönleutnerstr. 8, 85576 Oberschleißheim
(10 min from Lecture Hall)

WS1: Environmental monitoring (Claudia Guldemann)

WS2: AI-assisted Risk Negotiation (Alexandra Fetsch)

WS3: Diagnostic Test Evaluation without gold standard (Simon Firestone)

Program

Tuesday Sept 1st

09:00-18:00h **Workshops** (Part 1)

19:30-22:30h **Residents' Social
Evening**

Wednesday Sept 2nd

09:00-17:00 h **Workshops** (Part 2)

18:00-19:00 h **Residents' Meeting**

19:00-20:30 h **Joint welcome reception**



Leveraging AI for Veterinary Public Health

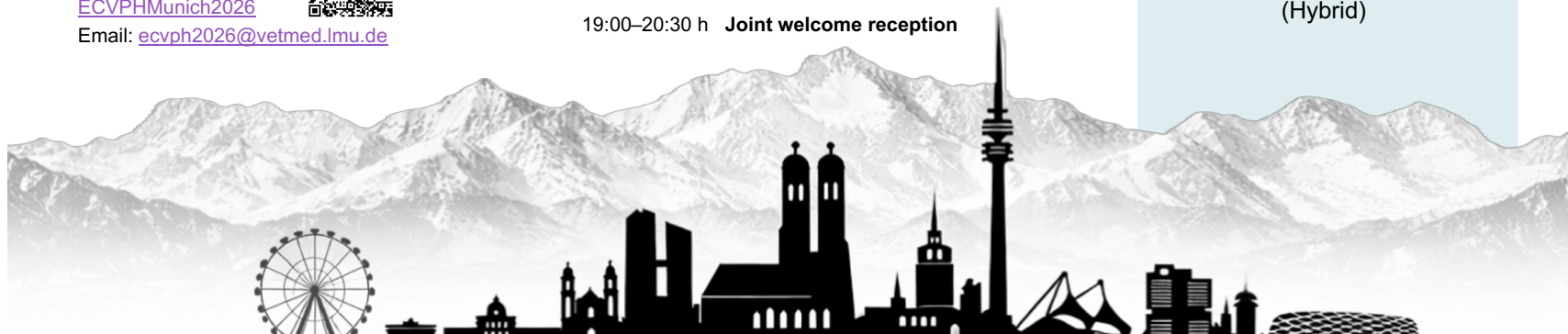
ECVPH

Conference & AGM

Sept. 1st – 4th 2026

Munich, Germany

(Hybrid)



Thursday, Sept. 3rd

08:00h **Arrival and Registration**

09:00h **Opening of the Conference**

SESSION 1: AI in Food Safety

Chair: Sophia Johler

09:10h Bas van der Velden (Wageningen University&Research): **AI foundation models for food safety**

09:50h Kacper Libera (Utrecht University), Michal Majewski (Technical University of Denmark): **AI in broiler meat inspection: are we ready?**

10:10h Mareike Wenning (LGL): **Prospects and challenges in predicting spoilage in minced meat along the food chain**

10:30h **Coffee break**

11:00h **Poster pitches & viewing**

Chair: Claudia Guldemann

12:15h **Lunch**

SESSION 2: AI in Population Medicine

Chair: Carola Sauter-Louis

13:20h Zsuzsa Farkas (University of Veterinary Medicine Budapest): **AI-Driven Risk Identification and Preparedness Systems**

Thursday, Sept. 3rd

14:00h Peter-John Noble (University of Liverpool): **Using language models of all sizes to identify disease signals in messy veterinary data**

14:20h Sandy Carmichael (Scotland's Rural College): **Bitesize Biosecurity: AI for Accessible Biosecurity Guidance for Farmers and Veterinarians**

14:40h Iurii Savvateev, Kangwei Hou (LMU Munich): **AI-based biosecurity measurements for conservation of endangered species**

15:00h **Conference Picture & Coffee break**

15:30h **Annual General Meeting**

18:30h **Guided Tour Munich City**

19:00h **Conference Dinner**

Friday, Sept. 4th

SESSION 3: Residents' presentations

Chair: Alexandra Fetsch

09:00h Luca Nalbone (University of Messina): **Leveraging machine learning to enhance official controls in the food industry**

09:15h Agathe Julie Verhulst (University Bern): **Towards a Determinants of Health Framework for Dairy Cattle**

Friday, Sept. 4th

09:30h Lapo Mughini-Gras (RIVM): **Salmonella source attribution in Dutch pig farms**

09:45h Jose Rodríguez Torres (University Las Palmas): **Free-text mining of farm animal veterinary records for syndromic surveillance**

10:00h **Coffee break**

SESSION 4: AI shaping food safety, animal welfare, and food security

Chair: Katharina Stärk

10:30h Eliana Lima (EFSA): **Specific needs of regulatory science: when and how to use AI for literature reviews**

10:50h Matthias Filter (BfR): **Data harmonization and knowledge graphs: their relevance in the age of AI**

11:10h Veronika Weber (Vion): **Transforming Monitoring through AI: An Industry Perspective**

11:30h Hila Cohen (UN WFP): **How can AI help support Food Security?**

11:50–12:00 h **Poster Award**

from 12:00 h **Closing with interactive feedback loop**

from 12:30 h **Lunch**

Invited Speaker



Bas van der Velden, PhD

Head of Data Science and Artificial Intelligence, Wageningen Food Safety Research

TALK TITLE

AI foundation models for food safety

Session 1: AI in Food Safety · Chair: Sophia Johler · Thursday, 3 September 2026, 09:10h

Biosketch

Bas van der Velden, PhD, is the head of Data Science and Artificial Intelligence at Wageningen Food Safety Research. He leads a diverse, international, and interdisciplinary team of 25 researchers in AI and data science. Bas sets strategic directions, fosters the personal growth of team members, leads projects, and contributes to EU consortia on AI in food safety research. Bas led Work Packages in the EU projects HOLiFOOD, EFRA, and ECO-READY and is deputy coordinator of HOLiFOOD. Bas authored many high-impact peer reviewed publications as well as the FAO report on artificial intelligence for food safety. Bas is a member of the European Food Safety Authority Advisory Group on Data Innovation subgroup and organizer and initiator of the Artificial Intelligence in Food Safety (AIFS) Conference.

Talk Outline

This talk will focus on the state of the art in artificial intelligence (AI) and specifically foundation models for food safety. The fundamentals and technical background of AI, machine learning, deep learning, and foundation models will be explained in lay-person terms. Several use cases will be discussed. This includes the CompreHensive European Food Safety (CHEFS) database, a database that enables AI tools by gathering over 400-million analytical lab results from all member states in the last decades and sharing them in an open access database and dashboard. These analytical lab results include chemical hazards, microbiological hazards, pesticide residues, and veterinary medicinal product residues. Other use cases focus on the PetriVision, an applied computer vision AI tool to analyze bacterial colonies in the lab; the use of large language models for knowledge extraction from text; and the use of dedicated foundation models to analyze high-resolution mass spectrometry data.

Invited Speakers



Michal Majewski

Postdoctoral Researcher, Technical University of Denmark (DTU) · Assistant Professor, Poznań University of Life Sciences



Kacper Libera

PhD Candidate, Utrecht University · Resident, European College of Veterinary Public Health (Food Safety)

TALK TITLE

AI in broiler meat inspection: Are we ready?

Session 1: AI in Food Safety · Chair: Sophia Johler · Thursday, 3 September 2026, 09:50h

Biosketch — Michal Majewski

Michal Majewski is a postdoctoral researcher at the Technical University of Denmark (DTU), working at the National Food Institute on food safety, epidemiology, and the control of foodborne pathogens. He is also an assistant professor at the Poznań University of Life Sciences and a third-year resident at the European College of Veterinary Public Health in the Food Safety sub-discipline. His research focuses on developing risk-based and harmonized approaches to broiler meat inspection, with a particular emphasis on improving food safety systems in poultry production. His current work contributes to advancing methodologies for post-mortem inspection of broilers, with a strong emphasis on standardization, data integration, and the development of camera vision systems for broiler post-mortem inspection. His broader goal is to support the transition toward more efficient, risk-based regulatory frameworks that enhance both consumer protection and animal health and welfare.

Biosketch — Kacper Libera

Kacper Libera – veterinarian passionate about veterinary public health and artificial intelligence (AI), dedicated to bridging the gap between these two fields. He graduated in 2021 in Poland and then worked as a research assistant at Poznan University of Life Sciences, Poland, and part-time as an official veterinarian. In 2022, Kacper moved to Utrecht, the Netherlands, to start a PhD focused on applying computer vision (a type of AI) to food safety and the automated monitoring of animal welfare and health. One year later, he began his Residency at the European College of Veterinary Public Health (food safety subspecialty) and is now in the 3rd year of the curriculum. At the College, he also serves as Chair of the Residents Committee. During his PhD, Kacper spent 2.5 months at the National Food Institute at the Technical University of Denmark (DTU) and was also invited as an expert speaker to the European Commission group working on the use of AI for meat inspection. In addition to his strong interest in meat inspection, Kacper is also training AI models to automate the monitoring of animal health and welfare on the farm, ensuring the entire food chain remains in focus. After defending his PhD (scheduled for October 2026), Kacper will continue working at Utrecht University as a postdoc.

Talk Outline

Artificial intelligence-based solutions are now supporting us in many areas of life, from simple generating text and images to enabling precise medical diagnostics and the development of autonomous vehicles. Often, we do not even notice their presence. At the same time, certain tasks, such as post-mortem inspection of broilers, are still performed manually by official veterinarians. Given the current intensification of broiler slaughter, post-mortem inspection has become a bottleneck that limits further increases in processing speed.

The VetInspector project, a computer-vision-based system, aims to automate both ante-mortem and post-mortem inspection of broilers. At the current stage, the project focuses on developing a system of camera stations for evaluating carcasses and internal organs after slaughter. These cameras have been installed as a demonstration line in one of Denmark's large broiler slaughterhouses, where they are currently undergoing testing and validation. The system consists of four camera stations, covering all elements required for meat inspection: detection of lesions visible on the carcass surface before evisceration, assessment of carcass hygiene status, detection of lesions in internal organs, and scoring of feet for footpad dermatitis.

Other imaging techniques such as X-ray and computed tomography scanning may provide further benefits, including the possibility of examining internal organs while still inside the carcass and enabling carcass "pre-screening" and early condemnation. X-rays are also proven to be very accurate in detecting bone or joint injuries, allowing automated detection of broken wings or legs as part of animal welfare monitoring. However, for such systems to be implemented across different slaughterhouses and countries, harmonization of post-mortem inspection procedures within the EU is essential and is currently being conducted by the authors' group, alongside modernization of EU legislation. Future work should focus on continually improving AI model performance, establishing clear benchmarking criteria for input data, and developing robust validation protocols, including explainability of AI models.

Invited Speaker

Mareike Wenning

Head of the Food Microbiology and Hygiene Laboratory for Southern Bavaria, Bavarian Health and Food Safety Authority (LGL)

TALK TITLE

Application of AI in food safety — Prospects and challenges in predicting spoilage in minced meat along the food chain

Session 1: AI in Food Safety · Chair: Sophia Johler · Thursday, 3 September 2026, 10:10h

Biosketch

Mareike Wenning is leading the lab for Food Microbiology and Hygiene for southern Bavaria at the Bavarian Health and Food Safety Authority (LGL) in Oberschleißheim. She graduated in Nutrition Science at the Technical University of Munich and holds a PhD and habilitation in Food Microbiology. Until 2018 she headed a research group at the Chair of Microbial Ecology of the Technical University of Munich focusing on microbial biodiversity in food and food processing environments as well as on bacterial taxonomy. At the LGL, her responsibilities cover several aspects of food safety: microbiological analysis of official food samples, investigation of food-borne outbreaks and development and implementation of analytical techniques. Mareike is, among others, a member of IDF and different ISO working groups.

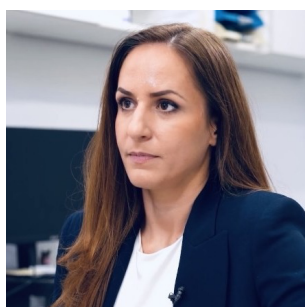
Talk Outline

The project "Zukunftslabor 2030" (Future Lab 2030) evaluates in a proof-of-concept study how food safety can benefit from different technical solutions. It aims to develop models to predict the quality of minced pork meat over shelf life by implementing digital twins that are based on a comprehensive description of meat characteristics through a variety of analytical methods. This is accompanied by a platform for exchanging data and information along the food chain based on GS1 EPCIS into which the digital twin will be embedded.

For data collection, model productions of minced pork were provided by one project partner. The meat samples were packed under different modified atmospheres (O₂ or N₂) and stored at various temperatures (2, 10 and 14°C) for up to 17 days, with analysis performed on different days of storage. Additionally, the impact of interrupting the cold chain at 2°C for 6 or 12 hours on meat quality was investigated. Data were collected on the microbiological status (bacterial count and diversity), physical parameters (pH and colour), biochemical parameters (peptide and metabolite profiles), volatile compounds in the packaging headspace, spectroscopic fingerprints, and overall sensory impression.

Analysis of single data sets revealed that different fast techniques such as MALDI-TOF mass spectrometry or fluorescence spectroscopy generate information that can be used to predict, for example, storage time of the meat. However, significant variations between production batches make it difficult to generalise about trends, which impairs accuracy. Overall, implementation of prediction models in food safety is a challenging task, requiring adequate analytical techniques, large datasets, and clearly defined questions to be answered by the model — but it also opens up a wide range of applications and can significantly speed up decision-making and communication processes.

Invited Speaker



Dr Zsuzsa Farkas, PhD

Head of the Department of Digital Food Science, University of Veterinary Medicine Budapest

TALK TITLE

Advancing AI in the food chain and animal health: AI-driven risk identification and preparedness systems

Session 2: AI in Population Medicine · Chair: Carola Sauter-Louis · Thursday, 3 September 2026, 13:20h

Biosketch

Dr Zsuzsa Farkas, PhD, is Head of the Department of Digital Food Science at the University of Veterinary Medicine Budapest, within the Institute of Food Chain Science. Her work focuses on data-driven food chain safety, veterinary public health, emerging risk identification, antimicrobial resistance, and the development of decision-support systems for One Health and food chain risk assessment. She has a strong interdisciplinary profile combining food safety, veterinary public health, risk assessment, digitalisation, artificial intelligence, and data integration.

Her research group develops analytical frameworks and practical tools that support evidence-based decision-making in complex food chain and public health contexts, including emerging risk monitoring systems, text-mining workflows, knowledge graph-based data integration, explainable machine learning applications, and dashboard-based decision-support solutions for risk assessors, risk managers, and other stakeholders.

Dr Farkas is actively involved in several international expert networks and regulatory science activities, contributing to EFSA-related scientific cooperation including the Emerging Risks Exchange Network, and serving as Vice-Chair of the Codex Committee on Methods of Analysis and Sampling. She also plays a leading role in national and international research initiatives related to food chain safety and One Health, including coordinating activities within the National Laboratory for Infectious Animal Diseases, Antimicrobial Resistance, Veterinary Public Health and Food Chain Safety that connect artificial intelligence, data analysis, and decision-support approaches to antimicrobial resistance and food chain risk management. Her work aims to bridge research, regulatory science, and practical veterinary public health by developing transparent, explainable and operationally relevant methods for identifying, interpreting and managing food chain risks.

Talk Outline

This presentation explores the practical applications of advanced artificial intelligence across the food chain and animal health sectors. It will highlight how AI-driven solutions can enhance decision-making, improve risk management, and support more sustainable and resilient systems. The presentation will feature two case studies: the first focuses on emerging risk identification within the food chain, demonstrating how data-driven models can assist in detecting and assessing potential threats at an early stage; the second presents an early warning system for antimicrobial resistance (AMR), showcasing how

predictive analytics can support risk forecasting and enable timely intervention strategies. Together, these examples illustrate the transformative potential of AI in safeguarding food safety and animal health.

Invited Speaker



Prof. Peter-John (PJ) Mäntylä Noble

Professor and Internal Medicine Clinician, University of Liverpool

TALK TITLE

Using language models of all sizes to identify disease signals in messy veterinary data

Session 2: AI in Population Medicine · Chair: Carola Sauter-Louis · Thursday, 3 September 2026, 14:00h

Biosketch

Professor Peter-John (PJ) Mäntylä Noble has worked at the University of Liverpool since 1992, progressing from clinical internship through PhD and post-doctoral research in gastric cell physiology to his current role as Professor and Internal Medicine Clinician. He co-founded the Small Animal Veterinary Surveillance Network (SAVSNET), now a major UK companion animal disease surveillance platform, and leads its AI/ML development programme, including domain-adapted transformer models (PetBERT, DogBERT) for clinical text classification used for disease and health surveillance, antimicrobial resistance and pharmacovigilance applications in veterinary medicine.

Talk Outline

Veterinary electronic health records (EHR) contain a great deal of valuable, searchable data about patient signalment and other tabular data, but a great deal of information resides in unstructured clinical free text which, when written by vets, includes inconsistent acronyms, abbreviations and initialisms, poor or absent punctuation, misspelling, word-truncation and spell-checker errors. The Small Animal Veterinary Surveillance Network (SAVSNET) collates EHR from over 400 veterinary premises around the UK, including signalment and treatment data as well as this challenging free-text material.

For the purpose of disease and health surveillance, the aim is to identify clinical signs and syndromes that may indicate emerging disease or health challenges. With a constantly growing database of over 20 million records, manual evaluation of free text to identify key features is unfeasible, requiring a range of strategies to capture these features. Prior to the use of language models, keyword searches were relied upon — useful but often complicated by negation (e.g. vomiting is negated more often than it is present in clinical notes); rule-based text pattern matching using regular expressions (regex) allows some mitigation of this challenge.

For more subtle contextual analysis of individual records, specialised neural language models (transformers) provide an excellent opportunity to screen records either alone or following filtering for keywords or word-patterns. Transformers range from encoders (BERT) — fast and efficient for specific classification tasks — to decoder architectures (GPT models), which can address more general tasks but more slowly and with greater energy consumption. Transformers can also be used for topic-modelling, allowing thematic clustering across millions of EHR to create topics that illustrate key themes such as disease syndromes or common activities reported in EHR, without the need for labelled training datasets.

This talk will review the application and outputs of all these methods to the SAVSNET data for disease, health and antimicrobial use research, with examples of ongoing AMU and syndromic surveillance projects.

Invited Speaker



Dr Sandy Carmichael

Research Associate, Scotland's Rural College (SRUC) — Centre for Epidemiology and Planetary Health (CEPH), RAVIC, Inverness

TALK TITLE

Bitesize biosecurity: AI for accessible biosecurity guidance for farmers and veterinarians

Session 2: AI in Population Medicine · Chair: Carola Sauter-Louis · Thursday, 3 September 2026, 14:20h

Biosketch

Dr Sandy Carmichael is a Research Associate at Scotland's Rural College (SRUC), where he works within the Centre for Epidemiology and Planetary Health (CEPH) at the Rural and Veterinary Innovation Centre (RAVIC) in Inverness. He completed his PhD in Computing Science at the University of Stirling in 2024, applying computer vision and machine learning to Atlantic salmon medical imaging.

Sandy applies computing science to veterinary and public health challenges, developing AI and data science tools across agriculture, aquaculture, and animal health. His particular interests include biosecurity, antimicrobial resistance, and salmon gill health. He is an advocate for responsible AI in animal health — believing technology should augment, not replace, expert judgement.

Talk Outline

Biosecurity measures are important to reduce the risk of disease on farms, but their implementation and ongoing use are variable across the livestock industry. One problem that persists is communication. There is authoritative guidance, but it is scattered across many sources and often written in technical language that is difficult to put into practice. Veterinarians are important advisers, interpreting this guidance for farmers, but they also have to deal with a similar volume and complexity of source material. Improved dissemination of biosecurity information could therefore increase adoption, reduce disease incidence and contribute to gains in productivity, profitability and animal welfare.

In this presentation, we will present Bitesize Biosecurity, a framework that leverages large language models (LLMs) to translate complex biosecurity guidance into information that farmers and the veterinarians who advise them can understand. The framework follows a systematic approach with three main components: advice curation from authoritative sources; prompt engineering to generate accessible content with LLMs; and the creation of a purpose-built, not-for-profit web platform to deliver the summaries. Source materials were obtained from publicly available UK government and veterinary advisory organisations, with a focus on incorporating expert validation and evaluation throughout the curation and summarisation process. Farmers were engaged during the design process to support acceptability and accessibility. The platform has initially focused on a series of livestock health challenges with a high economic impact, and is designed to be scalable and adaptable, so that more diseases and contexts can be added and further functionality, such as interactive chatbot support, can be incorporated in future. We will describe how the tool was built, the steps taken to keep its AI-generated content

accurate and trustworthy, and the role that expert and farmer input played throughout. We will also consider what LLMs can and cannot offer for knowledge translation in veterinary public health, and argue that, used with appropriate safeguards, they provide a practical and replicable way to bring scientific expertise closer to on-farm implementation.

Invited Speakers



Iurii Savvateev

AI in Biosystems and One Health Group, Competence Centre for Food Safety, LMU Munich



Kangwei Hou

Postdoctoral Research Associate, Chair of Fish Diseases and Fisheries Biology, LMU Munich (Project LIFE-PINNACARE)

TALK TITLE

AI-based biosecurity measurements for conservation of endangered species

Session 2: AI in Population Medicine · Chair: Carola Sauter-Louis · Thursday, 3 September 2026, 14:40h

Biosketch — Iurii Savvateev

Iurii Savvateev earned his bachelor's degree in physics from Saint Petersburg State University in Russia. With a scholarship from the German Academic Exchange Service (DAAD), he continued his master's studies at Otto-von-Guericke-University Magdeburg, Germany, specializing in neuroscience. He later completed his PhD at ETH Zürich in Switzerland, working at the crossroads of engineering, data analysis and neuroscience. After completing his PhD, Iurii worked at the German Federal Institute for Risk Assessment (BfR) in Berlin as a software engineer, focusing on the rapidly developing fields of generative artificial intelligence (GenAI) and semantic web technologies.

Recently, Iurii joined the newly formed group "AI in Biosystems and One Health" at LMU Munich to continue his work in GenAI and large language models (LLMs), focusing on the design, prototyping and integration of LLM-based agentic systems into existing workflows. His work also includes data analysis using both classical machine learning and deep learning methods. Iurii and his wife enjoy mountain skiing and indoor climbing in the winter, as well as tennis and cycling in the summer; he holds an entry-level professional mountain ski certification in Switzerland.

Biosketch — Kangwei Hou

Kangwei Hou is a Postdoctoral Research Associate in the Faculty of Veterinary Medicine at LMU Munich, working within the Chair of Fish Diseases and Fisheries Biology (Project LIFE-PINNACARE). In his current research, he applies veterinary epidemiology methodologies to design biosecurity and disease-surveillance frameworks for aquatic ecosystems and conservation.

Specifically, Kangwei leverages his expertise in qualitative risk assessment during his PhD study in Melbourne to translate subjective field observations and stakeholder compliance behaviors into structured parameters for analytical modeling. By bridging qualitative veterinary risk analysis with quantitative frameworks, he establishes the essential domain logic required to develop and implement AI-based biosecurity measurements in wildlife conservation.

Talk Outline

Ecological public-private partnerships (PPPs) often fail not because of a strategic disagreement, but due to unanticipated legal, institutional, and jurisdictional frictions. Resolving these challenges requires stakeholders to process large volumes of multimodal information under significant time pressure.

The presented project integrates a Large Language Model (LLM)-based multi-agent risk negotiation system to support policy development and stress testing. The system incorporates Retrieval-Augmented Generation (RAG) to enable the integration of multimodal information together with LLM-driven autonomous agents that simulate stakeholder interactions under defined governance conditions, aiming to identify potential compromises and implementation risks before policy deployment. Actions performed by LLM-based agents are documented and analyzed within the Langsmith ecosystem, allowing researchers to trace the origins of the obtained outcomes, account for potential biases, and perform cost/efficiency assessments. Furthermore, the approach establishes an objective, mathematical basis for evaluating potential compromises: rather than treating mere agreement as success, the framework applies formal concepts (e.g., Pareto optimality and Nash bargaining solution) to assess efficiency and fairness.

To link the project to a real-world scenario in which an ecological PPP is emerging, the framework is tested within the ongoing PINNACARE initiative for the conservation of the critically endangered *Pinna nobilis*. In this context, the PPP focuses, among other priorities, on multi-stakeholder negotiation where a saltworks owner permits juvenile shell hosting and research without disrupting salt production, while the government balances resource limitations with ecological preservation to prevent the site from being overly restricted.

Invited Speaker



Eliana Lima

Animal Health and Animal Welfare Unit, European Food Safety Authority (EFSA)

TALK TITLE

Specific needs of regulatory science: When and how to use AI for literature reviews

Session 4: AI Shaping Food Safety, Animal Welfare & Food Security · Chair: Katharina Stärk · Friday, 4 September 2026, 10:30h

Biosketch

Eliana Lima graduated as a veterinary surgeon in Lisbon, Portugal, in 2013. She earned a PhD at the University of Nottingham, United Kingdom, in 2019 on veterinary epidemiology. After a period at the World Organisation for Animal Health (WOAH) in Paris, France, she joined the European Food Safety Authority (EFSA) in 2021, working on animal health and animal welfare since then. At EFSA, she is currently part of a group dedicated to applying artificial intelligence to regulatory science production.

Talk Outline

One of the key tasks of the European Food Safety Authority is to review current scientific evidence to provide scientific advice to risk managers, such as national food safety authorities or the European Commission, on food-related matters. This requires undertaking a large number of systematic literature reviews every year across a wide range of topics, from nutrition and toxicology to plant and animal health and welfare.

The growing AI field makes it possible to substantially increase the speed of such literature reviews; however, regulatory science has certain requirements not necessarily covered by commercial solutions, such as full access to library databases and full-text articles, confidentiality of input data, legal European data storage requirements, robustness of data extraction, transparent screening criteria, and reproducibility of results. EFSA is exploring the potential use of AI and developed a custom Large Language Model (LLM)-based 'proof of concept' (POC) that automates two core, time-consuming tasks: screening titles and abstracts based on user-defined criteria, and extracting data based on frameworks like PICO (Population, Intervention, Control, Outcome).

This system ensures full control over data sources, maintains literature breadth, guarantees screening transparency and control, and allows cross-LLM comparisons. Although manual and human-led validation will remain necessary, preliminary results demonstrate substantial time savings. In parallel, the tool's functionalities are being compared against EFSA's current literature screening software, with planned activities including benchmarking the performance and robustness of existing commercial AI tools using manually validated datasets from previous EFSA projects. Because robustness and scientific quality remain paramount to EFSA, a rigorous evaluation of these diverse approaches for accelerating literature reviews is essential.

Invited Speaker



Matthias Filter

Head of the Innovation Centre Food Chain Modelling and Artificial Intelligence, German Federal Institute for Risk Assessment (BfR)

TALK TITLE

Data harmonization and knowledge graphs: their relevance in the age of AI

Session 4: AI Shaping Food Safety, Animal Welfare & Food Security · Chair: Katharina Stärk · Friday, 4 September 2026, 10:50h

Biosketch

Matthias Filter is the Head of the Innovation Centre Food Chain Modelling and Artificial Intelligence at the German Federal Institute for Risk Assessment (BfR). Holding a diploma in Biochemistry, he has been working at the BfR since 2008 as a research scientist and team leader in predictive microbiology, Quantitative Microbial Risk Assessment (QMRA), and software development. His recent research focus has extended to AI-based solutions that facilitate the generation and use of Linked Data and the efficient exchange of risk assessment models. He has initiated and coordinated several national and international research projects, among others the RAKIP Initiative, a joint effort of risk assessment agencies and universities to promote the provisioning of risk assessment models and related data as interoperable resources. He has led several national and international research projects in which his team developed innovative software solutions to support interdisciplinary knowledge and information integration; current projects focus on AI-based solutions for information extraction and information management, contributing significantly to the digital transformation of risk assessment practices.

Talk Outline

Artificial intelligence (AI) has proven capable of processing large, distributed, and heterogeneously structured data sources. Nevertheless, practical adoption is still hampered by missing solutions that guarantee reliability, data interoperability, and data provenance. As scientific evidence will remain distributed across various data sources and formats in the future, it is important to analyse whether ongoing data harmonization efforts and data integration technologies such as knowledge graphs are still needed to facilitate the use of AI in science, public health, and risk assessment.

The presentation will give a practice-oriented assessment of recent developments in the AI domain, with a specific focus on use cases from the food safety risk assessment domain. Based on experience from the German KIDA project, it will be demonstrated that in the age of AI the priorities should not be centred on the upfront harmonization of data sets or the adoption of the Linked Data paradigm, but instead on a more pragmatic approach to the "harmonizability" of data. At the same time, the definition of open data standards remains a critical enabler for AI adoption. This is illustrated using the FAIR Scientific Knowledge eXchange (FSKX) format, successfully applied to create an AI-ready knowledge base for risk assessment models in the RAKIP-Web model repository. As FSKX defines rules for capturing model code, metadata, dependencies, parameters, simulation settings, and documentation, this data standard can easily be used by AI agents to provide models in a harmonized format. Online repositories like RAKIP-Web can

then facilitate model discovery, curation, exchange, execution, and integration with AI-driven workflows for information extraction, validation, benchmarking, and decision support. In conclusion, data standards not only support AI systems in reliably accessing and using scientific knowledge, but also promote their own adoption by researchers, as this becomes easier due to AI itself.

Invited Speaker



Dr Veronika Weber

Chief Sustainability Officer, Vion Food Group

TALK TITLE

Transforming monitoring through AI: An industry perspective

Session 4: AI Shaping Food Safety, Animal Welfare & Food Security · Chair: Katharina Stärk · Friday, 4 September 2026, 11:10h

Biosketch

Dr Veronika Weber is Chief Sustainability Officer (CSO) and a member of the leadership team of Vion Food Group since January 2025. She studied Veterinary Medicine at Ludwig Maximilian University of Munich and earned her doctorate at the University of Veterinary Medicine Hannover. After completing an 18-month trainee programme in central quality management at Vion, she was appointed Group Quality Manager. In June 2023, she became Director Quality Assurance and, from June 2024, additionally assumed responsibility as Director Operations, overseeing operations across Vion's German sites before moving into the role as CSO. In her current position she leads the central Quality Assurance, Sustainability, Science & Innovation, and Communications teams for Germany and the Netherlands.

Veronika focuses on turning scientific knowledge into practical solutions and on creating improvements that can be implemented in everyday operations. Her experience includes the development and implementation of animal welfare and quality systems and the rebuilding and optimisation of slaughterhouses. Veronika and her team at Vion implement new technologies to support daily operations, including AI-supported camera surveillance systems, VR tools for employee education, infrastructure improvements, and innovative approaches to improvements along the supply chain that enhance animal welfare, food safety and product integrity.

Talk Outline

The food industry is undergoing a digital transformation, with Artificial Intelligence (AI), Virtual Reality (VR), DNA-based monitoring, and blockchain technologies reshaping traditional monitoring and quality assurance processes. The session will showcase practical AI applications for monitoring production processes to improve food safety and animal welfare, alongside the use of VR for training, process visualization, and knowledge transfer. It will further explore how DNA monitoring and blockchain technologies can reinforce product integrity and supply chain improvements to secure consumer trust.

Building on these examples, the presentation will discuss the opportunities, challenges, and future perspectives of AI-driven monitoring systems, highlighting emerging trends including their potential to support predictive quality management and data-driven decision-making across the meat supply chain. By combining technological innovation with practical implementation experience, the talk offers insights into how modern monitoring solutions can support quality assurance systems.

Invited Speaker



Hila Cohen

Deputy Head, United Nations World Food Programme (WFP) Innovation Accelerator

TALK TITLE

How can AI help support food security?

Session 4: AI Shaping Food Safety, Animal Welfare & Food Security · Chair: Katharina Stärk · Friday, 4 September 2026, 11:30h

Biosketch

Hila Cohen is the Deputy Head at the United Nations World Food Programme (WFP) Innovation Accelerator, is the co-chair of the UN Innovation Network (UNIN) on behalf of WFP, and an Advisory Board Member of the World Bank Group Innovation Awards. She connects the WFP Innovation Accelerator with global innovation networks, companies and impact actors to work towards Zero Hunger and to address the Sustainable Development Goals (SDGs).

Hila's leadership contributed to the WFP Innovation Accelerator supporting more than 530 start-ups and innovation teams, and being named one of the 'Best Workplaces for Innovators', 'Most Innovative Companies (Non-Profit)' and 'Innovation Team of the Year' by Fast Company over the years. Hila received the Silver Anthem Award for Non-Profit Leader of the Year in 2023.

Prior to joining WFP, Hila advised hi-tech clients, such as start-ups, venture capital firms and NASDAQ-traded companies, as a corporate lawyer at a leading law firm in Tel Aviv. She holds an MBA from the SDA Bocconi School of Management and a Bachelor of Law from the University of Haifa.

Talk Outline

As global food insecurity continues to affect hundreds of millions of people, humanitarian organizations are increasingly challenged to deliver impact at greater scale, speed, and efficiency. This session will explore the evolving global hunger landscape and the role innovation plays in addressing some of the world's most complex food security challenges.

Drawing on the experience of the United Nations World Food Programme (WFP), the discussion will highlight how innovation can help transform humanitarian action, from improving operational effectiveness to unlocking new ways of reaching vulnerable populations. The session will also draw on examples from a decade of the WFP Innovation Accelerator in Munich, which has supported and scaled promising solutions from both within and outside the organization. Through practical examples, including emerging applications of artificial intelligence, the talk will offer insights into how innovative approaches are helping shape the future of humanitarian assistance and contribute to a world with zero hunger.

Submitted Abstracts

A total of 59 abstracts were submitted for ECVPH Munich 2026: 4 selected for oral presentation in the Residents' Session, 10 selected for the Poster Pitch Session, and the remaining 45 presented as posters. Original submission numbers (Abstract No) are retained throughout for cross-reference.

Oral Presentations — Session 3: Residents' Presentations

- No. 2** *Salmonella* source attribution in Dutch pig farms — *Lapo Mughini-Gras*
- No. 13** Leveraging machine learning to enhance official controls in the food industry — *Luca Nalbone*
- No. 20** Towards a determinants of health framework for dairy cattle — *Agathe Julie Verhulst*
- No. 59** Free-text mining of farm animal veterinary records for syndromic surveillance — *Jose Rodríguez Torres*

Poster Pitch Session

- No. 30** Automated detection of asymmetrical udders in dairy goats using a camera and an artificial intelligence model YOLOv12 — *Kacper Libera*
- No. 46** AI-Assisted risk negotiation for One Health decision-making — *Alexandra Fetsch*
- No. 58** Automated scoring and localization of traumatic skin lesions in Italian fattening heavy pig carcasses: a pilot study — *Matteo Recchia*
- No. 39** Hospital kitchens as hotspots for the circulation of ESBL- and Carbapenemase-producing *E. coli*, *K. pneumoniae* and *Acinetobacter spp.* — *Anestis Tsitsos*
- No. 7** From antibiotic dependence to alternative strategies: Impact on animal welfare in livestock production — *Melanie Westermann*
- No. 45** Parameter inference for a complex agent-based model of Highly Pathogenic Avian Influenza — *Nacira Ramdani*
- No. 56** Another virus bites the dust: Electrostatic dust collectors for detection and sequencing of influenza A virus in pig herds — *Marina Meester*
- No. 11** A large-scale spatio-temporal epidemiological model for epidemic wave dynamics of African swine fever in wild boars — *Alice Diana*
- No. 36** Making data talk: an AI-assisted, user-friendly pipeline for data visualization and decision-making in Veterinary Public Health — *Stefano Di Nola*
- No. 10** Simulating vaccination scenarios for HPAI in turkeys using mechanistic simulation modelling — *Sandra Filipa Oliveira Carapeto*

Oral Presentation

ORAL PRESENTATION · ABSTRACT NO 2

Salmonella source attribution in Dutch pig farms

Session 3: Residents' Presentations · Chair: Alexandra Fetsch · Friday, 4 September 2026, 09:30h

Hester Bloem¹, Indra Bergval¹, Tryntsje Cuperus¹, Maren Lanzl¹, Greetje Castelijns², Ben Wit³, Marieke Opsteegh¹, Lapo Mughini-Gras^{1,4}

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3. Netherlands Food and Consumer Product Safety Authority (NVWA), Utrecht, the Netherlands.

4. Utrecht University, Utrecht, the Netherlands.

Key words: *Salmonella*; pig; source attribution; transmission; risk factors; serotyping

Social media message: Controlling *Salmonella* in pigs starts within the herd, but other species matter too.

Background: Effective control of *Salmonella* in pigs depends on understanding how the pathogen is introduced and transmitted within farms. This study aimed to identify potential sources of *Salmonella* infection in pig farms using both epidemiological and microbiological source attribution approaches.

Methods: A cross-sectional study was carried out on 148 fattening pig farms in the Netherlands. Fecal samples from pigs were collected and analyzed for the presence of *Salmonella*, alongside a questionnaire assessing farm characteristics. Farm-level risk factors associated with *Salmonella* detection were identified using logistic regression analysis. For source attribution based on microbial subtyping, serotyped *Salmonella* isolates from the Dutch national laboratory surveillance system (2016–2023) were used. *Salmonella* isolates (n = 494) from pigs were attributed to nine potential sources of infection (n = 4,171 *Salmonella* isolates in total, obtained from feed, broilers, laying hens, other poultry, cattle, small ruminants, mammal pests/vermin, avian pests/vermin, and horses and donkeys) based on their serotype distribution, as well as prevalence and exposure data, using the modified Dutch (mDM) and modified Hald (mHM) models for source attribution.

Results: A farm-level prevalence of 9.5% (14/148; 95% confidence interval [CI]: 5.3–15.4%) was observed. Cleaning pens between production batches (odds ratio [OR] 0.139, 95% CI: 0.030–0.625) and transferring piglets to the fattening unit at a later age (per week increase, OR 0.538, 95% CI: 0.290–0.998) were significantly associated with lower odds of *Salmonella* detection. In contrast, the presence of cattle on the pig farm was associated with increased odds of *Salmonella* detection in pigs (OR 4.860, 95% CI: 1.346–17.544). Both the mDM and mHM attributed the majority of pig isolates to pigs themselves (mDM: 43.0%; mHM: 72.6%), followed by cattle (mDM: 22.6%; mHM: 11.0%) and broilers (mDM: 9.2%; mHM: 5.0%).

Conclusion: The results suggest that pig-to-pig transmission is the primary pathway for *Salmonella* within pig farms, underscoring the importance of thorough cleaning and disinfection between production batches. On mixed-species farms, cattle may represent an important source of *Salmonella* introduction, as indicated by both risk factor analyses and subtyping-based source attribution models. Further research is needed to confirm the occurrence and direction of these transmission events.

Oral Presentation

ORAL PRESENTATION · ABSTRACT NO 13

Leveraging machine learning to enhance official controls in the food industry: A proof-of-concept for predicting regulatory non-compliance from establishments' risk-classification profiles

Session 3: Residents' Presentations · Chair: Alexandra Fetsch · Friday, 4 September 2026, 09:00h

Luca Nalbone^a, Maria De Salvo^a, Salvatore Pennisi^a, Filippo Giarratana^a, Graziella Ziino^a, Stefano Pardini^b, Luca Cianti^c, Maria Francesca Peruzi^c, Alessandro Giuffrida^a

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Key words: Official food control; Artificial intelligence; Risk-based inspection

Social media message: Can AI make food safety inspections smarter? Our proof-of-concept shows how machine learning, trained on ISO 17020-accredited inspection data, can predict regulatory non-compliance and support risk-based official controls. #FoodSafety #AI #ECVPH

Background: Regulation (EU) 2017/625 requires official controls along the agri-food supply chain to be proportionate to risk, and its Preamble No. 32 introduces a key principle: control efforts should also account for the expected likelihood of detecting non-compliance. While risk-based classification of food establishments is now standard practice, the integration of predictive, data-driven tools into routine inspection planning remains marginal. This study presents a proof-of-concept for embedding supervised machine learning into official food control systems, transforming routinely collected inspection data into predictive intelligence that estimates the probability of regulatory non-compliance based on establishments' risk-classification profiles.

Methods: The analysis used 2024 inspection records from a competent authority accredited under ISO 17020:2012, covering 108 food establishments approved under Regulation (EC) 853/2004 across three provinces of Tuscany (Central Italy). The integrated dataset combined the compliance outcome of 13 regulatory parameters (structural, hygienic and managerial requirements) assessed during 484 inspections (2,347 parameter-level observations) with the 12 risk-classification criteria defined by the Italian "Intesa Stato-Regioni" guideline (CSR 212/2016). After exploratory Multiple Correspondence Analysis (MCA), four supervised algorithms (Random Forest, CART, C5.0, Naïve Bayes) were trained and benchmarked against models generated by H2O AutoML. Class imbalance was addressed through synthetic resampling of the training set, while the test set remained unaltered. Performance was assessed using rare-event-sensitive metrics (PR AUC, F1 score, balanced accuracy) integrated into a composite Rank Score.

Results: Non-compliances accounted for 3.3% of assessments (77/2,347), concentrated in structure and equipment (24.7%), cleaning and disinfection (18.2%), hygiene during production (15.6%) and pest control (11.7%). Notably, elevated non-compliance rates also emerged in establishments classified at lower-risk levels, particularly for HACCP management and traceability. Among classical algorithms, predictive power was limited (sensitivity 0–32%). An Extremely Randomized Trees (XRT) model selected via AutoML achieved the best performance (sensitivity 77%, balanced accuracy 77%, highest F1 and PR AUC). Variable-importance analysis indicated that establishment-level features contributed more strongly to prediction than individual inspection parameters. The best model was embedded in an interactive Shiny web application enabling authorities to simulate inspection scenarios and visualise compliance probabilities.

Conclusion: Although predictive power remained constrained by the rarity of non-compliant cases, the framework proved robust, transparent and transferable. Discrepancies between official risk classes and observed outcomes suggest that current classification schemes may benefit from revision and complementary criteria. AI-based tools are not yet sufficient as stand-alone predictors, but can meaningfully complement risk-based inspection systems, supporting smarter prioritisation, resource efficiency and evidence-informed food safety governance.

Oral Presentation

ORAL PRESENTATION · ABSTRACT NO 20

Towards a determinants of health framework for dairy cattle: LLM-enhanced topic modelling and expert perspectives

Session 3: Residents' Presentations · Chair: Alexandra Fetsch · Friday, 4 September 2026, 09:15h

Agathe Verhulst¹, Laura Cunha Silva¹, Reda Zahri¹, Jasmin Widmer¹, John Berezowski², Luis Pedro Carmo¹

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Key words: Dairy cattle health, Determinants of Health, LLM topic modelling

Social media message: What shapes dairy cattle health beyond disease? Combining LLM-enhanced topic modelling with expert perspectives, we developed a Determinants of Health framework highlighting the systemic drivers influencing cattle health and prevention.

Background: Health in dairy cattle is a complex and multidimensional state shaped by biological, environmental, managerial, socio-economic, and policy-related factors. However, livestock medicine and animal health research have traditionally remained largely disease-centred. In contrast, human public health frameworks such as the Determinants of Health (DoH) model consider health as the product of many interacting systemic influences extending beyond the absence of disease. Applying a similar perspective to livestock systems may support more holistic and prevention-oriented approaches to bovine health. This study aimed to develop a DoH framework for dairy cattle by integrating large-scale computational literature analysis with expert perspectives.

Methods: Abstracts related to dairy cattle health published between 2000 and 2025 were retrieved from PubMed and Scopus (n=74,003). A large language model (LLM)-enhanced topic modelling pipeline integrating BioBERT embeddings, BERTopic clustering, and LLaMA 3.1-assisted topic labelling was used to identify thematic structures and health-related factors within the literature. Following filtering and expert curation, 9,570 abstracts were retained for final analysis and clustered thematically. The literature-derived clusters informed an initial conceptual DoH framework, which was subsequently expanded through semi-structured online interviews with 17 participants from academia, veterinary practice, consultancy, government veterinary services, and farming. Collaborative digital mapping boards were used to iteratively organize determinants and visualize relationships between factors.

Results: The computational analysis identified 128 validated thematic clusters, of which 110 were retained for further exploration following expert review, showing a strong concentration of literature around disease-oriented and production-related research areas, while broader systemic dimensions of health appeared less represented. Expert interviews broadened the framework by highlighting the wide systemic influences shaping dairy cattle health, which was consistently described as extending beyond the absence of disease to include physiological functioning, welfare, resilience and adaptation to the production environment. The resulting DoH framework organized determinants into four levels: (i) individual animal; (ii) herd farm-level; (iii) socio-economic and policy level; (iv) environmental determinants, with human management, labour conditions and broader economic structures emerging as central drivers of health outcomes.

Conclusion: This study presents a preliminary systems-based DoH framework for dairy cattle developed through the integration of computational literature synthesis and expert knowledge. Similar to human DoH frameworks, the model highlights health as an emergent property shaped by multiple interacting determinants rather than solely the absence of disease. By combining LLM-enhanced evidence synthesis with participatory systems exploration, the proposed framework may support more holistic approaches to dairy cattle health surveillance, prevention, and policy.

Oral Presentation

ORAL PRESENTATION · ABSTRACT NO 59

Free-text mining of farm animal veterinary records for syndromic surveillance: Regular expressions, guided topic modelling and anomaly detection in a pilot veterinary surveillance network

Session 3: Residents' Presentations · Chair: Alexandra Fetsch · Friday, 4 September 2026, 09:45h

Jose Rodríguez Torres¹, Antonio Espinosa de los Monteros y Zayas¹, Ifan Lloyd², Rob Smith², P. Davies³, P.J. Noble³, Alan Radford³

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Key words: syndromic surveillance; natural language processing; farm animal health

Social media message: Do we really need LLMs for vet syndromic surveillance? Regex + unsupervised topic modelling on FAVSNET farm records identified 21 syndromes, validated them & detected anomalies — no labelled data needed. #VPH #VetEpi

Background: Farm animal veterinary electronic health records (EHRs) contain free-text consultation narratives that, if mined at scale, can underpin near real-time syndromic surveillance. In an era of growing enthusiasm for large language models (LLMs), this study asks whether lighter, more interpretable and transparent tools such as regular expressions (regex) and guided topic modelling (GTM) are sufficient to extract actionable and trustworthy disease information from farm animal veterinary records, and how well anomaly detection can translate these signals into surveillance alerts.

Methods: Free-text narratives from FAVSNET, a small pilot network of farm animal veterinary practices across Wales and England, were analysed using two complementary natural language processing (NLP) approaches. Six regex patterns were developed for mastitis, pneumonia, lameness, joint ill, watery mouth, and abortion. GTM was implemented using BERTopic, guided by domain-expert seed word lists. Both approaches were validated by expert narrative review, by comparison of temporal patterns against known biological seasonality, and by direct cross-method comparison of weekly syndrome counts. Aberration detection was piloted on both regex- and GTM-derived syndrome counts using the vetsyn R package.

Results: Regex PPV ranged from 65% (watery mouth) to 96% (lameness). GTM produced 129 topics, of which 21 syndrome groups (spanning 38 topics) were retained for surveillance, covering a broad range of cattle and sheep conditions including pneumonia, mastitis, lameness, parasites, and several syndromes with no regex equivalent (acorn toxicity, *Listeria*, Texel throat). GTM PPV ranged from 38% (watery mouth) to 84% (pneumonia, ectoparasites). Both approaches agreed closely on temporal patterns, providing quasi-independent validation. Anomaly detection identified biologically plausible signals: for instance, pneumonia proportion rose from ~3.5% of all consultations at baseline to 4.45–4.76% during alarm weeks, a pattern consistent across both methods.

Conclusion: Regex and GTM, without recourse to LLMs or manual data labelling, are sufficient to build a validated, multi-syndrome surveillance system from farm animal EHR free text, requiring much lower computational resources. The unsupervised nature of GTM is a particular strength: it discovers clinically meaningful syndromes from the data itself, including unexpected ones. As a pilot study, FAVSNET currently represents a limited sample of farm animal practices; expanding the network will increase case counts and strengthen the robustness of both syndrome identification and aberration detection — a compelling case for joined-up data infrastructure in veterinary public health.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 30

Automated detection of asymmetrical udders in dairy goats using a camera and an artificial intelligence model YOLOv12

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

Kacper Libera¹, Maxime A.M. Pals², Yvette de Geus^{1,2}, Gerrit Koop², Lidwien A.M. Smit¹, Alex Bossers¹

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Key words: computer vision, mastitis, precision livestock farming

Social media message: Researchers from Utrecht University trained an AI (computer vision) model to detect asymmetrical udders in dairy goats. Asymmetrical udders are a sign of (past) mastitis and should therefore be closely monitored on the farm, both for individual animals and at the herd level.

Background: Udder asymmetry is a clinical sign in dairy goats frequently linked to udder inflammation (mastitis). Goats identified with udder asymmetry should therefore be examined and specifically checked for (past) mastitis, and the prevalence of udder asymmetry should be monitored at the herd level. However, in many countries dairy goat herds consist of hundreds to thousands of goats, making it practically impossible and labor-intensive to regularly examine all of them. New automated solutions, including computer vision models, are therefore highly desirable. In this study, we trained and validated a custom computer vision model to detect udder asymmetry in goats.

Methods: To develop the model, 4,321 annotated goat backside udder images and 373 background images were collected during milking sessions on a dairy goat farm on 3 different days. The 3 ground truth labels for the goat udders — symmetrical, left asymmetry, and right asymmetry — were provided by 2 independent dairy goat veterinarians. The dataset was randomly split into 60% training, 20% validation, and 20% unseen test subsets. The model was trained for 300 epoch cycles including hyperparameter optimization for 300 iterations.

Results: The performance of our model on the test dataset was satisfactory, with a mean average precision of 0.891 (95% CI 0.869–0.912) for mAP50, indicating detection success with 50% overlap between the predicted and actual udder area, and 0.766 (95% CI 0.747–0.789) for mAP50–95, the average performance across stricter localization requirements.

Conclusion: The detection of udder asymmetry in dairy goats can be automated using a simple camera and our computer vision model. The model is currently being tested in a validation study on three other dairy goat farms with a rotary milking parlor. This solution can facilitate more effective udder health monitoring, ultimately improving animal health, animal welfare, and milk quality.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 46

AI-Assisted risk negotiation for One Health decision-making

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

Alexandra Fetsch¹, Iurii Savvateev^{1,2}, Thomas Schuler², Monika Ehling-Schulz³, Sophia Johler¹, Matthias Filter²

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Key words: Risk analysis, Negotiations, LLM-based agents, Multi-agent frameworks

Social media message: New work: AI-assisted risk negotiation for food safety. LLM agents + RAG help stakeholders reach Pareto-optimal, evidence-grounded consensus — tested on Campylobacter & oak moth scenarios. Scalable One Health blueprint.

Background: Effective mitigation of food safety risks requires timely and systematic risk analysis, encompassing hazard recognition, probability and impact evaluation, and identification of suitable management and communication strategies. Under the One Health framework, this process is further complicated by competing stakeholder interests across human, animal, and environmental health domains — constrained by information complexity and time pressure. To support evidence-grounded and balanced decision-making, we developed an AI-assisted risk negotiation framework centred on large language model (LLM)-based multi-agent negotiation among relevant stakeholders.

Methods: The framework integrates LLM-based autonomous agents into a human-supervised, multi-step negotiation pipeline targeting risk assessment, valuation, and negotiation. Each stakeholder is represented by an LLM-based agent; agent descriptions are generated from stakeholder-provided materials using retrieval-augmented generation (RAG). The pipeline proceeds in four steps: (1) RAG-based methods extract stakeholder positions from submitted evidence, prompting agents in a preliminary discussion round; (2) human participants rank the proposed issues and options to align the agenda with stakeholder preferences; (3) the agreed issues, options, and preference scores are fed into a simulated negotiation game in which LLM-based agents negotiate while inferring opponents' agendas; (4) output deal distributions are evaluated against Pareto optimality (efficiency) and the Nash bargaining solution (fairness).

Results: The approach was evaluated in a workshop involving independent domain experts across two real-world scenarios: food safety criteria for *Campylobacter* in broiler meat and oak processionary moth management. In both cases, the framework enabled participants to reach consensus within the allotted time. Deals were characterised by frequency and temporal evolution, and assessed against Pareto and Nash criteria, providing a structured basis for evaluating outcome quality.

Conclusion: AI-assisted risk negotiation can substantially reduce the time required to make science-based, balanced management decisions. The framework offers a scalable and adaptable blueprint for evidence-grounded stakeholder negotiation across One Health disciplines, with demonstrated applicability to real-world food safety and environmental management scenarios.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 58

Automated scoring and localization of traumatic skin lesions in Italian fattening heavy pig carcasses: A pilot study

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

Matteo Recchia¹, Abbey Olsen², Lis Alban^{2,3}, Camilla Allegri¹, Sergio Ghidini⁴, Adriana Ianieri⁵, Giorgio Bontempi¹, Giorgio Varisco¹, Giovanni Loris Alborali¹

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Key words: *Abattoir, computer vision, welfare*

Social media message: *AI is changing the way we monitor animal welfare. Our pilot project shows that computer vision can automatically localize and score skin lesions on pig carcasses, providing more objective and continuous welfare data from abattoirs.*

Background: Traumatic skin lesions in slaughtered pigs are a relevant indicator of animal welfare (AW). Their distribution and morphology may help identify potential aetiologies, and whether injuries originated from the farm, during transport, or at lairage. Their assessment at slaughter could generate data for AW monitoring systems like ClassyFarm, designed by the Italian Ministry of Health for risk-based farm categorization. However, manual lesion scoring is time-consuming and difficult to standardize. This pilot study evaluated the feasibility of a computer vision (CV) model for scoring and localizing traumatic skin lesions on Italian heavy pig carcasses at slaughter.

Methods: A trained veterinarian scored 1,194 carcasses for traumatic skin lesions after scalding and dehairing, by carcass region (cranial, caudal, and dorsal) using a semiquantitative severity scale (0–3). The same carcasses were video-recorded, and a single extracted frame per carcass was rescored to assess intra-rater agreement. After excluding unsuitable images, 1,092 images were annotated for carcass regions and skin lesions, and split into training (70%), validation (20%), and test (10%) sets to train a commercial CV segmentation model. Model performance was evaluated on the test set using recall, precision, and F1 score, while predicted severity scores were compared with human scores.

Results: Intra-rater agreement between slaughter- and image-based scores was high, with weighted Cohen's kappa values of 0.89, 0.92, and 0.94 for the cranial, caudal, and dorsal regions, respectively. Model performance peaked at a confidence threshold of 42% (recall: 90.6%, precision: 91.5%, F1 score: 91.0%). Agreement between CV-predicted and image-based scores was also high, with correct classification rates of 91.7%, 89.9%, and 89.0% for the cranial, caudal, and dorsal regions, respectively. Most disagreements involved mild lesions and adjacent scores, whereas moderate and severe lesions were generally identified correctly.

Conclusion: High agreement between slaughter- and image-based scores supports the suitability of image-based scoring for CV model training. The CV model showed promising performance under commercial slaughterhouse conditions, particularly for identifying moderate and severe lesions. Future studies should validate the approach under different operational conditions. CV systems could support ClassyFarm by providing continuous, standardized slaughter-derived AW data.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 39

Hospital kitchens as hotspots for the circulation of ESBL- and Carbapenemase-producing *Escherichia coli*, *Klebsiella pneumoniae* and *Acinetobacter spp.*: Evidence from two Greek hospitals

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: broiler meat; hospital kitchens; β -lactam resistance

Social media message: Hospital kitchens may act as reservoirs for ESBL- and carbapenemase-producing bacteria. Our study highlights links between broiler meat, kitchen environments, staff and patients, underlining the need for strict hygiene, AMR monitoring and targeted food safety training.

Background: Extended-spectrum- β -lactamase (ESBL) and carbapenemase-producing Enterobacterales and *Acinetobacter spp.* are important nosocomial pathogens, frequently exhibiting multidrug resistance and limiting therapeutic options. Although hospital kitchens are responsible for preparing meals for vulnerable patients, their role as reservoirs and potential transmission points for antimicrobial-resistant bacteria remains insufficiently investigated. This study aimed to assess the prevalence, antimicrobial resistance characteristics, and epidemiological relationships of β -lactam-resistant *E. coli*, *K. pneumoniae*, and *Acinetobacter spp.* isolated from kitchen environments, broiler meat, and kitchen staff in two Greek hospitals.

Methods: A cross-sectional study was conducted in the kitchens of two Greek hospitals from different geographical regions. Samples were collected from kitchen environmental sites, broiler meat, and hospital kitchen staff. Strains were recovered after selective isolation using β -lactams and identified by MALDI-TOF MS. Antimicrobial susceptibility testing determined resistance profiles, phenotypic confirmation of ESBL and carbapenemase production was conducted, followed by molecular screening for β -lactamase genes. Protein profile analysis was used to investigate potential relationships among food, environmental, staff, and clinical strains, and *E. coli* isolates were further assigned to phylogenetic groups.

Results: Among 200 kitchen environmental samples, β -lactam-resistant strains were recovered from 42 samples (4.5% *E. coli*, 1.5% *K. pneumoniae*, 15.0% *Acinetobacter spp.*). Moreover, 35.0% of broiler meat samples were positive for ceftazidime-resistant *E. coli*, while *Acinetobacter spp.* were detected in 4.0% of staff skin samples. All *E. coli* isolates were multidrug-resistant ESBL producers, mainly phylogroups A (73.9%) and B1 (17.4%); all *K. pneumoniae* isolates were multidrug-resistant carbapenemase producers; 84.2% of *Acinetobacter spp.* were multidrug-resistant and 18.4% were carbapenemase producers. Protein profile analysis revealed close relationships between broiler meat and kitchen environmental strains, as well as between kitchen environmental and clinical strains from the same and other hospitals.

Conclusion: Hospital kitchens may act as important reservoirs and circulation points for β -lactam-resistant bacteria within healthcare environments. The detection of related strains across broiler meat, kitchen surfaces, utensils, staff, and patients highlights the need for strict hygiene practices, regular monitoring of clinically significant antimicrobial-resistant strains, and targeted food safety training for hospital kitchen personnel.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 7

From antibiotic dependence to alternative strategies: Impact on animal welfare in livestock production

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: Livestock welfare; Antimicrobial use reduction; Non-antibiotic interventions

Social media message: Reducing antibiotics in livestock while safeguarding animal welfare: this scoping review maps global evidence on the impact of reduced antibiotic use and non-antibiotic interventions on livestock welfare, highlighting key gaps for One Health action.

Background: The global spread of antimicrobial resistance (AMR) represents a major One Health challenge, threatening animals, humans, and the environment alike. Antimicrobial use (AMU) is considered a key driver of AMR, particularly in high-density settings such as global livestock production. Although various strategies to reduce antibiotic use and implement non-antibiotic interventions in food-producing livestock have been suggested, the available evidence regarding their effects on animal welfare remains fragmented and insufficiently synthesized. This study aimed to comprehensively map the scope and nature of the available literature on this topic, using a scoping review approach.

Methods: This study followed the Joanna Briggs Institute (JBI) methodology for scoping reviews. A systematic literature search was conducted in MEDLINE, Scopus, and Web of Science Core Collection, including relevant publications from regulatory authorities, for literature published from January 2015 onwards. Search strategies were developed and validated with professional librarians per the PRESS checklist. Screening was performed in two stages (title/abstract and full-text) by two independent reviewers using a predefined Population-Concept-Context (PCC) framework, managed in DistillerSR, with reporting following the PRISMA-ScR checklist.

Results: We retrieved 7,133 records across the three databases, of which 3,250 duplicates were removed. Titles and abstracts of the remaining 3,883 records were screened for inclusion, followed by full-text screening and data extraction. This study provides a comprehensive overview of the existing literature on the impact of reduced antimicrobial use and non-antibiotic interventions in food-producing livestock on animal welfare.

Conclusion: By mapping the breadth and characteristics of available evidence, this scoping review identifies key knowledge gaps and supports researchers, veterinarians, and policymakers in designing and implementing sustainable, evidence-informed strategies to mitigate AMR while safeguarding animal health and welfare within a One Health framework.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 45

Parameter inference for a complex agent-based model of Highly Pathogenic Avian Influenza: From approximate Bayesian Computation to sequential neural posterior estimation for rapid outbreak analysis and decision support

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: Agent-based modeling; simulation-based inference; decision support

Social media message: Comparing ABC and SNPE to calibrate a complex HPAI agent-based model, we show that neural simulation-based inference enables efficient parameter estimation and supports near real-time outbreak forecasting and decision-making.

Background: Highly Pathogenic Avian Influenza (HPAI) poses major challenges for disease control due to rapid transmission, heterogeneous poultry systems, and complex intervention strategies. Mechanistic epidemiological models can support outbreak management, but their calibration is often hindered by computationally intractable likelihood functions. Approximate Bayesian Computation (ABC) has been widely used for likelihood-free inference, yet it becomes computationally prohibitive in high-dimensional settings, particularly for stochastic agent-based models. This study investigates Sequential Neural Posterior Estimation (SNPE) for calibrating a complex HPAI epidemiological model, conducted within an international HPAI modelling challenge (WiLiMan-ID Horizon Europe project).

Methods: A stochastic, spatio-temporal agent-based model was developed in NetLogo to simulate HPAI transmission with farms as epidemiological units, explicitly representing farm characteristics and between-farm movements. Transmission occurred through local spread, wild bird introductions, and poultry movements, with delays between infection, detection, confirmation, and culling. Control measures included movement restrictions, surveillance, zoning, and culling. Parameter estimation used two successive approaches: an initial ABC exploratory phase, followed by SNPE implemented in Python via the sbi package.

Results: The model successfully reproduced the epidemiological patterns observed across the challenge, enabling prediction of epidemic dynamics and assessment of control measures. In the exploratory phase, ABC involved a high computational cost and posterior distributions showed limited divergence from priors, reflecting weak parameter identifiability. In contrast, SNPE efficiently produced informative posterior distributions, yielding simulated epidemic trajectories consistent with observed temporal dynamics, including peak timing.

Conclusion: SNPE provides a scalable and efficient alternative to ABC for calibrating computationally intensive epidemiological models, enabling robust parameter estimation while preserving epidemiological realism. This approach shows strong potential for near real-time outbreak analysis and decision support, representing a valuable asset for veterinary public health and improved preparedness for future epizootics.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 56

Another virus bites the dust: Electrostatic dust collectors as non-invasive alternative for detection and sequencing of Influenza A virus in pig herds

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: Swine flu; surveillance; whole genome sequencing

Social media message: Can you imagine that the dry sweeping cloths you use to dust your desk can unravel the evolution of flu? Colleagues from the Netherlands have shown that the cloths can detect and characterize influenza virus in pig farms without ever touching a pig!

Background: Pigs are reservoirs of former human influenza A virus (IAV) lineages, and act as mixing vessels for diverse strains, facilitating the emergence of novel IAVs. IAV surveillance in pig herds is crucial to assess zoonotic risk, but is complex, as the viremic period is short and clinical signs are aspecific, and the gold standard, nasal swabbing, causes discomfort. Here we tested whether passive air sampling through electrostatic attraction of dust could be a non-invasive, practical alternative for detection and genomic characterization of IAVs circulating in pig herds.

Methods: During a first pilot in three herds, we collected dust on horizontally placed petri dishes and electrostatic dust collectors (EDCs), testing three exposure periods (1, 2, and 7 days), and compared outcomes to nasal swabs and chewing ropes. A Bayesian latent class analysis determined sensitivity and specificity of the matrices. A second pilot was performed in one herd, with EDCs placed both horizontally and vertically and preserved in DNA/RNA Defend buffer. Samples with Ct values below 32 were selected for Oxford Nanopore sequencing to assess whole genome sequencing (WGS) feasibility.

Results: The first pilot showed 90% sensitivity and 91% specificity for EDCs exposed to air for two days, comparable to chewing ropes and grouped nasal swabs. Although EDCs had Ct values below 32, the quality of obtained viral sequences was substandard, while WGS were retrieved from other matrices — likely due to long aerosol exposure time or storage without stabilizing buffer. Preliminary data from the second pilot showed improved sequencing quality for samples from vertically placed EDCs stored in buffer.

Conclusion: Airborne dust samples collected by EDCs can be used to detect IAVs by qPCR in pig farms with high sensitivity and specificity, and show promise for IAV lineage classification by sequencing. Advantages of sampling dust instead of pigs include its non-invasive nature, lower costs, and the opportunity for farmers to do the sampling themselves, reducing biosecurity risks. After further optimization, the team aims to apply this technique to unraveling the long-term evolutionary dynamics of IAVs on farms.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 11

A large-scale spatio-temporal epidemiological model for investigating epidemic wave dynamics of African swine fever in wild boars

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: African swine fever, spatio-temporal modelling, epidemic wave speed

Social media message: How fast would African swine fever spread through Swiss wild boar if left unchecked? Our large-scale model shows that, without human intervention, wave speed is density-driven: ASF can travel up to 25 km/year and halving wild boar numbers cuts spread speed by up to 60%.

Background: African Swine Fever (ASF) is spreading across Europe and poses a growing threat to boar populations and domestic pig production^{1,2}. Given the high risk of ASF spreading to disease-free countries, understanding how fast it could naturally spread through this population, without human intervention, is essential for preparedness. This study builds and tests a large-scale mathematical model to answer one question: at what speed would ASF spread through wild boar populations when only natural transmission drives the epidemic?

Methods: We developed a modified SIR spatio-temporal compartmental model extended to include infectious cadavers as a persistent environmental source of transmission³. The model describes temporal changes in susceptible, infected, recovered, and cadaver densities across a simulated landscape divided into a 5×9 grid of 10×10 km² compartments, totalling 4,500 km². Wild boar movement is modelled as isotropic diffusion and population dynamics follow logistic growth. Under these idealised conditions, we ran eight scenarios varying population density, reproduction rate, infection rate, cadaver decay rate and population recovery. We measured how each parameter set influenced wave speed and peak infection density.

Results: The model produced epidemic waves travelling outward from the index compartment at speeds between 5 and 25 km/year, depending on wild boar density and infection rate. This is consistent with empirically estimated spread velocities under comparable conditions^{4,5}. Figure 1 links the controllable variable (population density) to the output of interest (wave speed), illustrating that wave speed is density-driven and that halving susceptible density substantially reduces it (i.e., 25–60% reduction across scenarios). Faster cadaver removal reduced spread speed, but only when cadaver infectivity was comparable to that of live animals⁶. Higher animal dispersal increased baseline wave speed without altering the sensitivity of speed to density reduction.

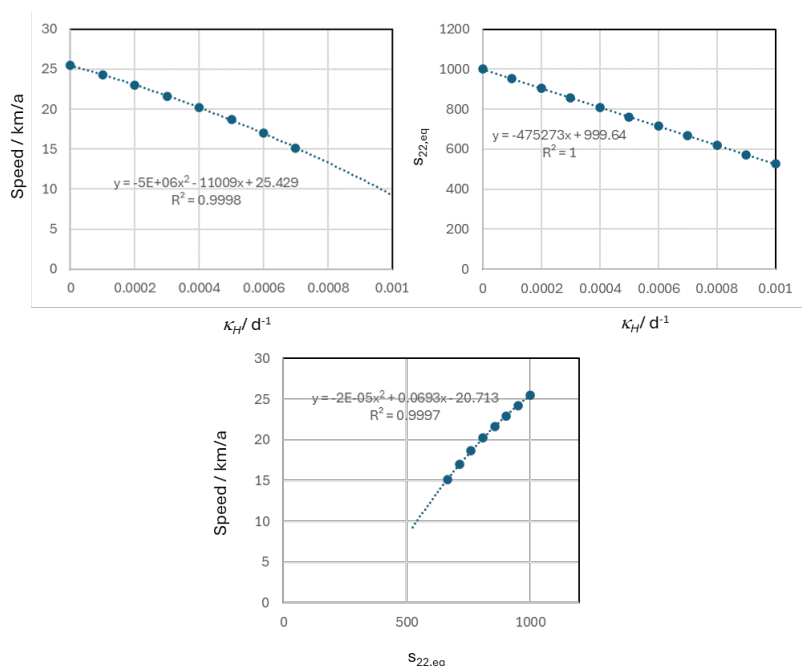


Fig. 1. Epidemic wave speed (A) and equilibrium density of the susceptible population (B) as a function of susceptible population density reduction (e.g., hunting intensity) and wave speed as a function of the equilibrium level (C) for scenario 1 — high density and low infectiousness.

Conclusion: Under natural transmission conditions and without human intervention, ASF can spread through a wild boar population at up to 25 km/year. Results suggest that wild boar density is the strongest driver of spatial spread and that density reduction is a key lever to slow epidemic waves. The model provides a theoretical basis to evaluate how population size affects ASF spread. It operates at a coarse resolution appropriate for large-scale dynamics and is not intended to predict outbreak trajectories or directly inform management decisions without further calibration and validation. However, it can be extended to incorporate seasonality⁷, non-isotropic dispersal⁸, sounder social structures and demographics⁷. Exploring the wild boar-domestic pig interface represents the next step toward a field-applicable model⁹.

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Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 36

Making data talk: A proof-of-concept AI-assisted, user-friendly pipeline for supporting data visualization and decision-making in Veterinary Public Health

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: AI-assisted, dashboard, surveillance

Social media message: What if turning surveillance data into an interactive dashboard required no coding skills, no proprietary software and less than half a working day? We designed and validated a four-stage, code-free pipeline producing a fully functional, portable dashboard in 3 hours.

Background: Veterinary public health surveillance programs generate continuous streams of data that often remain underexploited beyond static reports. Building custom dashboards traditionally requires dedicated programming expertise and proprietary software, limiting uptake in field veterinary and official control settings. The growing availability of accessible, web-based tools, including Large Language Model (LLM) assistants and open-access mapping platforms, offers an opportunity to substantially lower these barriers.

Methods: A four-stage, code-free pipeline was designed and tested: (1) data preparation from a structured CSV export with standard variable harmonization and anonymization; (2) AI-assisted code generation via iterative LLM prompting to produce a self-contained interactive HTML dashboard; (3) geographic visualization via a free-tier web mapping tool; (4) human validation, systematically cross-checking all AI-assisted outputs. The pipeline was first validated on a synthetic *Salmonella spp.* monitoring dataset, then applied to a real-world, anonymized foodborne pathogen surveillance dataset.

Results: Validation on the synthetic dataset confirmed that the pipeline produces a functional, visually coherent dashboard within a ~3-hour working session, with AI-generated code requiring only minor conversational refinements. Application to the real dataset demonstrated seamless transferability, yielding a presentation-ready dashboard providing annual positivity trends, matrix-specific detection rates, and a fully annotated serotype register — a single portable HTML file deployable in any browser without server infrastructure.

Conclusion: AI-assisted dashboard production offers a practical, low-barrier approach to operationalize surveillance data in veterinary public health. The proposed workflow is scalable and accessible to many professionals, aligning with One Health digital transformation goals. Input data should always be appropriately anonymized in compliance with data protection regulations, and this approach may serve as a replicable model for official control laboratories and competent authorities.

Poster Pitch

POSTER PITCH SESSION · ABSTRACT NO 10

Simulating vaccination scenarios for HPAI in turkeys using mechanistic simulation modelling

Poster Pitches & Viewing · Chair: Claudia Guldemann · Thursday, 3 September 2026, 11:00h

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Key words: Disease control, vaccine efficacy, outbreak dynamics

Social media message: A SEIRD model using Danish HPAI data assessed vaccination in turkeys. Vaccination reduced mortality but did not prevent within-flock spread; boosters improved control. High efficacy is key, and vaccination should complement biosecurity.

Background: Highly pathogenic avian influenza (HPAI) has had a dramatic influence on wild birds and poultry populations worldwide during the last six seasons. Vaccination has been used in certain poultry species to control and prevent outbreaks, but there is an additional need for mathematical models to simulate disease spread and explore the effects of vaccination across different poultry species and scenarios. This project assessed the effect of different HPAI vaccination scenarios in turkey flocks.

Methods: A SEIRD compartmental model was fitted to mortality data from HPAI outbreaks in Denmark. Five vaccine efficacy curve functions were explored — linear, exponential, plateau, differential primer-booster, and Weibull-beta distributions — with the latter selected based on model fit and biological plausibility. Two vaccination strategies were evaluated: a single dose at 1 day of age, and a two-dose plan administered at 1 and 36 days of age, using both documented parameter values and an optimistic scenario.

Results: Vaccination alone was insufficient to prevent spread in a flock once the virus was introduced, protecting highly against mortality but less against susceptibility and shedding. With vaccine efficacy above 80%, the model predicted around 6.5% of animals remained uninfected throughout the production cycle. Modelled outbreaks were more severe in the absence of a booster, while booster vaccination led to more controlled outbreaks. Scenarios using conservative parameters showed higher mortality associated with earlier or later virus introduction days than more optimistic estimates, particularly when immunity onset was delayed or waning occurred faster.

Conclusion: Following HPAI virus introduction, vaccination does not prevent within-flock spread, with outbreaks occurring in all tested scenarios. However, vaccination can significantly reduce associated mortality, which may complicate surveillance. Vaccination should complement, not replace, biosecurity measures, and achieving high levels of protection remains essential, especially in highly susceptible species such as turkeys. Future work should focus on practical implementation of vaccination and surveillance scenarios to inform policy for optimal protection, animal welfare and international trade.

Poster Presentations

The following 45 abstracts, submitted for ECVPH Munich 2026, are presented as posters.

- No. 1** Attributing sources of foodborne pathogens in the Netherlands: a structured expert elicitation — *Lena I. Wijnen*
- No. 3** Dairy goats can be super shedders of *Staphylococcus lugdunensis* and *Staphylococcus simulans* — *Y. de Geus*
- No. 4** Biopesticide-associated *Bacillus thuringiensis* on retail fresh produce: occurrence, typing and implications for food-safety surveillance — *Carolyn Schmidt*
- No. 5** Growth conditions drive CytK1 toxin dynamics in *Bacillus cytotoxicus* — *Arina Khalili*
- No. 6** Detection of Udder Pathology and Unexpected Neoplastic Lesions in Adult Small Ruminants During Post-Mortem Inspection: Implications for Risk-Based Post-Mortem Inspection — *Madalena Vieira-Pinto*
- No. 8** ESBL Potential and Multidrug Resistance in *Salmonella* Strains Isolated from Chicken Meat — *Ali AYDIN*
- No. 9** Farmers' experiences of biosecurity work and their future perspectives on Swedish animal production — *Alexis Rydell*
- No. 12** Bovine respiratory syncytial virus : Comparative analysis of humoral immune response induced by different vaccines — *Anneliese Demil*
- No. 14** OutCost Tool: Estimating the Impact of African Swine Fever in the Balkans — *Mafalda Mil-Homens*
- No. 15** Generative AI in Veterinary Case-Based Learning for Clinical Reasoning Training — *Jasmin Widmer*
- No. 16** Identification of very high users among veterinary practices for antibiotic use in cats and dogs with different indicators — *Anaïs Léger*
- No. 17** Quantitative evaluation of bovine tuberculosis surveillance in Belgian slaughterhouses — *Mickael Cargnel*
- No. 18** Genomic analysis of *Staphylococcus aureus* in the Zambian dairy value chain reveals widespread circulation of a pandemic clone with high virulence potential — *Ângelo J. F. Mendes*
- No. 19** A glimpse on emerging hazards: the FoodSafer Project — *M. Wagner*
- No. 21** Farmers and veterinarians' perceptions and adaptive management of tick-borne disease risk on endemic dairy farms — *Sarah Shanks*
- No. 22** Environmental Drivers of Tick Density in UK Dairy Farms: Implications for Livestock Health and Agri-Environment Policy — *Sarah Shanks*
- No. 23** Beyond KAP in AMR: Integrating Psychometrics and Choice Tasks in a Mixed-Methods Study with Nepalese Poultry Farmers — *Jorge Pinto Ferreira*
- No. 24** Co-construction and governance of a nationwide HPAI vaccination strategy in ducks: Drivers, success factors, and future challenges in France — *Marie Pelgrin*
- No. 25** A Novel Agent-Based Model framework for Simulating Multidrug-Resistant Organism Transmission Dynamics in a Veterinary Teaching Hospital Environment — *Nicolo Mezzasalma*
- No. 26** Epidemiology of Pain in the Brain A Review and Conceptual Framework for Operationalizing Pain in Veterinary Neurology as a Quantifiable Cognitive State in Dogs — *Dr. med. vet. Julia D. Kschonek*
- No. 27** From awareness to preparedness: a gap in veterinary students' training on public health knowledge related to game meat? — *Sara Marques*
- No. 28** Hepatitis E virus detection in effluent samples collected from a swine slaughterhouse: A one-year molecular surveillance — *Gianluigi Ferri*
- No. 29** Stability of therapeutic bacteriophages against intestinal infections in formulations for oral application in veterinary medicine — *Sofiia Merkureva*
- No. 31** Construction of an integrated data collection network in the context of multi-hosts zoonoses persistence communities — *Alexis Peutot*
- No. 32** Rapid detection and mitigation of a filarioid nematode outbreak in the Canadian Arctic. — *Rachele Vada*
- No. 33** What matters most in avian influenza surveillance? Veterinarians' perspectives from Italy — *Liliana Martella*
- No. 34** Pathogen Transmission by Flies and Beetles in Poultry Houses — *Iryna Makovska*
- No. 35** Educational needs and biosecurity competencies in veterinary medicine: a multinational survey — *Claude Saegerman*
- No. 37** Microbiological Safety of Heat-Treated Plant-Based Meat Alternatives During Refrigerated Storage — *Erënesa Gorcaj*
- No. 38** Understanding How Livestock Impact Refugee Health and Nutrition: A Grounded-Theory Approach — *HERRINGTON, Rosie*
- No. 40** Human Carriage of β -Lactam-Resistant Bacteria along the Broiler Meat Production Chain: A One Health Perspective — *Anestis Tsitsos*
- No. 41** Prevalence and Molecular Characteristics of ESBL-producing *Escherichia coli* in Foods of Animal Origin in Europe: A Systematic Review and Meta-Analysis — *Alexandros Damianos*
- No. 42** Validation of the Pour-Plate Method as an Alternative to the MPN Technique for *E. coli* Quantification in Bivalve Molluscs — *Rosa Luisa Ambrosio*
- No. 43** Dry-Curing of Seabass and Cod: Process Characterisation and *Listeria monocytogenes* Challenge Test — *Giulia Polizzi*

No. 44 Evaluation of Official Data on the Surveillance and Control of *Salmonella* in Meat of Domestic Ungulates in Portugal — João Bettencourt Cota

No. 47 Trustworthy AI for Food: An Architecture for Verifiable, Accountable Decision Support — Alexandra Fetsch

No. 48 Agrifood-OneAI: A Pan-European COST Action Leveraging Artificial Intelligence to Operationalise One Health in Agrifood Systems Transformation — Sophia Johler

No. 49 Assessing the performance of a rapid test in integrated bite case management for One Health rabies control — Rabina Ghimire

No. 50 'Monitoring wildlife matters': study on the presence of *Cryptosporidium spp.* in Portuguese wild boars and related hygiene risk factors — Ana Carolina Abrantes

No. 51 Gastric Lesions in Pig Stomachs: An Exploratory Study — Ana Francisca Oliveira

No. 52 Veterinary Career Preferences in Europe: Determinants of Sector Choice Among Students and Early-Career Veterinarians — Panagiotis Maroulidis

No. 53 Evaluation of the public health risks from broiler carcasses rejected with localised perihepatitis during post-mortem inspection — Nikolaos Dadios

No. 54 Assessing pathogen surveillance in swine barn sedimentation dust via metagenomic profiling of environmental RNA — Frederik Kiene

No. 55 Relevance of cattle as source of resistant *E. coli* in Cameroon — Rodrigue FOKA FONKAM

No. 57 Report of control and surveillance measures against enzootic bovine leukosis in French Reunion Island over a 10-year period — Camille DEMASSIEUX

Poster

POSTER PRESENTATION · ABSTRACT NO 1

Attributing sources of foodborne pathogens in the Netherlands: a structured expert elicitation

Poster Session · Thursday, 3 September 2026

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Key words: Calibration questions; Foodborne pathogens; Source attribution; Structured expert judgment; Transmission pathways

Social media message: Source attribution results based on expert knowledge elicitation help improve understanding of where foodborne pathogen risks come from and how to better target prevention

Background: Foodborne pathogens impose a substantial burden on public health, even in high-income countries. However, quantifying the relative contributions of different sources of human infection with foodborne pathogens remains difficult due to limited data availability and uncertainty in empirical evidence. Structured expert elicitation (SEE) offers a useful methodological alternative to improve understanding of source attribution for foodborne pathogens.

Methods: We performed a SEE study to attribute human cases of infection with 26 foodborne pathogens in the Netherlands to seven major transmission pathways (food, drinking water, environmental water, other environmental pathways, animal contact, person-to-person, and international travel), 20 food groups within the foodborne pathway, and two animal groups within the animal contact pathway. The analysis was conducted using Cooke's classical model for structured expert judgement. The elicitation process included snowball sampling of experts, self-assessment of expertise, and a calibration workshop in which experts responded to seed questions designed to quantify their uncertainty for model weighting. Subsequently, experts provided estimates for target questions to derive attributable proportions at the 'kitchen door' level.

Results: The results showed that transmission was predominantly foodborne (>50%) for several pathogens, particularly *Staphylococcus aureus*, *Listeria monocytogenes*, *Yersinia spp.*, *Bacillus cereus*, *Clostridium perfringens*, certain non-typhoidal *Salmonella* serotypes, *Campylobacter spp.*, hepatitis E virus, and *Toxoplasma gondii*. In contrast, person-to-person transmission was the main route for astrovirus, rotavirus, norovirus, and sapovirus. *Brucella spp.* and typhoidal *Salmonella* were largely (>85%) associated with international travel. For the remaining pathogens, no single pathway accounted for more than half of cases. When foodborne transmission was further disaggregated into 20 food groups, substantial heterogeneity was observed. Key contributing sources actually included food handlers and vermin, as well as various meat products (including pork, beef, and chicken) and shellfish.

Conclusion: The obtained SEE-based source attribution estimates complement existing empirical evidence from public health surveillance data and epidemiological studies by providing detailed, pathogen-specific insights into transmission pathways in the Dutch context.

Poster

POSTER PRESENTATION · ABSTRACT NO 3

Dairy goats can be super shedders of *Staphylococcus lugdunensis* and *Staphylococcus simulans*

Poster Session · Thursday, 3 September 2026

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Key words: *Staphylococcus lugdunensis*; *Staphylococcus simulans*; bulk milk total bacterial count; dairy goats

Social media message: In goats, mastitis caused by *Staphylococcus lugdunensis* and *Staphylococcus simulans* can significantly increase the total bacterial count in bulk milk.

Background: The bulk milk total bacterial count (BMTBC) is a key milk quality indicator since bacterial byproducts reduce the shelf life of milk and dairy products. Factors influencing BMTBC include milking hygiene, cooling and cleaning of the bulk tank, and milking technique. Also, goats with intramammary infections (IMI) can shed bacteria into the milk. How many bacteria are shed during IMI, and to what extent individual goats can contribute to BMTBC is not known yet.

Methods: A cross-sectional study with 98 goats (n=196 milk samples) was conducted on a Dutch dairy goat farm with a recurrent elevated BMTBC. Milk was cultured on blood agar plates followed with track dilutions, and bacteria were identified using matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Additionally, TBC was determined using flow cytometry.

Results: Based on BAPC results, we showed that goats with IMI caused by *Staphylococcus lugdunensis* or *Staphylococcus simulans* can shed extremely high numbers of bacteria into the milk with a maximum of ~700 million cfu/mL. Due to a high proportion of goats with abnormal milk, TBC could not be measured in these samples using flow cytometry.

Conclusion: Some super shedder goats with *Staphylococcus lugdunensis* or *Staphylococcus simulans* IMI had such a high BAPC that only even one goat significantly elevated the BMTBC. Identifying, and excluding high bacterial shedders, along with improved hygiene measures, enhanced the milk quality, and helped to control BMTBC at the studied farm. Perspectives: A larger study could investigate whether IMI with these staphylococcal species also play a role in high BMTBC on other dairy goat farms.

Poster

POSTER PRESENTATION · ABSTRACT NO 4

Biopesticide-associated *Bacillus thuringiensis* on retail fresh produce: occurrence, typing and implications for food-safety surveillance

Poster Session · Thursday, 3 September 2026

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Key words: biopesticide residues, *Bacillus cereus* group, enterotoxins, whole genome sequencing, FTIR

Social media message: Retail fresh produce can harbour biopesticide-associated *Bacillus thuringiensis*: detected in 22% of 280 samples. FTIR showed a highly uniform population, and WGS linked 20/22 isolates closely to commercial biopesticide strains. Implications for exposure and food-safety monitoring.

Background: *Bacillus thuringiensis* is one of the most widely used microbial biopesticides and is likely to gain further relevance in the agrifood systems transformation. However, as a member of the *B. cereus* group, *B. thuringiensis* may harbour enterotoxin genes linked to diarrheal illness, raising food-safety concerns about its occurrence on minimally processed fresh produce. This study aimed to assess the prevalence and genetic diversity of *B. thuringiensis* on retail fresh produce to better understand its potential role in food contamination and risk.

Methods: A total of 280 fresh produce samples, including leafy greens, vegetables, and fruits, were collected from a retail distribution centre. Samples were analysed by selective cultivation and PCR-based characterization of presumptive *B. cereus* group isolates, including screening for enterotoxin genes, and *B. thuringiensis*-associated insecticidal toxin genes (cry genes). Isolates were further characterized using FTIR spectroscopy and whole-genome sequencing for clustering and phylogenetic analyses.

Results: *B. thuringiensis* was detected in 22% of produce samples. Isolates predominantly showed biopesticide-associated profiles, and 20/22 sequenced isolates showed close genomic relatedness to commercially used biopesticide strains.

Conclusion: These findings underscore that residues of biopesticides lead to the widespread occurrence of *B. thuringiensis* on retail fresh produce.

Poster

POSTER PRESENTATION · ABSTRACT NO 5

Growth conditions drive CytK1 toxin dynamics in *Bacillus cytotoxicus*

Poster Session · Thursday, 3 September 2026

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Key words: foodborne toxico-infection; enterotoxin regulation; food matrix; starch-rich foods; cytotoxicity; qPCR

Social media message: *Tiny spores, big questions: Bacillus cytotoxicus is an emerging foodborne pathogen linked to severe toxin-mediated diarrheal disease. This study explores how food-relevant nutrient conditions shape cytK-1 expression, CytK-1 production, and cytotoxicity using qPCR, ELISA, and cell-based assays. Our findings point to highly strain-specific and condition-dependent toxin regulation --- highlighting how food matrix components may influence the pathogenic potential of B. cytotoxicus.*

Background: Foodborne toxico-infections associated with *B. cytotoxicus* have resulted in severe or even fatal diarrheal illness caused by the CytK 1 toxin. Its thermotolerance may allow it to escape routine screening, increasing the importance of understanding CytK 1 regulation. Contamination with the pathogen is almost exclusively associated with dried, starch rich products such as potato-based foods as well as with insect derived foods. Although *B. cytotoxicus* is frequently detected in these products, only comparatively few outbreaks have been reported. However, documented cases include severe and even fatal disease. This discrepancy suggests that environmental conditions and matrix composition may influence CytK 1 production and cytotoxicity.

Methods: In this study, we investigated environmental factors shaping cytK1 expression by comparing nutrient conditions in CGY and minimal media with different carbon sources. Eight strains of *B. cytotoxicus* were compared, including the reference strain NVH 391 98. Gene expression was measured using qPCR, and CytK 1 production and activity were assessed via ELISA and Vero and CaCo₂ cell cytotoxicity assays at 0, 1, and 5 h. QPCR results indicate strain specific and condition dependent differences in cytK1 expression. Several strains peaked after 5 h in CGY supplemented with fructose, whereas others showed higher expression as early as 1 h in CGY without added sugars.

Results: These findings suggest that cytK1 expression in *B. cytotoxicus* is highly variable across strains and growth conditions

Conclusion: We therefore hypothesize that specific food relevant matrix components, such as starch and its breakdown products, modulate CytK 1 production and cytotoxic activity.

Poster

POSTER PRESENTATION · ABSTRACT NO 6

Detection of udder pathology and unexpected neoplastic lesions in adult small ruminants during post-mortem inspection: Implications for risk-based post-mortem inspection

Poster Session · Thursday, 3 September 2026

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Key words: Small ruminants, post mortem inspection, udder

Social media message: Visual inspection missed udder lesions in 484 adult small ruminants. Incision revealed 3.9% mastitis and two neoplasms, including a carcinoma, showing the need for enhanced udder assessment to improve Risk Based Post-Mortem Inspection

Background: Udder pathology is a frequent finding during post-mortem inspection of adult small ruminants in slaughterhouses. Under Commission Implementing Regulation (EU) 2019/627, udder and respective lymph nodes examination is restricted to visual inspection in adult small ruminants. This limited approach may hinder the detection of relevant lesions, particularly those not externally visible. Reports of udder neoplasms in small ruminants are scarce, and malignant lesions carry direct implications on post mortem condemnation criteria applied by official veterinarians. This study aimed to determine the prevalence and characteristics of udder lesions in adult small ruminants and to evaluate the diagnostic limitations of visual inspection alone.

Methods: A total of 484 adult small ruminants were examined on the slaughter line. Inspection procedures included visual assessment, systematic incision of the udder parenchyma, and evaluation of the medial iliac and precrucial lymph nodes. Udders presenting macroscopic abnormalities or altered consistency were sampled and fixed in 10% buffered formalin for histopathological analysis. Lesions were classified as inflammatory or neoplastic, and lymph node reactivity was recorded to assess potential implications for carcass condemnation.

Results: Among the 484 udders examined, no macroscopic alterations were detected upon visual inspection. Following systematic incision of the udder parenchyma, 3.9% (n = 19) presented lesions consistent with mastitis. Histopathological examination confirmed and further characterized the macroscopically identified inflammatory lesions, enabling precise classification of mastitis subtypes based on the nature and distribution of the inflammatory infiltrate. These included purulent mastitis with abscessation (n = 9), fibrinopurulent mastitis (n = 4), chronic mastitis (n = 4), and necrotic mastitis (n = 2). Medial iliac and precrucial lymph node reactivity was observed in 7 of the 9 purulent and necrotic mastitis cases, resulting in total carcass condemnation due to evidence of systemic involvement. Importantly, histopathological examination of two udders initially not subjected to total condemnation revealed previously unrecognized neoplastic lesions: one fibroadenoma and one carcinoma. The malignant lesion would have required total condemnation, underscoring the public health relevance of detecting such changes.

Conclusion: Visual inspection alone is insufficient for detecting udder pathology in adult small ruminants. A combined approach incorporating palpation and systematic parenchymal incision significantly improves diagnostic sensitivity. The incidental identification of a malignant mammary adenocarcinoma in an animal that would otherwise have passed routine inspection highlights critical gaps in current post-mortem protocols. Reports of udder neoplasms in small ruminants are scarce, and these findings contribute novel information to the field. Adult small ruminants should be considered a priority category for enhanced udder assessment, and incorporating routine palpation and parenchymal incision into post-mortem protocols may improve lesion detection and support more accurate Risk-Based Post-Mortem Inspection. **Acknowledgments:** This work was funded as part of the AICanceR[∞]Hub project (NORTE2030-FEDER-02687800), co-financed by the European Regional Development Fund (ERDF) under the 2021--2027 Northern Portugal Regional Program [NORTE2030].

Poster

POSTER PRESENTATION · ABSTRACT NO 8

ESBL potential and multidrug resistance in *Salmonella* strains isolated from chicken meat

Poster Session · Thursday, 3 September 2026

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Key words: *Salmonella*, ESBL, Sanger Sequencing, One Health

Social media message: The relationship between human health, animal health, and food consumption is complex and interdependent, forming an interconnected system known as "One Health." The ESBL-producing *Salmonella* found in chicken meat, which has developed antibiotic resistance, clearly demonstrates how the uncontrolled use of antibiotics in livestock farming directly threatens human health. To ensure that even the simplest infections are not left untreated in the future, we must use antibiotics responsibly---both in our own lives and in animal production---and wage a collective battle that encompasses nature and all living beings. Consequently, the One Health approach is of critical significance in the struggle against antibiotic resistance.

Background: *Salmonella*, a major foodborne pathogen, poses a threat to global public health due to its role in the spread of antibiotic resistance. This study aimed to investigate the presence, genetic diversity, and resistance profiles of *Salmonella* in chicken meat, addressing the inseparable link among animal-derived foods, humans, and the environment within the framework of the "One Health" concept.

Methods: A total of 210 raw chicken meat samples collected from retail outlets across İstanbul were analyzed in accordance with ISO 6579-1. The isolated strains were confirmed and serotyped using PCR, agglutination, and Sanger sequencing. Antibiotic susceptibilities were determined using disk diffusion and E-test methods in accordance with EUCAST and CLSI standards, while resistance genes were investigated using PCR.

Results: *Salmonella* was isolated from 6.2% of the samples (n=13); the predominant serotype was *S. Infantis* (84.6%), followed by *S. Enteritidis* (7.7%) and *S. Virchow* (7.7%). In the disk diffusion test, multidrug resistance was identified in 84.6% of the strains. According to E-test results, the highest resistance was observed against tetracycline at 84.6%. The double-disk synergy test confirmed that 38% of the strains phenotypically produced Extended-Spectrum Beta-Lactamases (ESBL). Genetic analyses identified the resistance genes bla~TEM~ (30.7%), bla~CTX-M~ group 9 (30%), and bla~CTX-M~ group 1 (7.7%). No colistin or carbapenem resistance genes were detected.

Conclusion: This pioneering study has revealed that retail chicken meat poses a serious public health risk and serves as a reservoir for the spread of potential ESBL-producing multidrug-resistant *Salmonella* strains. It is clear that multidisciplinary surveillance studies based on the One Health approach are of vital importance for limiting the uncontrolled use of antibiotics in animal production and preventing zoonotic risks.

Poster

POSTER PRESENTATION · ABSTRACT NO 9

Farmers' experiences of biosecurity work and their future perspectives on Swedish animal production

Poster Session · Thursday, 3 September 2026

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Key words: Farm biosecurity, work environment, challenges

Social media message: Farmer interviews reveal conflicting interests between regulatory requirements, administrative burdens, workload, animal welfare, and economic sustainability

Background: Climate change, political instability, changing trade patterns and wildlife population dynamics all contribute to increased risk of emergence and spread of animal diseases. With infectious diseases such as e.g. African swine fever and highly pathogenic avian influenza increasingly challenging pig and poultry production, there is a need for a high level of farm biosecurity. Farm biosecurity includes all measures to prevent spread of infectious agents within and between animal holdings, to minimise the risk of disease outbreaks. Disease outbreaks as well as the effort needed to prevent them impact on farmer's work and work environment. This can also be expected to affect their views of the future. This study focused on experiences of biosecurity work in commercial pig and poultry production in Sweden. It was conducted within the EU Horizon project 101136346 EUPAHW.

Methods: The purpose of the study was to explore how changing requirements for farm biosecurity affect the farmers' current work and what they expect in the future. We employed an interdisciplinary approach including researchers from work science, sociology and veterinary medicine. Twenty-one semi-structured interviews were conducted with farmers with larger commercial holdings with pigs or poultry, in different parts of the country. The respondents were either the farm owner or their operation manager. The focus on large farms was motivated by their key role in national food production and their complex challenges in biosecurity due to the involvement of several employees in the work.

Results: The results demonstrate that the farmers view biosecurity as an integral and important part of their operations. Biosecurity is believed among the farmers to play an even more significant role in the future. The results also highlight various tensions between demands and interests that affect farmers' work situation. These tensions lie in the intersection of regulatory requirements, administrative burdens, workload, animal welfare, and economic sustainability. Although biosecurity efforts contribute to a more reliable production as well as a safer and cleaner work environment, there are challenges regarding employee compliance with procedures, economic costs associated with external biosecurity, access to skilled labour, and the public perception of changes toward closed-system production farming, all of which may impact farmers' future outlooks in different ways.

Conclusion: Farm biosecurity is not performed in isolation but is affected by external context and involves a complex interaction between human behaviour, organizational strategies, regulations and guidelines, and the environment.

Poster

POSTER PRESENTATION · ABSTRACT NO 12

Bovine respiratory syncytial virus : Comparative analysis of humoral immune response induced by different vaccines

Poster Session · Thursday, 3 September 2026

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Key words: BRSV; vaccination; seroneutralization

Social media message: Modified live BRSV vaccines induced stronger neutralizing antibody responses than inactivated vaccines against circulating Belgian subgroup II strains. Future studies will assess cross-neutralization against the newly identified subgroup VIII strain.

Background: Bovine respiratory syncytial virus (BRSV), classified within the genus Orthopneumovirus, is a major contributor to bovine respiratory disease complex (BRD). Recent phylogenetic investigations in Belgium identified the circulation of BRSV subgroup II strains and, for the first time, subgroup VIII strains. Commercial vaccines currently marketed in Belgium are based on subgroup II or III strains, raising questions regarding their capacity to induce cross-protective immunity against circulating field strains. This study aimed to evaluate and compare the humoral immune response induced by commercially available BRSV vaccines in seronegative cattle.

Methods: Seronegative cattle were vaccinated using commercially available BRSV vaccines, including both modified live and inactivated formulations administered through parenteral routes. Humoral responses were evaluated longitudinally by measuring BRSV-specific IgG1 levels and serum neutralization titres against a subgroup II BRSV strain. Samples were collected at multiple time points following vaccination, including days 14 and 28 post-vaccination. Comparative analyses were performed between vaccine groups to assess differences in antibody kinetics and neutralizing capacity.

Results: IgG1 levels increased rapidly after vaccination and stabilized within the first month post-vaccination, with a slight subsequent increase observed for most vaccines. Vaccine C, a multivalent inactivated vaccine, induced significantly higher IgG1 levels compared with the other vaccines evaluated. This enhanced humoral response may be associated with adjuvant use in inactivated formulations. Despite high IgG1 responses, inactivated vaccines A and C showed the lowest serum neutralization titres against subgroup II BRSV. In contrast, the two parenterally administered modified live vaccines (vaccines D and E) generated higher neutralizing antibody levels. A statistically significant increase was observed for vaccine D at days 14 and 28 post-vaccination. Notably, live attenuated vaccine strains originating from subgroup II (vaccine E) or subgroup III (vaccine D) both demonstrated effective neutralization of subgroup II field strains, suggesting the presence of cross-neutralizing activity between phylogenetic subgroups.

Conclusion: Parenterally administered modified live vaccines appear to induce stronger neutralizing antibody responses against subgroup II BRSV in seronegative cattle compared with inactivated vaccines. High IgG1 levels alone were not predictive of neutralizing capacity. These findings highlight potential differences between quantitative humoral responses and functional antibody activity. Future work will focus on isolating a Belgian subgroup VIII field strain to further evaluate cross-neutralization and vaccine-induced protection against this recently identified subgroup.

Poster

POSTER PRESENTATION · ABSTRACT NO 14

OutCost Tool: Estimating the impact of African swine fever in the Balkans

Poster Session · Thursday, 3 September 2026

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Key words: Economic impact; OutCost; African Swine Fever

Background: African swine fever (ASF) is a highly lethal disease of domestic pigs and wild boar, spreading mostly through the informal trade of contaminated products and wild boar movements. In the absence of effective vaccines, control relies on total stamping out, generating economic consequences through mortality, reduced pig production, costly eradication strategies, and disruption of trade and tourism. ASF reached Europe via Georgia in 2007 and the Balkans in 2017, with 19 countries reporting outbreaks in 2025. Balkan nations have adopted control strategies combining stamping out, surveillance, movement restrictions, and biosecurity measures. Despite multiple studies documenting ASF's economic impacts on swine production globally, its full financial burden in the Balkan region remains underexplored. Considering this, the objective of the study was to quantify the direct economic costs of ASF outbreaks across seven Balkan countries/territories using the OUTbreak COSTing Tool (OutCostT), a FAO corporate Excel-based tool.

Methods: ASF outbreaks were assessed in Albania, Bulgaria, Kosovo, Montenegro, North Macedonia, Romania, and Serbia. A total of 431 outbreaks were evaluated: 4.2% in commercial farms (n=18), 3.3% in family/smallholder farms (n=14), and 92.6% in backyard farms (n=399). Assessment periods ranged from three months (Kosovo) to one year (Romania). Cost data were collected and entered into the OutCostT tool, capturing expenses related to culling, carcass disposal, compensation, movement restrictions, surveillance, and training and communication, among others.

Results: Estimated annual ASF costs varied widely across territories: Albania €0.22 million (1 commercial farm outbreak), Bulgaria €24 million (44 outbreaks, mostly backyard farms), Kosovo €0.24 million (25 backyard farm outbreaks), Montenegro €0.001 million (2 wild boar cases), North Macedonia €0.47 million (3 outbreaks in family and backyard farms), Romania €26 million (340 outbreaks, 329 in backyard farms), and Serbia €0.85 million (18 backyard farm outbreaks). Bulgaria and Romania costs were driven primarily by culling, carcass disposal, and farmer compensation. In territories with fewer outbreaks, costs were shaped by distinct measures: movement bans (Albania), wildlife surveillance (North Macedonia and Montenegro), and surveillance in the general population (Serbia). Cost coverage also differed: official veterinary services bore most expenses in Bulgaria, Montenegro, North Macedonia, and Romania, while farmers absorbed the majority in Albania and Kosovo.

Conclusion: Total ASF costs and expenditure distribution across the seven Balkan territories were primarily driven by the number of outbreaks and the type of affected holding. OutCostT proved to be a valuable tool for retrospective economic analysis, providing information that can be used for resource allocation and guiding evidence-based decisions on ASF control strategies.

Poster

POSTER PRESENTATION · ABSTRACT NO 15

Generative AI in veterinary case-based learning for clinical reasoning training

Poster Session · Thursday, 3 September 2026

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Key words: *Clinical Reasoning; Veterinary Education; Generative Artificial Intelligence; AI Literacy; Case-Based Learning; Clinical Competence*

Social media message: *Generative AI holds promise for veterinary education. In our study, most students gained valuable insights, yet AI integration alone didn't improve clinical reasoning. Are scaffolded systems and AI literacy the missing pieces?*

Background: Clinical reasoning is a core competency in veterinary education. Generative AI (GenAI) holds promise for case-based learning (CBL), yet its effectiveness as a reasoning support tool remains unclear. This study evaluated whether the integration of a commercially available GenAI chatbot into CBL would support veterinary students in clinical reasoning tasks.

Methods: Following an evaluation of accessibility, functionality, and data protection compliance, Microsoft Copilot was selected as the GenAI tool of choice. Students received a user-oriented instruction manual and access to a tailored prompt to support effective use. Sixty fourth-year veterinary students at a Swiss university participated in an interventional crossover study, alternating between AI-supported and traditional CBL across four clinical case scenarios. Clinical reasoning outcomes were assessed per case scenario by a dedicated lecturer using 34 scored items. A post-class survey completed by students and lecturer reflections provided additional depth.

Results: Despite almost two thirds of students reporting that the AI tool provided relevant inputs they had not previously considered, clinical reasoning outcomes showed no meaningful difference between groups ($W = 6719$, $p = 0.464$). Notable variation across individual case scenarios was observed. Post-class surveys ($n = 38$) further revealed largely positive experiences, with most students perceiving reduced task difficulty (58%) and finding the AI-generated starting point effective (61%). At the same time, nearly half (45%) reported negative effects on case understanding and dissatisfaction with the overall learning experience. Qualitative feedback highlighted benefits such as information retrieval and a lower barrier to case initiation with a ready-made AI output to build on, alongside concerns about superficial or inaccurate AI outputs.

Conclusion: These findings highlight both the promise and the complexity of integrating GenAI into veterinary education to support clinical reasoning training. AI integration alone appears insufficient to improve clinical reasoning outcomes. The missing pieces may lie in adequate AI literacy training to build student confidence and competence, and thoughtfully scaffolded systems to alleviate cognitive demand. Realizing what GenAI could offer for clinical reasoning training will require collaboration among educators, developers and students to ensure AI integration is aligned with student learning needs and clinical experience.

Poster

POSTER PRESENTATION · ABSTRACT NO 16

Identification of very high users among veterinary practices for antibiotic use in cats and dogs with different indicators

Poster Session · Thursday, 3 September 2026

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Key words: Antibiotic, companion animals, benchmark

Background: In the veterinary sector, numerous tools have been implemented to support reducing antibiotic use (ABU), among which benchmarking (BM) has proven particularly effective. In Switzerland, the Information System for Veterinary Antibiotic Use (IS ABV) collects AB use data from all veterinary practices across all animal species. A BM tool based on a count-based indicator using days of active substance activity as its numerator -- the pATI -- was introduced for small animal practices in 2024. This study compares the pATI with four alternative indicators of ABU to assess its suitability and the influence of each indicator in identifying high-volume users.

Methods: Analyses are based on 2024 data for antibiotic use for cats and dogs in Switzerland among all veterinary practices with more than 100 consultations per year. We compared the pATI against three other consultation-normalized indicators --- number of antibiotic treatments (pPAT), number of treatment days (pTDAI), and Defined Daily Dose (pDDD) --- and one weight-normalized indicator based on the amount of active ingredient (pTAB). Descriptive analyses assessed differences in the classification of very high users across indicators, and Spearman's rank correlations compared practice rankings by species and practice type.

Results: In 2024, 12.9% (89/689) of cat practices and 16.9% (116/686) of dog practices were classified as very high users (above the 95th percentile) by at least one indicator. Spearman's analyses revealed significant positive correlations across all indicator pairs and species ($p < 0.05$; min $p = 0.40$), confirming broadly comparable rankings. However, pTAB showed weaker correlations with all other indicators ($p = 0.40$ -- 0.70). Practices identified as very high users by at least four indicators had significantly fewer consultations, but a higher number of animals treated ($p < 0.05$).

Conclusion: Count-based and dose-based indicators performed similarly in identifying very high users, which means that regardless of the indicator chosen, largely the same group of practices would be identified. This gives decision-makers confidence that indicator selection can be guided by practical or contextual considerations rather than concerns about outcome differences. The weight-based indicator (pTAB), however, showed notably weaker alignment with the others and is harder to interpret in terms of actual ABU patterns.

Poster

POSTER PRESENTATION · ABSTRACT NO 17

Quantitative evaluation of bovine tuberculosis surveillance in Belgian slaughterhouses

Poster Session · Thursday, 3 September 2026

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Key words: bovine tuberculosis; slaughterhouse surveillance; meat inspection

Social media message: Quantitative evaluation of bovine tuberculosis surveillance in Belgian slaughterhouses revealed marked heterogeneity in suspicion reporting and detection performance, highlighting potential surveillance gaps, particularly in high-throughput facilities.

Background: Bovine tuberculosis (bTB) remains an important zoonotic disease despite the official bTB-free status achieved by several European countries, including Belgium. In such low-prevalence settings, early detection of disease re-emergence is essential to maintain disease-free status and protect both animal and public health. Slaughterhouse surveillance constitutes a key component of the Belgian bTB monitoring system, as all slaughtered cattle undergo routine post-mortem inspection. However, the effectiveness of this surveillance component remains poorly documented. The objective of this study was to quantitatively evaluate the performance of slaughterhouse-based bTB surveillance in Belgium by assessing reporting practices, predictive value of reported suspicions, and detection performance across slaughterhouses.

Methods: Data from routine post-mortem inspections and laboratory confirmation tests were collected from January 2019 to June 2025. Slaughterhouse data were extracted from the Belgian national traceability database, while laboratory results were obtained from the Belgian National Reference Laboratory for bTB. Three complementary indicators were calculated at slaughterhouse level. First, reporting ratios were estimated by comparing the observed number of bTB suspicions with the number expected under different epidemiological assumptions. Second, positive predictive values (PPV) were calculated as the proportion of reported suspicions subsequently confirmed as bTB. Third, observed-to-expected true positive (O/E TP) ratios were used as a proxy for detection performance by comparing the number of confirmed cases with the number expected under model assumptions. Two modelling scenarios were explored, including a constant detection sensitivity and an age-dependent sensitivity.

Results: A total of 41 slaughterhouses were included in the analysis. During the study period, 506 bTB suspicions were reported, of which only eight were laboratory-confirmed. Reporting practices were highly heterogeneous between slaughterhouses. Nineteen slaughterhouses reported no suspicions throughout the study period, including the two largest facilities, which processed more than 1.3 million and 500,000 cattle respectively. Under both modelling scenarios, all slaughterhouses experienced at least one year with reporting ratios below expected levels, while eight slaughterhouses consistently remained below expectations throughout the study period. Positive predictive values were generally low, reflecting the rarity of confirmed infections in an officially bTB-free context. Only four slaughterhouses detected confirmed bTB cases. Similarly, O/E TP ratios indicated limited detection performance, with most slaughterhouses failing to detect the number of true positive cases expected under model assumptions.

Conclusion: This study highlights substantial heterogeneity in slaughterhouse-based bTB surveillance in Belgium, together with evidence of under-reporting and limited detection performance. The absence of suspicions in several high-throughput slaughterhouses is particularly concerning, as it may reduce the effectiveness of early detection. These findings suggest that targeted monitoring and performance evaluation of slaughterhouses should be strengthened to improve surveillance sensitivity and support the maintenance of Belgium's official bTB-free status.

Poster

POSTER PRESENTATION · ABSTRACT NO 18

Genomic analysis of *Staphylococcus aureus* in the Zambian dairy value chain reveals widespread circulation of a pandemic clone with high virulence potential

Poster Session · Thursday, 3 September 2026

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Key words: *Staphylococcus aureus*, dairy, Africa, bioinformatics, one health

Social media message: Analysis of *S. aureus* isolates from the Zambia dairy sector reveals circulation of a multidrug-resistant strain with high virulence potential. Targeted control measures are needed to mitigate associated risks to human and animal health.

Background: Milk is an important nutritional resource in livestock-dependent communities of low- and middle-income countries. In these settings, raw milk consumption is a common pathway of exposure to zoonotic pathogens. *S. aureus* is among the most relevant, causing food intoxication and severe infections. Certain pandemic clones circulate globally across human and animal reservoirs, raising One Health concerns about cross-species transmission and food-chain spread. This study aimed to characterise the genomic diversity, antimicrobial susceptibility, and virulence potential of *S. aureus* from the dairy value chain in Zambia, and to assess the global phylogenetic context of local strains to infer potential transmission routes across hosts and supply chain levels.

Methods: This study used whole-genome sequencing (Illumina) and susceptibility testing (broth microdilution) data from 94 *S. aureus* isolates. These data were obtained from a previous project that collected almost 2,000 samples along the dairy value chain in Zambia (Lusaka, Southern, and Western Provinces), including farms, milk collection centres, processing plants, traders, and traditional markets.^{1,2} Sample types included milk, environmental (e.g. milk buckets), and human swabs (nasal and hand). A global dataset of bovine- and human-derived *S. aureus* assemblies was retrieved from GenBank. Analyses included multilocus sequence typing (MLST), core-genome MLST (cgMLST), antimicrobial resistance and virulence gene detection, and maximum-likelihood phylogenetic inference from core-genome alignments.

Results: Predominant local sequence types were ST97 (n=22; 23.4%), ST152 (n=15; 16.0%), and ST7344 (n=13; 13.8%). Among global assemblies (n = 7,054), the most common sequence types were ST1 (n=1,002; 14.2%), ST8 (n=754; 10.7%), and ST5 (n=662; 9.4%). Local ST152 assemblies were most closely related (29-46 allelic differences) to isolates from human blood cultures in Malawi. At least one antimicrobial resistance gene was detected in 65 (69.1%) local assemblies. The most prevalent resistance determinants among local assemblies were point mutations linked with fosfomycin resistance: *murA* E291D and T396N (n=59; 62.8%), and *glpT* A100V (n=61; 64.9%). No genes conferring methicillin resistance were detected among local assemblies. All local ST152 assemblies carried genes linked to resistance to ≥3 antimicrobial classes. The collagen adhesin precursor (*cna*) gene (n=17; 18.1%), exfoliative toxin E (*ete*) gene (n=50; 53.2%), and toxic shock syndrome toxin-1 (*tsst-1*) gene (n=17; 18.1%) were present at relatively high levels, compared to global assemblies. Genes encoding Panton-Valentine leukocidin (PVL) components were detected in all ST152 isolates. The *tsst-1* gene was present in all ST7344 isolates and in four ST152 isolates. Phylogenetic analyses revealed generally low local genetic diversity, with identical or closely related (cgMLST distance ≤ 8) isolates spanning farms, multiple supply chain levels, and provinces, indicating active transmission events.

Conclusion: The circulation of highly virulent *S. aureus* strains, including the pandemic clone ST152, in the Zambian dairy value chain is of One Health concern, and effective control measures are advised.

Poster

POSTER PRESENTATION · ABSTRACT NO 19

A glimpse on emerging hazards: the FoodSafer project

Poster Session · Thursday, 3 September 2026

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Key words: Risk preparedness, emerging disease, risk estimation, risk communication

Social media message: Europe faces challenges via emerging disease and contamination patterns. How we better prepare ourselves in a dramatically changing world can be learnt at www.foodsafer.com

Background: EFSA defines an emerging risk as "a risk resulting from a newly identified hazard to which a significant exposure may occur, or from an unexpected new or increased significant exposure and/or susceptibility to a known hazard." The latter increased exposure can be the result of the increased presence of the known hazard and/or the increased exposure to this hazard. Food safety "hazards" or "issues" are the (biological, physical or chemical) agents present in our food system (existing or emerging) which may cause a harmful impact on public health of our European citizens. The risk of a particular food safety hazard or issue will depend on the occurrence (prevalence, concentration) of the hazard in our food, the applied food preparation method by the consumers, the consumption of the food (dose), and its potential impact on human health (acute or chronic effect, short- or long-term effect). All this happens in a changing physical and political environment and the resilience of the European food system has been critically hallmarked.

Methods: The EU-funded project FoodSafer is testing future impacts on food safety and develops indicators for the trends that reach out into the future. Eleven main drivers have been found and more than 30 subdrivers have been found from literature and tested in stakeholder group consultations. The consortium has furthermore selected eight microbiological and chemical hazard scenarios that include food system structures, foodborne pathogens and chemicals. Microbiologically we looked into underresearched ways of food distribution, persistence of pathogens, emerging viruses and transmission of AMR in aquaculture. The persistence case will be demonstrated to the audience. A central activity is fully interoperable risk screening and communication tool that is now under operation and can be accessed via www.foodsafer.com.

Results: Conclusively, FoodSafer critically asks for improvements of the currently food safety management practices and how this may be achieved via modern communication tools.

Poster

POSTER PRESENTATION · ABSTRACT NO 21

Farmers and veterinarians' perceptions and adaptive management of tick-borne disease risk on endemic dairy farms

Poster Session · Thursday, 3 September 2026

Sarah Shanks, Jennifer Duncan, Caroline Millins, Nicholas Johnson, Bethan V. Purse, Tamzin Furtado
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Key words: Tick-borne disease, livestock, qualitative

Background: Tick-borne diseases are an increasing challenge for UK livestock farming, yet decision-making processes and risk perceptions remain poorly understood. This qualitative study explores how dairy farmers and veterinarians perceive and manage tick-borne disease risk, and how these interpretations shape farm-level actions.

Methods: Using a constructivist framework and reflexive thematic analysis, we analysed three focus group discussions with eight farmers and seven veterinarians from endemic areas of southwest England.

Results: Four themes were constructed: (1) perceived risk in relation to farm geography, ecology and land history; (2) knowledge gaps and diagnostic uncertainty; (3) disease management and decision-making; and (4) impacts on farm systems and farmer wellbeing. Risk was understood as embedded within the physical and ecological features of farms, with management guided largely by experiential knowledge rather than formal evidence. Participants described balancing deliberate exposure to ticks to maintain immunity with the risk of clinical disease, amid substantial uncertainty around pathogen distribution and the durability of protection. Emotional strain, economic loss and herd disruption represented a significant, under-recognised consequence of outbreaks. Concerns were also raised that Environmental Land Management Schemes may inadvertently expand tick habitat and introduce disease risk into previously unaffected areas.

Conclusion: Overall, tick-borne diseases represent a complex, context-specific challenge for UK dairy systems operating within increasingly biodiverse and environmentally regulated landscapes. In the absence of formal surveillance and standardised guidance, farmers rely on pragmatic, adaptive strategies developed through trial and error, highlighting critical gaps in advisory support, research and policy integration.

Poster

POSTER PRESENTATION · ABSTRACT NO 22

Environmental drivers of tick Density in UK dairy farms: Implications for livestock health and agri-environment policy

Poster Session · Thursday, 3 September 2026

Sarah Shanks, Jennifer Duncan, Nicholas Johnson, Jake Goswell, Catherine Hartley, Richard Hassall, Bethan V. Purse, Caroline Millins

University of Liverpool

Key words: Tick-borne disease, cattle, dairy systems

Background: Ticks are important vectors of livestock and human pathogens in Europe. Environmental policies promoting woodland creation and habitat restoration are increasing habitat suitability for *Ixodes ricinus* but impacts on livestock tick-borne disease risk remain unclear. This study examined how landscape features influence tick distribution on UK dairy farms with a recent history of tick-borne disease.

Methods: Questing ticks were sampled on 72 pastures in 12 dairy farms in southwest England (2,376 transects), stratified by distance from pasture boundaries and adjacency to woodland or non-woodland habitats. Environmental variables were measured at transect, boundary, and pasture scales. Generalized linear mixed models identified predictors of tick presence in pastures, and nymph density at pasture boundaries. Farm-level associations between tick abundance, woodland cover, and cattle pathogen prevalence were assessed descriptively.

Results: A total of 1,701 ticks were collected (91.3% nymphs). Ticks were detected on 20% of transects and in 89% of pastures, with densities strongly aggregated at pasture boundaries. The proportion of woodland cover within 50 m buffers was the dominant environmental driver at both boundary and pasture scales, with greater cover associated with higher nymph densities and increased probability of tick presence. Boundaries adjacent to water also supported significantly higher nymph densities.

Conclusion: Local landscape features, particularly woodland cover and small water bodies at boundaries, strongly influence tick distribution in UK dairy pastures. Woodland expansion through environmental schemes may therefore be associated with increased tick distribution and densities in farmed landscapes, with implications for livestock exposure and public health.

Poster

POSTER PRESENTATION · ABSTRACT NO 23

Beyond KAP in AMR: Integrating psychometrics and choice tasks in a mixed-methods study with Nepalese poultry farmers

Poster Session · Thursday, 3 September 2026

Jorge Pinto Ferreira¹, Diletta Topazio¹, Anica Buckel¹, Jeffrey LeJeune¹, Sakar Shivakoti¹, Megha Raj Banjara²

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Key words: AMR; KAP; AMU

Social media message: AMR: knowledge is not enough -- we must ACT!

Background: Inappropriate antimicrobial use (AMU) in food-producing animals like poultry is a major driver of antimicrobial resistance (AMR), threatening global health. While Knowledge, Attitudes, and Practices (KAP) surveys are a common tool in AMU research, they often miss psychological and contextual drivers of behaviour. This study goes beyond KAP by integrating psychometric measures and behaviour change models to explore AMU among Nepalese poultry farmers.

Methods: We adopted a two-phase mixed-methods approach. Phase 1 involved a KAP survey and psychometric assessments with 107 smallholder poultry farmers in Chitwan. Phase 2 used qualitative interviews based on Phase 1 results, analysed thematically through the COM-B model.

Results: Despite moderate knowledge and positive attitudes, these did not predict antimicrobial misuse. Misuse correlated significantly with psychological factors: higher risk aversion and temporal discounting increased misuse, while higher financial scarcity correlated with lower misuse. Common practices included using Colistin (48%), antibiotics without prescriptions (42%), and self-prescribing (31%). Growth promotion use was rare (2%). Qualitative findings highlighted how economic pressure, entrenched habits, limited service access, and informal markets shaped AMU. Financial anxiety drove early selling and disregard for withdrawal periods. Habitual prophylactic use and challenges accessing trustworthy veterinary services led to unregulated AMU. Availability of banned drugs and market uncertainty further influenced behaviour.

Conclusion: AMU practices are shaped by complex psychological and contextual factors, often overriding farmers' knowledge and attitudes.

Poster

POSTER PRESENTATION · ABSTRACT NO 24

Co-construction and governance of a nationwide HPAI vaccination strategy in ducks: Drivers, success factors, and future challenges in France

Poster Session · Thursday, 3 September 2026

Marie Pelgrin, Sophie Le Bouquin, Morgane Salines

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Key words: HPAI vaccination; public policy; co-construction

Social media message: France's HPAI duck vaccination campaign reduced outbreaks dramatically. This study shows how co-construction between public authorities, scientists, and industry enabled an effective and widely accepted animal health policy.

Background: Since October 2023, France has implemented a nationwide vaccination campaign against highly pathogenic avian influenza (HPAI) in ducks. This policy contributed to a sharp decline in outbreaks, from 2,266 cases between 2020 and 2023 to only 150 between 2023 and May 2026. This unprecedented success reflects a shift from the traditional European paradigm, where vaccination was historically excluded from HPAI control strategies. This study examines how the French HPAI vaccination strategy emerged as a co-constructed public policy, mobilising diverse actors, knowledge systems, and interests, and how this process shaped both its effectiveness and social acceptability.

Methods: A multi-level qualitative approach was used. First, a bibliographic and institutional review explored frameworks of co-construction and shared governance in animal health policies. Second, a field-based qualitative study was conducted using semi-structured interviews with key stakeholders, including public authorities, scientists, veterinarians, poultry industry representatives, and pharmaceutical actors. Third, the interviews were used within a prospective approach to explore future evolutions and anticipate upcoming challenges. Data were analysed using thematic content analysis to identify decision-making processes, actor roles, governance mechanisms, and drivers of policy adoption.

Results: Around twenty semi-structured interviews were conducted via videoconference in spring 2026 with key stakeholders. The results highlight that the vaccination policy emerged from the convergence of several factors, including repeated epidemic crises, mounting economic losses, and growing scientific evidence supporting vaccine efficacy. The policy was co-constructed through iterative discussions and negotiations between public and private actors, leading to a shared governance model and a hybrid funding mechanism. Scientific expertise played a central role in legitimising decisions amid uncertainty. Strong stakeholder engagement and adaptive implementation strategies were key to achieving high levels of adherence. The campaign significantly reduced viral circulation, reinforcing its legitimisation. However, challenges remain regarding long-term sustainability, surveillance adaptation, and international trade implications.

Conclusion: The French HPAI vaccination strategy illustrates how a co-constructed, multi-actor governance framework can enable the successful implementation of an innovative animal health policy. The resulting socio-technical compromise balanced sanitary effectiveness with economic and social acceptability. This model provides valuable insights for future vaccination strategies, including extension to other species or diseases, and highlights the importance of integrating scientific, political, and sectoral dynamics in veterinary public health decision-making.

Poster

POSTER PRESENTATION · ABSTRACT NO 25

A novel agent-based model framework for simulating multidrug-resistant organism transmission dynamics in a veterinary teaching hospital environment

Poster Session · Thursday, 3 September 2026

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Key words: Antimicrobial resistance, Veterinary Teaching Hospital, Agent Based Modeling

Social media message: We developed a stochastic agent-based model in R to simulate MDRO transmission within a Veterinary Teaching Hospital. The model explores how students, staff, and contaminated environments may contribute to pathogen spread, supporting future infection prevention and AMR control strategies

Background: Hospital-acquired infections (HAIs) caused by multidrug-resistant organisms (MDROs) are an increasing concern in both human and veterinary healthcare settings. While several stochastic mathematical models have been developed for human healthcare settings, veterinary medicine has seen only one stochastic model specifically designed for a veterinary hospital environment, focusing on the impact of canine patient movements on the transmission dynamics of antibiotic-susceptible and antibiotic-resistant pathogens.

Methods: In our study developed a novel agent-based model (ABM) to simulate the transmission dynamics of MDROs within a VTH environment. The framework, developed in R language, simulated the daily activities of 45 human agents including students and VTH personnel, moving dynamically across different hospital locations. For each human agent, mean visitation times were defined to emulate the distinct daily routines of student and hospital personnel. Human agents could transition through different epidemiological states, including exposure, infection, symptom development, and recovery during the simulation. Environmental contamination was also incorporated, allowing rooms to act as potential sources of pathogen transmission. Different transmission probabilities were assigned to human agents and rooms according to hypothetical minimum exposure durations required for pathogen transmission and converted into hourly transmission probabilities. Pathogen introduction into the hospital environment could occur either through a simulated human agent or an external visitor in a room.

Results: In the human-introduction scenario, one randomly selected individual was initially infected and able to transmit the pathogen and contaminate the environment. In the room-introduction scenario, one randomly selected room was initially contaminated and capable of transmitting the pathogen to human agents. The model simulated hospital activity over a 365-day period with a fixed time spent in the VTH based on human agent characteristics. Individual daily movement trajectories were randomly generated as sequences of visited rooms, and the time spent in each room was sampled from room- and agent-specific distributions. For each agent, visited locations and corresponding exposure times were stored to support the subsequent transmission module.

Conclusion: The model suggests that the risk of exposure to the pathogen was closely linked to agent characteristics and activities. The model also identified specific categories of agents that could act as potential superspreaders within a VTH environment, highlighting their key role in pathogen dissemination dynamics. To our knowledge, this is the first ABM developed to investigate the role of veterinary students in an MDRO outbreak within a VTH setting. Our findings highlighted spatial heterogeneity in environmental exposure risk across the VTH and suggested that veterinary students may play an important role in MDRO transmission dynamics. These preliminary findings support the applicability of ABM frameworks for identifying high-risk individuals and locations involved in pathogen dissemination and provide a useful basis for future infection prevention and control strategies in VTH.

Poster

POSTER PRESENTATION · ABSTRACT NO 26

Epidemiology of pain in the brain: A review and conceptual framework for operationalizing pain in veterinary neurology as a quantifiable cognitive state in dogs

Poster Session · Thursday, 3 September 2026

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Key words: pain epidemiology, quantifiable cognitive states, canines

Social media message: How can we build epidemiology around something we do not yet define consistently? Recognizing pain in the brain as a quantifiable cognitive state could fundamentally change veterinary public health, transforming how we assess disease burden, design prevention strategies, and interpret pain as a self-standing cognitive state in dogs. Initial results of a review capture current approaches and assess whether existing methods are sufficient for epidemiological purposes.

Background: Epidemiology studies the distribution and determinants of health-related states and diseases in populations, including methods for their measurement, diagnosis, and surveillance. Beyond descriptive analysis, it also addresses prevention, disease control, and translational applications within a One-Health framework. Within this framework, pain represents a particular methodological challenge. It may function as a clinical sign of acute disease, a long-term consequence of pathological processes, or a self-standing disorder. Especially in veterinary medicine, pain is inconsistently conceptualized and reported across studies and clinical settings as the clinical expression may be subtle or masked. This raises a fundamental question: how can epidemiological investigations be conducted on a phenomenon that lacks consistent definition and operational criteria? The aim of this study was to address this gap by focusing on "pain in the brain", defined as the central neurocognitive processing of pain independent of temporal classification or peripheral origin. Following analogous approaches in human pain epidemiology, a review was conducted to evaluate the utility and limitations of existing measurement approaches, particularly outlined by Ahmad & Barkana regarding brain-based pain biomarkers recently. In addition, relevant canine population-level parameters were explored as a first step toward defining pain as an epidemiologically measurable entity.

Methods: A systematic review was conducted including publications from 2020 onwards addressing dogs with neurological disorders in which pain was explicitly assessed, discussed, or inferred. Data extraction focused on explicit pain definitions, methodological approaches to pain assessment, and the use of validated pain scales or biomarkers. The methodological framework was informed by translational neurobiological approaches to pain assessment. Findings were synthesized to identify methodological gaps and opportunities for epidemiological operationalization.

Results: The review identified only a limited number of studies explicitly addressing "pain in the brain" as a primary outcome in canine neurological disease. No standardized framework was identified that allows consistent classification of pain as an independent epidemiological outcome in veterinary neurology yet. Pain was commonly inferred from inflammatory or degenerative processes rather than directly measured. Existing approaches relied predominantly on generalized clinical pain scales, while neurobiological markers remained largely unexplored. The findings highlight a lack of cohort-based descriptions and emphasize the need for validated, condition-specific pain metrics tailored to canine neurological populations.

Conclusion: The epidemiological study of pain in veterinary medicine remains underdeveloped. Pain (in the brain) is frequently present but inconsistently defined, measured, and reported as an independent health state, limiting its integration into population-level analyses and preventive veterinary medicine. Standardized operational definitions, improved pain-specific biomarkers, and cohort-based epidemiological studies are needed to enable robust quantification of pain as a cognitive state in canines. Establishing pain as a measurable epidemiological entity may improve prevention strategies, clinical decision-making, and the conceptual framework of veterinary public health.

Poster

POSTER PRESENTATION · ABSTRACT NO 27

From awareness to preparedness: a gap in veterinary students' training on public health knowledge related to game meat?

Poster Session · Thursday, 3 September 2026

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Key words: Game meat; One health; Veterinary education

Social media message: Public health awareness related to game meat among EU veterinary students is limited, and training remains insufficient. Bridging this gap is essential to further support veterinary roles in One Health and food safety.

#OneHealth #ECVPH2026

Background: Hunting and game meat consumption are associated with public health risks, including zoonotic infections, contamination by environmental hazards, and inadequate or absent veterinary inspection. Within a One Health framework, veterinarians play a key role in mitigating these risks. However, veterinary students' awareness of these issues and training adequacy remains unclear. These aspects are currently being investigated within the COST-Action SafeGameMeat CA22166 through a large European survey. Herein, the preliminary results focussing on public health awareness of students are presented.

Methods: A cross-sectional survey between November 2025 and March 2026 was conducted among veterinary students from European countries. Data were collected on sociodemographic characteristics, perceptions of public health risks, and perception of adequacy of curriculum coverage on topics related with hunting and game meat. The selection of the response options No official veterinary inspection and/or Environmental contaminants, of the question "What do you associate with the consumption of game meat?" was used to indicate that students had Public health awareness. These response rates were compared between respondents who perceived the adequacy of the veterinary curriculum to be either adequate or inadequate, and between those enrolled in different years. Descriptive statistics were used to summarise the data, and the associations were assessed using the chi-square test.

Results: A total of 1,545 veterinary students participated from 48 universities in 29 European countries. Among respondents, 29.7% identified lack of official veterinary inspection and 16.8% identified environmental contamination as associated with game meat consumption, resulting in an overall public health awareness of 36.6%. Twenty-five percent of respondents considered adequate curriculum coverage on topics related to hunting and game meat. No significant association was found between public health awareness and perceived curriculum adequacy ($\chi^2 = 1.94$, $df = 1$, $p = 0.164$) or year of enrolment ($\chi^2 = 3.5$, $df = 5$, $p = 0.619$), with response rates on public health awareness between years of enrolment ranging between 34 to 40%.

Conclusion: Public health awareness related to game meat among veterinary students across Europe appears to be limited. Despite a quarter of the respondents considering the curriculum adequate, the veterinary training appears to result in restricted knowledge acquisition. The proportion of students with public health awareness does not change significantly as they progress through their years of study. Main limitations of this study include the use of a survey to assess perceptions and knowledge, and the voluntary participation. Future analysis will consider the socio-cultural and geographical specificities. These results suggest that teaching future veterinarians more about wildlife, hunting and meat safety could ensure safer food and healthier ecosystems following a One Health framework.

Poster

POSTER PRESENTATION · ABSTRACT NO 28

Hepatitis E virus detection in effluent samples collected from a swine slaughterhouse: A one-year molecular surveillance

Poster Session · Thursday, 3 September 2026

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Key words: Hepatitis E virus; Effluent samples; Slaughterhouse; Public health

Social media message: Hepatitis E virus (HEV) is a sanitary and environmental concern. We analyzed 72 effluent samples collected over one year from a swine slaughterhouse in Central Italy, revealing a prevalence of 26.39%. This is the first Italian report of HEV RNA in effluents, highlighting the environmental risk.

Background: Among zoonotic foodborne pathogens, Hepatitis E virus (HEV) is recognized for its environmental persistence. The Suidae family are the primary target hosts for HEV genotype 3. Based on these considerations, this study aimed to molecularly screen effluent samples collected from a swine slaughterhouse in Central Italy.

Methods: Between January and December 2025, a total of 72 effluent samples (1.0 liter each) were collected every 10 days over one year. More in detail, 36 samples were collected from the collection tank at the stocking yard point (V~1~), and the remaining 36 at the wastewater treatment plant (WWTP) level (V~2~) after the depuration processes. The number of slaughtered pigs per each sampling day was also registered. All samples were centrifugated at 180,000 x g for 2 hours and the obtained pellets were resuspended in 500 µL of RNase-free water and stored at -80 °C. RNA was extracted from all samples and molecularly screened using real time RT-qPCR and nested RT-PCR assays. The obtained amplicons were sequenced and successively published on the GenBank platform. Finally, a phylogenetic tree was constructed based on the Neighbor Joining method and realized using the iTOL Software.

Results: From a general perspective, HEV RNA was detected in 26.39% of the total samples. More in detail, it was found in 27.78% of V~1~ and 25.00% of V~2~ ones. The highest viral load, 10⁵ GE/mL, was observed in two V~1~ samples collected in December and January months, corresponding to the periods with the highest slaughtering volumes. Statistically significant differences of HEV RNA loads were observed between V~1~-V~2~ (p<0.001) and cold-warm seasons (p=0.02). Finally, the obtained sequences were deposited and published on the GenBank platform with the following accession numbers: PX925942, PX925944, PX925945, PX925946, and PX925948.

Conclusion: The detection of HEV RNA in effluent samples collected at the swine slaughterhouse represents the first report of this finding in Italy. Similar approaches have been applied in Brazil and Spain, with reported prevalences of 50.0% and 0.4%, respectively. The demonstrated ability of HEV to overcome the WWTP highlights the need for further investigation and the development to find new solutions to this environmental issue

Poster

POSTER PRESENTATION · ABSTRACT NO 29

Stability of therapeutic bacteriophages against intestinal infections in formulations for oral application in veterinary medicine

Poster Session · Thursday, 3 September 2026

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Key words: Bacteriophage therapy, one health, novel antimicrobials

Social media message: Bacteriophages (phages) hold significant potential to reduce antibiotic use in veterinary medicine and improving food safety. They can serve as alternatives or complementary agents in the management of bacterial infections, mitigating the occurrence and spread of antimicrobial resistance in a One Health approach. By specifically infecting target bacteria and preserving beneficial microbiota, they offer a highly selective approach to manage infectious diseases. Unlike traditional antibiotics, phages can replicate and evolve alongside bacterial pathogens, making them a promising tool against the growing challenge of antimicrobial resistance. Suitable formulation technologies can foster the development of stable and effective oral phage therapies for livestock. Our findings can help to develop effective and environmentally friendly novel antimicrobial treatments for poultry, swine, and other livestock species, promoting animal health, enhancing food safety, and supporting global One Health objectives while reducing dependence on traditional small molecule antibiotics.

Background: The growing threat of antimicrobial resistance has increased interest in approaches that can reduce antibiotic use in veterinary medicine while maintaining animal health and welfare. Phages are viruses that specifically infect bacterial cells and can be used to treat or prevent bacterial infectious disease in humans and animals. However, effective therapeutic or preventive phage application in livestock animals requires stable and effective formulations that meet operational demands of livestock farming. This study addresses a critical gap in phage delivery by systematically evaluating the performance of phage formulation blends in enhancing the stability of orally administered lytic bacteriophages targeting zoonotic *Enterococcus* species.

Methods: We evaluated the stability of three newly isolated Caudoviricetes phages, representing three distinct morphologies (siphovirus, myovirus, and podovirus). The impact of various environmental stresses on phages in the absence of protective formulations was evaluated (i. shear forces, ii. elevated temperature, iii. low pH, and iv. enzymatic digestion). Subsequently, we screened nine candidate delivery systems, microbial polysaccharides, cellulose ether, natural hydrocolloids, and starches A and B, for their ability to protect phages during environmental stresses by evaluating phage concentrations after exposure.

Results: Our results demonstrate that phages incorporated into cellulose ether exhibited superior stability across all tested conditions, maintaining high infectivity even after exposure to low pH and digestive enzymes. In contrast, natural hydrocolloids caused a complete loss of phage viability, indicating a destabilizing interaction. Furthermore, formulations based on flours A and B provided moderate protection, preserving phage function during processing and release into the surrounding environment.

Conclusion: These findings highlight cellulose ether as the most effective and robust formulation for oral phage delivery, offering strong protection while remaining simple to produce and suitable for large-scale application. This work provides a foundation for the development of cost-effective, stable, and practical phage-based novel antimicrobial therapeutics for poultry and other livestock.

Poster

POSTER PRESENTATION · ABSTRACT NO 31

Construction of an integrated data collection network in the context of multi-hosts zoonoses persistence communities

Poster Session · Thursday, 3 September 2026

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Key words: Multi-host pathogens, multisectoral network, collaborative approach

Social media message: In the understanding of multi-hosts disease emergence, collaboration is a much-needed process. Our approach tends to facilitate the implementation and evaluation of local networks specialized in gathering comprehensive ecosystemic and socio-economic data.

Background: The rapid expansion of human-animal interfaces has increased the risk of zoonotic outbreaks worldwide. Most zoonotic agents are multi-host pathogens whose persistence depends on the host-environment assemblage within an ecosystem, referred to as the pathogen maintenance community. However, the absence of structured surveillance for many emerging multi-host diseases, combined with socio-ecosystem diversity, limited access to key host species, logistical constraints, and restricted environmental monitoring, limits comprehensive field investigations. Addressing these challenges requires integrated ecosystem approaches and participatory surveillance. Stakeholders not traditionally engaged in health surveillance, particularly within the environmental sector, may provide critical insights on specific nodes of the maintenance community. This study develops a visual and analytical tool to map and analyze ecosystem-related information shared among stakeholders to better characterize maintenance communities and support investigations of multi-host pathogen outbreaks.

Methods: We developed an approach built on available eco-epidemiological knowledge, structured around the source-pathway-target framework, combined with interactions driven by socio-economic activities, political context and legal framework. From that detailed picture of pathogen cycle and drivers, relevant local stakeholders can be identified and engaged through semi-structured interviews. These interviews allow to collect information on the nature, strength, and frequency of links between stakeholders. Those links are then modelled as an information flow (cases notification, data ...) network, enabling detailed analysis of communication patterns and coordination related to multi-host disease risk. This network modelling was also used to investigate many scenarios of information transmission.

Results: This method was applied to the context of leptospirosis risk in a mountainous ecosystem and 45 stakeholders were identified of which 26 were interviewed. From stakeholders involved in animal management, water use and management, land practices, economic activities and public health, network analysis identified connected or isolated ones. It revealed strengths and weaknesses in inter-sectoral linkages, thereby highlighting potential gaps in surveillance, prevention, or control systems. In addition, it showed uncovered discrepancies between risk exposure and information flow that will require special attention or information hub that concentrates data. It also reveals sectorial compartmentalisation that needs to be addressed.

Conclusion: Eventually, this framework will provide comprehensive data on the ecosystem which could lead to a higher level of knowledge on the studied multi-host pathogen. These standardized, reproducible approach and method can be applied to any multi-host disease and represents a foundational step toward operationalizing a multisectoral One Health approach. By strengthening cross-sectoral understanding and collaboration, it contributes to co-benefits across human, animal, and environmental health sectors, supporting more resilient and context-adapted One Health systems and responses.

Poster

POSTER PRESENTATION · ABSTRACT NO 32

Rapid detection and mitigation of a filarioid nematode outbreak in the Canadian Arctic

Poster Session · Thursday, 3 September 2026

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Key words: Emerging vector disease - Disease surveillance - Filarioid nematodes

Social media message: In the Canadian Arctic, collaboration among Indigenous communities, government and researchers promptly detected a outbreak of disease syndrome associated with filarioid nematodes and mitigated its impacts on food security and caribou conservation.

Background: Climate change is reshaping the epidemiology of vector-borne diseases in the Arctic, with important implications for wildlife conservation, food security, and Indigenous well-being. Species like the barren-ground caribou (*Rangifer tarandus groenlandicus*) are a keystone element of the Arctic ecosystem and are also a fundamental part of Indigenous food security and culture. Since before 2015, filarioid nematodes, namely *Setaria yehi* and *Onchocerca* sp. lineage 2, have been circulating in caribou from the Arctic, but not disease syndrome had yet been associated to them in this species.

Methods: In 2023, harvesters near Kugluktuk, Nunavut, Canada, reported a novel disease syndrome in 11 barren-ground caribou, detected as yellow exudate in the abdominal cavity and fibrin attachments on the organs. In one case, the thoracic cavity was involved as well. This raised immediate concerns among harvesters regarding meat safety, resulting in carcasses being discarded, with impact on Indigenous food security and mental health and caribou conservation, as replacing tags increased the hunting pressure. Samples were sent to the University of Calgary for a pathological assessment of the causes of these alterations, which included macroscopic examination, histological exam and DNA detection of the suspected agent through a droplet digital PCR (ddPCR) assay.

Results: In September 2023, 26.3% of the caribou tags presented abnormalities compatible with filarioid infestation (peritonitis and myositis). DNA of *S. yehi* and *Onchocerca* sp. lineage 2 was detected through ddPCR. More species, including *Rumenfilaria andersoni*, may be circulating. The strong collaboration among community members, conservation officers, biologists, and researchers enabled a proactive intervention to identify the cause of the observed abnormalities, and the rapid development of culturally appropriate risk communication and outreach. Within one year, the solid collaboration and communication network, as well as the underlying trust among its members, and the availability of diagnostic tools helped restore confidence in country food safety, reduce meat wastage, and support community resilience. Subsequent reports from the Kitikmeot and Kivalliq regions of Nunavut and Northwest Territories suggested a broader geographic distribution and increasing health impacts in caribou populations. While the investigation on the drivers of the emergence of this disease syndrome is still ongoing, literature data suggest that being vector-borne parasites, the increase in temperature and the expansion of the summer season may be the underlying factor boosting these outbreaks; community observations support this theory, reporting an increasing number of insects.

Conclusion: This work forms part of a broader community-partnered caribou health surveillance initiative aimed at developing sensitive diagnostic tools, and understanding the environmental drivers and health impacts of parasite emergence in Arctic ecosystems. The project illustrates the importance of integrating wildlife health surveillance, Indigenous knowledge, and risk communication within a One Health and veterinary public health framework in the context of climate change.

Poster

POSTER PRESENTATION · ABSTRACT NO 33

What matters most in avian influenza surveillance? Veterinarians' perspectives from Italy

Poster Session · Thursday, 3 September 2026

Liliana Martella¹, Marco Zago², Stefania Crovato², Elena Catelli¹, Caterina Lupini¹, Katia Capello², Giovanni Cattoli², Francesca Scolamacchia², Paolo Mulatti², Marco De Nardi¹

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Key words: surveillance, surveillance evaluation, avian influenza, expert elicitation

Social media message: Regular evaluation of infectious diseases surveillance systems is essential to ensure they remain effective, efficient and fit for purpose. Surveillance performance can be assessed through a range of attributes reflecting different operational and epidemiological dimensions of the system. In this study, we explored veterinarians' perspectives on the Italian avian influenza surveillance programme. Using a structured questionnaire, veterinarians working in the public sector and poultry production chains were asked to prioritize ten surveillance evaluation attributes according to their perceived importance, and to provide their views on the system's effectiveness, strengths and weaknesses. Incorporating stakeholder perspectives into surveillance assessment may strengthen the evaluation process by providing operationally relevant and diverse insights.

Background: Disease surveillance programmes must be regularly evaluated to ensure they provide valuable information in an efficient and effective manner. This study aimed to investigate veterinarians' perspectives on the evaluation of the Italian avian influenza surveillance system, including the perceived importance of key evaluation attributes, overall system effectiveness, and major strengths and weaknesses.

Methods: Ten surveillance evaluation attributes (acceptability, benefit, cost, representativeness, data quality, communication and dissemination, simplicity and stability, risk-based criteria definition, sensitivity and timeliness) were selected based on literature review and programme relevance. A structured questionnaire, developed in LimeSurvey, was administered to 104 veterinarians, working in public sectors or poultry production chains, together with supporting information and instructions. Participants distributed 100 points among attributes according to their perceived importance for surveillance evaluation. Additional information was collected on professional roles, years of experience, working area, and perceived effectiveness of the programme. Open-ended questions captured perceived strengths and weaknesses of the system.

Results: Eighty-one veterinarians completed the survey (77.9% response rate). The majority of respondents worked in the public sector (81%) and had six or more years of professional experience (74%). Participants were distributed across provinces classified as low (16%), medium (5%) and high (51%) risk for avian influenza introduction and spread, while the remaining respondents worked across mixed-risk areas. Respondents showed a balanced prioritization across evaluation attributes, suggesting recognition of the multidimensional nature of surveillance performance. Timeliness and sensitivity received slightly higher importance scores, while communication, simplicity and cost were rated marginally lower. Differences across risk groups were assessed using non-parametric tests. Only acceptability differed significantly, with higher scores among respondents from medium-risk than high-risk regions. Respondents' explanations of the point allocation exercise indicated heterogeneous rationales for prioritizing attributes. The perceived effectiveness of the surveillance programme was rated using a 1-7 Likert scale, with a median score of 5 (IQR 5-6). Reported strengths of the surveillance system included its early detection capacity and the implementation of a risk-based approach. Weaknesses were mainly related to planning and funding constraints in wild bird surveillance and insufficient attention to medium/low risk regions and small-scale or rural farms.

Conclusion: Veterinarians' perceptions showed a generally balanced prioritization of evaluation attributes for the avian influenza programme. The slightly greater emphasis placed on timeliness and sensitivity suggests that particular value is attributed to the system's early detection capacity. Integrating stakeholder perspectives into surveillance evaluation may support more context-adapted and operationally relevant improvements of avian influenza surveillance systems.

Poster

POSTER PRESENTATION • ABSTRACT NO 34

Pathogen transmission by flies and beetles in poultry houses

Poster Session • Thursday, 3 September 2026

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Key words: *Campylobacter*, house flies, *Salmonella*

Social media message: Systematic review (2007--2025; 42 studies) shows flies and beetles in poultry houses can carry key pathogens. While confirmed transmission is rare (9.5%), evidence links them to *Campylobacter* and *Salmonella* ---highlighting their role as overlooked disease vectors in poultry systems.

Background: Flies and beetles are ubiquitous in poultry production systems and move freely between birds and potentially contaminated substrates, creating opportunities for the spread of numerous pathogens, including zoonotic agents. The aim of this systematic review was to evaluate the evidence for the role of flies and beetles present in poultry house environments in transmitting pathogenic agents to poultry.

Methods: A systematic review was conducted according to PRISMA guidelines. Relevant publications published between 2007 and 2025 were identified through searches of PubMed®, Scopus, and Web of Science. Eligible studies were English-language, peer-reviewed publications that examined potential interactions between target insect species and poultry farms in Europe and North America.

Results: A total of 2,319 publications were identified through the literature search. Following screening and eligibility assessment, 42 studies fulfilled the predefined inclusion criteria. Most studies were conducted in the USA (n = 17), followed by Denmark (n = 6) and the Netherlands (n = 5). Flies were the primary focus in 26 studies, beetles in 13 studies, and both insect groups were investigated together in 3 studies. Overall, the findings suggest that flies may contribute to the transmission of 12 different pathogens, while beetles may be involved in the spread of 8 pathogens. The pathogens most frequently investigated were *Campylobacter* (n = 17), *Salmonella* (n = 13), and *Escherichia coli* (n = 5). Evidence of confirmed transmission was reported in 9.5% of studies (n = 4). Transmission was considered likely in 38.1% (n = 16) and potentially possible in 47.6% (n = 20) of studies. Only 4.7% (n = 2) concluded that pathogen transmission via flies or beetles was unlikely.

Conclusion: Our findings emphasize the epidemiological importance of flies and beetles in poultry house environments. Although evidence for viral transmission appears limited, the ability of flies and beetles to carry zoonotic pathogens and antimicrobial-resistant bacteria highlights the need to shift from reactive pest control measures to proactive vector management within standardized biosecurity programs.

Poster

POSTER PRESENTATION · ABSTRACT NO 35

Educational needs and biosecurity competencies in veterinary medicine: a multinational survey

Poster Session · Thursday, 3 September 2026

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Key words: Animal; biosecurity; education

Social media message: Competency growth during the first decade of veterinary practice highlights the value of experiential learning and the need for structured support of early-career practitioners.

Background: Animal biosecurity has become increasingly important and is now embedded into veterinary medicine curricula, as well as in the European Animal Health Law.. Despite these developments, few studies have been conducted so far on the competencies acquired and the educational needs of veterinary students and practitioners in the field of applied animal biosecurity.

Methods: To address this gap, an online survey was conducted and involving 651 participants from 66 countries across 5 continents. It was subdivided into three parts (participant profiles, perceptions of their competencies, and additional training needs). The questionnaire survey was disseminated across different continents initially through the World Animal Biosecurity Association (WABA) and subsequently using a snowball sampling strategy. The perception of the agreement level regarding each biosecurity competency related to the animal species was assessed using a Likert scale with six modalities (disagree [D], partially disagree [PD], neutral [N], partially agree [PA], agree [A] and does not apply to my practice [NA]). The ratio $([D] + [PD]) / ([A] + [PA])$ allowed the identification of the competencies to improve in priority. A cluster analysis to group competency priorities was carried out using a regression tree analysis. Statistical difference between medians after grouping competencies in clusters was assessed using a non-parametric Kruskal-Wallis equality-of-populations rank test and an ordered regression analysis.

Results: The participants mainly work in veterinary clinics, ambulatory practices and academic environments. The main animal species managed included cattle, companion animals, small ruminants, equids, poultry and pigs. The level of agreement regarding the competencies acquired in relation to the managed species was consistent (8.9-16.7% for both disagree and partially disagree; 9-12.2% neutral, 71.1-81.2% for both partially agree and agree), except for the biosecurity audits (21.9%, 15.5% and 62.6%, respectively). Competencies related to biosecurity audit and animal isolation were identified as priority for improvement, particularly for traditional and non-traditional companion animals, horses, camelids, fish and bees. A significant increase in competencies was observed between the time of graduation and the tenth year of professional practice, followed by a more moderate increase thereafter. Overall, of 276 participants (45.4%) expressed a high need for training. This need was lower for cleaning and disinfection protocols. Comparing Africa, America and Europe, for which enough participants were available, no significant difference was observed between the three continents for the group of competencies in risk analysis and biosecurity audit. However, for all other competency groups (cleaning and disinfection procedures, animal isolation procedures, and information sourcing), the median priority score was significantly lower in Africa compared with America and Europe.

Conclusion: Identifying priority competencies and training gaps will enable better-targeted educational interventions, thereby contributing to sustainable development goal (SDG) 3 (Good Health and Well-Being) and SDG 10 (Reduced Inequalities) in animal biosecurity.

Poster

POSTER PRESENTATION · ABSTRACT NO 37

Microbiological safety of heat-treated plant-based meat alternatives during refrigerated storage

Poster Session · Thursday, 3 September 2026

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Background: Plant-based meat alternatives (PBMA) are becoming increasingly popular as substitutes for conventional meat products, but their microbiological safety during refrigerated storage is still not well documented, especially under industrial production conditions. This study aimed to evaluate the microbiological status of heat-treated PBMA during refrigerated storage and to provide practical information relevant to food safety and industrial monitoring.

Methods: A total of 100 PBMA formulations were produced under standardized industrial conditions, including salami-type and frankfurter-type products. All products were thermally processed until reaching a core temperature of ≥ 92 °C and then stored at 0-4 °C. Microbiological analyses were carried out at four storage intervals: day 0, day 15, day 35, and day 60. The analysis included selected foodborne pathogens and hygiene indicator microorganisms: *Salmonella* spp., *Listeria monocytogenes*, Enterobacteriaceae, *Escherichia coli*, coagulase-positive *Staphylococcus aureus*, and *Bacillus cereus*. In addition, pH, water activity, moisture content, and salt content were evaluated to better understand the internal product conditions during storage.

Results: *Salmonella* spp., *Listeria monocytogenes*, and Enterobacteriaceae were not detected in any sample throughout the storage period. During early refrigerated storage from day 0 to day 15, no hygiene indicator microorganisms were detected. However, at extended storage on day 60, limited microbial occurrence was observed, including *Escherichia coli* in 3% of samples, coagulase-positive *Staphylococcus aureus* in 20%, and *Bacillus cereus* in 15%. The detected levels of *Staphylococcus aureus* ranged from 10^3 to 10^5 CFU/g.

Conclusion: Taken together, the results indicate that heat-treated PBMA can maintain good microbiological stability during early storage when produced under controlled industrial conditions. However, the presence of selected microorganisms at day 60 shows that extended storage requires careful attention, particularly regarding post-processing hygiene, raw material quality, packaging integrity, and cold-chain control. These findings provide useful baseline for the safety evaluation of heat-treated PBMA and may support the development of product-specific storage limits and routine microbiological monitoring strategies.

Poster

POSTER PRESENTATION · ABSTRACT NO 38

Understanding how livestock impact refugee health and nutrition: A grounded-theory approach

Poster Session · Thursday, 3 September 2026

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Key words: Livestock ; Refugee ; Nutrition

Background: Livestock-keeping is for many refugee communities, the only available source of income after aid in Dadaab. Although evidence exists in pastoralist contexts, no empirical evidence to date has been found investigating the potential health/nutrition benefits or drawbacks of such in refugee camps. This is especially relevant as livestock-rearing in the camp context has a specific set of circumstances such as restricted movement, access to inputs, access to markets, and different housing/WASH/food preparation facilities. It is therefore important to understand the potential beneficial or disadvantageous effects of such so that investment can be best directed, positive impacts maximised and disadvantageous effects minimised. This study sought create a novel theory through examining which processes explain the impact of livestock-keeping on the community and which processes contribute to the hinderance or support of livestock-keeping in Dadaab Refugee Camp.

Methods: This study was conducted using a grounded theory approach as described by Corbin and Strauss. 20 key informant interviews were undertaken with theoretically, purposively selected key stakeholders in the Dadaab agriculture and health sectors. As is key to this methodology, a systematic constant comparative method of analysing the data was undertaken through the use of memo-ing in-between interviews resulting in 40 memos. Upon theoretical saturation, three levels of coding were conducted. Firstly, line-by-line, in-vivo coding fragmented the data by inductively assigning codes to the transcripts. Secondly, axial coding categorised the data, focussing on the core phenomenon and its relative strategies, context and consequences. This produced a visual axial coding paradigm. Lastly, selective coding described the inter-relationship of the categories in the process model.

Results: The analysis of these interviews is currently in progress. As of the date of submission of this abstract (May 31st 2026), the first stage of coding has been completed which involved the creation of over 231 codes. In addition, 40 memos were created during the data collection period which have been reviewed. The axial and selective coding will be completed by June 2026, well in advance of the ECVPH Annual Scientific conference. At this stage the results demonstrate the needs for a systems-thinking approach, with major emerging categories on climate change, lack of animal health services, use of livestock-related income and multiple benefits of livestock-ownership in the camp. Likewise, the preliminary results indicate emerging barriers to livestock ownership that are specific to refugee communities and potential risks in regards to waste management and zoonotic diseases.

Conclusion: This study will produce a novel theory of the process of how livestock impact health and well-being in the refugee camp context. By doing so it will highlight the need for a systems-thinking approach and identify leverage points in this system for action by the humanitarian sector, policy-makers and communities themselves.

Poster

POSTER PRESENTATION · ABSTRACT NO 40

Human carriage of β -Lactam-resistant bacteria along the broiler meat production chain: A One Health perspective

Poster Session · Thursday, 3 September 2026

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Key words: antimicrobial resistance; broiler meat; human carriage

Social media message: Workers along the broiler meat chain may carry β -lactam-resistant bacteria. Our findings highlight non-optimal practices of antibiotic use and the need for improved hygiene and education to reduce carriage and cross-contamination of antibiotic-resistant bacteria.

Background: β -lactam-resistant *Escherichia coli*, *Klebsiella pneumoniae* and *Acinetobacter spp.* are frequently isolated from hospitalized patients and represent an important public health concern due to their multidrug-resistant profiles and limited treatment options. However, data regarding their occurrence in healthy individuals from the community remain limited. Similar resistant bacteria have also been recovered from foods of animal origin, including broiler meat, suggesting that persons working along the broiler meat production chain may act as potential carriers and contribute to the circulation of antimicrobial resistance between humans, animals, food and the environment. This study aimed to investigate the prevalence and possible factors associated with the isolation of β -lactam-resistant *E. coli*, *K. pneumoniae* and *Acinetobacter spp.* from persons working along the broiler meat production chain.

Methods: A total of 160 skin and oropharyngeal swab samples were collected seasonally over a one-year period from broiler farmers, slaughterhouse workers and hospital kitchen staff across two Greek regions. Samples were subjected to selective isolation using β -lactam antimicrobials for the recovery of resistant *E. coli*, *K. pneumoniae* and *Acinetobacter spp.* Isolates were identified by MALDI-TOF MS. Antimicrobial susceptibility testing was performed to characterize resistance profiles, and molecular screening was conducted for the detection of β -lactamase genes. In addition, broiler farmers and hospital kitchen workers completed a questionnaire regarding antibiotic consumption practices by themselves and by broiler flocks, as well as demographic, health-related and behavioral factors potentially associated with the carriage of resistant strains.

Results: β -lactam-resistant bacteria were recovered only from skin samples, whereas no resistant isolates were detected in oropharyngeal samples. The prevalence of resistant *E. coli* and *Acinetobacter spp.* on human skin was 1.8% and 5.3%, respectively, while no β -lactam-resistant *K. pneumoniae* isolates were recovered. Overall, one *E. coli* strain and four *Acinetobacter spp.* strains were isolated from positive individuals. Most isolates (80.0%) were multidrug-resistant. No acquired β -lactamase genes were detected among the recovered strains; however, the *E. coli* isolate was phenotypically confirmed as an extended-spectrum β -lactamase producer. Questionnaire data indicated inappropriate antibiotic-use practices among both participants and broiler flocks. Statistical analysis also showed a higher probability of recovering resistant strains from male participants.

Conclusion: Although the observed prevalence was relatively low, the findings suggest that persons working along the broiler meat production chain may serve as potential carriers of antimicrobial-resistant bacteria, even in the absence of clinical disease. The recovery of multidrug-resistant strains from human skin highlights the need for improved hygiene practices and targeted education on prudent antibiotic use. Strengthening awareness among community members and food-chain workers is essential to reduce bacteria carriage, prevent cross-contamination events and limit the dissemination of antimicrobial resistance between humans and foods of animal origin.

Poster

POSTER PRESENTATION · ABSTRACT NO 41

Prevalence and molecular characteristics of ESBL-producing *Escherichia coli* in foods of animal origin in Europe: A systematic review and meta-analysis

Poster Session · Thursday, 3 September 2026

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Key words: *Escherichia coli*; ESBL; Animal-origin foods

Social media message: This study highlights chicken meat as a major reservoir of ESBL *E. coli* (40%), with lower prevalence (<10%) in almost all the other animal-origin foods examined. Key ESBL genes (*bla*_{CTX-M-1}, *bla*_{CTX-M-15}, etc.) were widespread in almost every food type.

Background: The emergence of extended-spectrum β -lactamase (ESBL)-producing *Escherichia coli* poses a significant threat to both public and animal health. While antimicrobial use in human and veterinary medicine is a key driver for ESBL emergence, the role of non-human reservoirs, such as animals, food, and the environment, remains unclear. The food chain may contribute to the transmission of resistant strains to humans, but evidence is still limited. This study aimed to estimate the pooled prevalence of ESBL-producing *E. coli* in different foods of animal origin in Europe and to characterize the molecular and phenotypic features of the isolates.

Methods: A systematic review and meta-analysis were conducted in accordance with PRISMA guidelines. Three electronic databases (MEDLINE via PubMed, Scopus, and epistemonikos.org) were searched for relevant studies, published between 2011 and December 2023.

Results: In total, 67 studies met the inclusion criteria for systematic review, with 63 of these being eligible for meta-analysis. The pooled prevalence (95% confidence interval) of ESBL *E. coli* in Europe was 40% (n = 33, 30--52%) in chicken meat, 5% (n = 19, 3--9%) in pork, 3% (n = 12, 2--5%) in beef, 5% (n = 4, 0--28%) in minced meat, 4% (n = 3, 0--32%) in game meat, 11% (n = 7, 0--40%) in poultry meat, 0% (n = 5, 0--1%) in RTE foods, 2% (n = 7, 0--4%) in seafoods, 2% (n = 6, 0--10%) in milk, 0% (n = 3, 0--2%) in cheese, and 3% (n = 2, 1--6%) in eggs. Several ESBL genes (n = 29) and sequence types (STs, n = 145) were observed across all food types. The most frequently detected ESBL gene was *bla*_{CTX-M-1}, while *bla*_{CTX-M-14}, *bla*_{CTX-M-15}, *bla*_{SHV-12}, and *bla*_{TEM-52} were identified in most food types. The pandemic clone ST131 was found in chicken meat and seafood samples, highlighting the possibility of zoonotic and foodborne transmission pathways.

Conclusion: These findings highlight chicken meat as a potential reservoir for ESBL-producing *E. coli*. Effective mitigation should include strengthened food safety measures and coordinated monitoring throughout the food production chain, guided by a One Health approach, to limit the spread of resistant bacteria to humans.

Poster

POSTER PRESENTATION · ABSTRACT NO 42

Validation of the pour-plate method as an alternative to the MPN technique for *E. coli* quantification in bivalve molluscs

Poster Session · Thursday, 3 September 2026

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Key words: Trueness; Accuracy; Food Safety

Social media message: New validation of the ISO 16649-1 pour-plate method for *E. coli* in bivalves. Shifting from the probabilistic MPN reference to direct counting delivers superior statistical precision and a faster workflow for food safety monitoring.

Background: Bivalve molluscan shellfish (BMS) can bioaccumulate enteric pathogens from contaminated waters, posing public health risks via raw consumption. *Escherichia coli* remains the primary indicator for regulatory classification. Currently, the Most Probable Number (MPN) technique is the reference method; though sensitive, it is labor-intensive and characterized by low precision with high variability. Conversely, classical plate-count methods offer improved reproducibility and shorter turnaround times. This study evaluates the comparative advantages and limitations of these approaches.

Methods: To assess the trueness and accuracy of the pour-plate method, a comparative validation was conducted following ISO 16140-2 guidelines, comparing the reference MPN method (ISO 16649-3:2015) against the alternative plate-count method (ISO 16649-1:2018). A total of 57 naturally contaminated BMS samples were analysed. Additionally, matrix-matched water samples were artificially contaminated with *E. coli* ATCC 25922 across six concentration levels (2.5 to 6.0 Log CFU/100 mL) to evaluate the method's accuracy profile. Relative trueness was assessed via Bland-Altman plots, while accuracy and equivalence were verified using the AP Calculation Tool.

Results: In the relative trueness assessment using artificially contaminated matrices, individual sample differences were visualized via Bland-Altman plots. Analysis showed a mean bias of -0.07013 ± 0.2804 . All data points remained within the 95% confidence limits (CLs) of agreement (-0.6197 to 0.4794). The relative trueness of the alternative method was deemed satisfactory, as no outliers exceeded the predefined acceptability limits. For naturally contaminated BMS, the Bland-Altman plot revealed that only two out of 57 samples exhibited differences exceeding the CLs (-1.058 to 0.8848), thereby supporting the validity of the alternative method. Specifically, results obtained from *Mytilus galloprovincialis* confirmed the suitability of the pour-plate technique, with only one out of 16 samples falling outside the CLs (-0.8327 to 0.6609). The accuracy of the method was evaluated using the AP Calculation Tool (MCS) on data from artificially contaminated samples. In accordance with validation standards, the alternative method is considered equivalent to the reference method if the upper and lower β -expectation tolerance intervals (β -ETI) fall within the established Acceptability Limits (AL), which are set at ± 0.500 . Within this framework, the repeatability standard deviation of the reference method was 0.429, showing high inherent variability compared to 0.162 of the alternative method. The findings demonstrated a satisfactory accuracy profile, as all calculated β -ETI values strictly fell within the AL at all tested concentrations.

Conclusion: This study validates the pour-plate method as a reliable alternative to the reference MPN method for BMS, confirming both trueness and precision. The tendency of MPN to yield higher estimates aligns with the Gronewold and Wolpert (2008) model, which attributes such discrepancies to the method's probabilistic basis rather than to an actual methodological bias. Consequently, the pour-plate method provides a robust and time-efficient approach for shellfish monitoring, optimizing laboratory workflow without compromising safety.

Poster

POSTER PRESENTATION · ABSTRACT NO 43

Dry-curing of seabass and cod: Process characterisation and *Listeria monocytogenes* challenge test

Poster Session · Thursday, 3 September 2026

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Key words: Dry-curing; fishery products; innovative technology; *Listeria monocytogenes*; RTE foods; food safety; process validation.

Social media message: As dry-curing gains popularity in the seafood sector, ensuring product safety becomes increasingly important. Our research on sea bass and cod investigated process performance and *Listeria monocytogenes* behaviour, providing data to support process validation and safe industrial application.

Background: The seafood industry continuously seeks innovative and sustainable preservation strategies capable of improving product stability and safety while maintaining nutritional and sensory quality. Among the available technologies, dry curing has gained increasing attention as a mild preservation technique based on the combined effects of dehydration, salt diffusion, and controlled environmental conditions.

Methods: In this study, sea bass (*Dicentrarchus labrax*) and cod (*Gadus morhua*) fillets were subjected to a 96-hour (h) dry-curing process using a patented cabinet specifically designed for fishery product transformation. The protocol included salting (48 h), dripping (4 h), drying (18 h), and aging (4 h) phases under controlled climatic conditions. Samples collected at different time points (T0, T48, T52, T70, T96) were analysed to evaluate physicochemical (pH, $a_{w\sim}$) and microbiological changes, including total mesophilic count, total psychrotrophic count, Enterobacteriaceae, and lactic acid bacteria (LAB).

Results: A challenge test was performed to assess the behaviour of *Listeria monocytogenes* during processing. Fish fillets were inoculated with adapted reference strains according to ISO 20976-1:2019 guidelines, reproducing contamination scenarios potentially occurring during handling operations, and pathogen dynamics were monitored throughout transformation.

Conclusion: During processing, pH values remained stable in both species. Water activity progressively decreased in cod, showing statistically significant differences between T0 and T96, with values decreasing from 0,990 to 0,960. A greater reduction was observed in sea bass, where $a_{w\sim}$ declined from 0,999 to 0,939 over the processing period. Microbiological analyses revealed dynamic changes in microbial populations. In sea bass, mesophilic and psychrotrophic bacterial counts initially decreased after salting, likely due to the combined effects of salt, temperature, and ventilation, before increasing toward the final stages of processing. LAB showed a similar pattern, whereas Enterobacteriaceae resulted mostly below the detection limit. In cod, mesophilic and psychrotrophic bacteria progressively increased throughout transformation, while Enterobacteriaceae and LAB were generally undetectable. Challenge test results showed an initial reduction of *L. monocytogenes* counts occurred in both species ($\Delta\sim T48-T0\sim = -27.57\%$ in sea bass; $\sim T48-T0\sim = -30.06\%$ in cod), suggesting an inhibitory effect of salting and environmental conditions. In the subsequent stages, *L. monocytogenes* counts showed stable trends in sea bass, with no statistically significant differences, whereas cod exhibited a moderate increase in *L. monocytogenes* counts from 3.36 to 4.67 log CFU/g ($\Delta\sim T96-T0\sim = +20.3\%$), possibly related to the higher $a_{w\sim}$ values observed in this species. Overall, the results indicate that dry curing contributed to limiting the growth of *L. monocytogenes* during the early stages of transformation; however, pathogen persistence throughout processing highlights the need for appropriate control measures. As dry-cured fishery products fall within the category of ready-to-eat foods capable of supporting the growth of *L. monocytogenes* under Regulation (EC) No 2073/2005, strict hygiene management and process validation are essential to ensure product safety.

Poster

POSTER PRESENTATION · ABSTRACT NO 44

Evaluation of official data on the surveillance and control of *Salmonella* in meat of domestic ungulates in Portugal

Poster Session · Thursday, 3 September 2026

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Key words: Salmonella; Domestic Ungulates; Surveillance and Control

Social media message: Longitudinal assessment (2004--2024) of Salmonella in Portuguese domestic ungulates meats shows an overall declining trend. Surveillance splits between abattoir self-checks and official controls at processing/retail.

Background: Salmonellosis is the second most reported foodborne zoonosis in the European Union (EU), with pork identified as a major food vehicle. The systems for the surveillance and control of *Salmonella* in animal populations and foodstuffs are largely similar across the various EU Member States, based on a common legal framework, although different approaches are applied. The aim of this study is to evaluate trends in data relating to the surveillance and control of *Salmonella* in meat of domestic ungulates in Portugal, comparing official results with European indicators.

Methods: Data on surveillance and control activities carried out during the period 2004--2024 were collected and analyzed from the national zoonosis surveillance reports submitted to the European Food Safety Authority (EFSA), the zoonosis monitoring reports from EFSA and the European Centre for Disease Prevention and Control Diseases and EFSA's online '*Salmonella* Dashboard' platform.

Results: The reported data on the detection of *Salmonella* in animals is mostly associated with clinical investigations or with the EU baseline study on *Salmonella* in fattening pigs and breeders during the period 2004-2011. Several serotypes were identified, including some of the most associated with human salmonellosis cases, namely Typhimurium and its monophasic variant. Consistent reported data on abattoir level surveillance is only available from 2020 onwards, except for pigs, with results available since 2015, based on Food Business Operators (FBOs) own checks. Generally, in Portugal, the isolation rate of *Salmonella* does not surpass 2% of all carcasses tested of all the domestic ungulate species, with levels steadily below 1% for cattle and small ruminants. Regarding meat, the data available is almost exclusively from Competent Authorities' (CA) sampling activities. There is an inconsistent number of samples tested throughout the study period, and likewise, the levels of isolation are also quite variable, within the same species and between species. The largest number of samples focuses on pig meat samples, but on the other hand, no sampling was performed on horse meat. The highest levels of *Salmonella* contamination were reported in 2011, reaching 11% of all samples tested, both for bovine and pig meat, with an overall decreasing trend being observed from that point on.

Conclusion: The data analyzed shows a two-sided *Salmonella* surveillance and control approach regarding the meat of domestic ungulates in Portugal: at abattoir level, based on FBOs own checks, and at processing and retail levels based on official controls performed by CA. The compiled results also point out a generally decreasing trend of *Salmonella* contamination in Portugal throughout the years, though the actual impact of such efforts in the incidence of human salmonellosis cases have not been fully studied.

Poster

POSTER PRESENTATION · ABSTRACT NO 47

Trustworthy AI for food: An architecture for verifiable, accountable decision support

Poster Session · Thursday, 3 September 2026

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Key words: Risk analysis, Negotiations, LLM-based agents, Multi-agent frameworks

Social media message: Can AI support food safety decisions without hallucinating? Our new conversational system for the dairy sector combines RAG, FSKX simulations, stakeholder negotiation & GS1 audit trails. Verifiable. Transparent.

Accountable. #FoodSafety #AI #OneHealth

Background: In food production, operators must navigate an expanding body of regulations, guidelines, and scientific evidence that no individual can fully master. Large Language Models (LLMs) offer substantial opportunities to support decision-making here, but hallucinations, opaque reasoning, and unverifiable advice are unacceptable where food safety and public health are at stake.

Methods: We present the design of a conversational decision-support system in development for the dairy sector addressing these challenges through four integrated components targeting verifiability, uncertainty transparency, multi-stakeholder balance, and regulatory accountability.

Results: First, the system extends conventional retrieval-augmented generation (RAG) systems with dual-source evidence grounding. Each claim is anchored either in a curated, customizable document corpus of HACCP guidelines, SOPs, regulations, and scientific literature, or in a live predictive model executed via the FSKX (Food Safety Knowledge Exchange) simulation framework. A control layer requires the LLM to decompose responses into individually verifiable claims, each linked to a source handle; any claim that cannot be substantiated is automatically removed before it reaches the user. Second, uncertainty is explicitly modeled and treated as a primary output. Confidence levels, explicit assumptions, and evidence-gap notices are communicated transparently alongside every response, indicating what additional information would improve the answer. Third, the system addresses multi-stakeholder trade-offs by extending an AI-assisted risk negotiation framework that structures competing interests into explicit negotiation spaces. It surfaces conflicting perspectives, proposes balanced compromises, and makes its reasoning transparent, rather than obscuring value-laden choices behind a single AI-generated recommendation. Fourth, every claim, citation, and simulation is logged as an EPCIS (Electronic Product Code Information Services) event, producing a GS1-compatible audit trail. This integrates with existing food-industry traceability systems and allows auditors and regulators to reconstruct the evidential basis of any decision.

Conclusion: Although instantiated in the dairy sector, the architectural pattern is transferable to other high-stakes scientific decision-support domains.

Poster

POSTER PRESENTATION · ABSTRACT NO 48

Agrifood-OneAI: A Pan-European COST Action leveraging artificial intelligence to operationalise One Health in agrifood systems transformation

Poster Session · Thursday, 3 September 2026

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Key words: One Health, artificial intelligence, food safety risk governance

Social media message: Agrifood-OneAI --- a new pan-European COST Action --- unites >200 experts to harness AI for One Health food safety. From AMR to Risk Negotiation, we're building the network to move from data to decision. #OneHealth #FoodSafety #AI

Background: Agrifood systems face compounding increasing pressures from climate change, biodiversity loss, antimicrobial resistance (AMR), and evolving food safety risks. The One Health framework offers a holistic approach to managing problems characterized by human--animal-environment interdependencies, yet its operationalisation remains fragmented. Artificial Intelligence (AI) holds significant potential to enable integrated, real-time data analysis and predictive risk assessment across One Health domains. However, siloed data ecosystems, divergent national governance frameworks, and the absence of harmonised data and model-sharing standards impede cross-sectoral integration. Deep-rooted sectoral silos and inadequate financial and human resources further hinder translation of One Health concepts into coordinated action. A pan-European, transdisciplinary network is therefore essential to align methodologies, build consensus, and ensure AI tools serve One Health objectives equitably.

Methods: Agrifood systems face compounding increasing pressures from climate change, biodiversity loss, antimicrobial resistance (AMR), and evolving food safety risks. The One Health framework offers a holistic approach to managing problems characterized by human--animal-environment interdependencies, yet its operationalisation remains fragmented. Artificial Intelligence (AI) holds significant potential to enable integrated, real-time data analysis and predictive risk assessment across One Health domains. However, siloed data ecosystems, divergent national governance frameworks, and the absence of harmonised data and model-sharing standards impede cross-sectoral integration. Deep-rooted sectoral silos and inadequate financial and human resources further hinder translation of One Health concepts into coordinated action. A pan-European, transdisciplinary network is therefore essential to align methodologies, build consensus, and ensure AI tools serve One Health objectives equitably.

Results: Agrifood-OneAI will deliver harmonised, interoperable data and metadata standards for One Health agrifood applications; conceptual frameworks and European roadmaps for AI-enabled risk prediction and AMR mitigation; and governance guidelines for responsible, FAIR, and GDPR-compliant data sharing. Validated demonstration pilots will illustrate AI-assisted, real-time food safety management. The Action integrates multi-criteria decision analysis (MCDA) and AI-based Risk Negotiation to support participatory, trade-off-aware governance across food safety, sustainability, and public health objectives. Capacity-building outputs include training resources, a customised AI tutor, and two international scientific conferences.

Conclusion: Agrifood-OneAI positions AI as a facilitator of governance and informed decision-making rather than a purely technical solution. By coordinating dispersed European efforts under a shared One Health framework, the Action establishes the conceptual and organisational foundations for safe, resilient, and trusted agrifood system transformation -- with direct relevance to the veterinary public health community.

Poster

POSTER PRESENTATION · ABSTRACT NO 49

Assessing the performance of a rapid test in integrated bite case management for One Health rabies control

Poster Session · Thursday, 3 September 2026

Rabina Ghimire, Caroline Pannrucker, Sonja Hartnack

Key words: Rabies, Rapid Test, BLCM, IBCM

Social media message: In this study, we evaluated the specificity and sensitivity of the "Bionote Rapid Rabies Ag Canine Test" under field conditions using the Bayesian latent class model, with the aim of expanding the options for integrated management of bite cases and thereby moving closer to the "Zero by 30" goal (zero human deaths from rabies by 2030).

Background: Globally, an estimated 59,000 human deaths occur because of rabies each year, with about 99% of these resulting from dog bites. The disease disproportionately affects poorer, rural, and Indigenous communities, as well as children. Uganda currently lacks sufficient rabies diagnostic capacity across both human and veterinary sectors. In other endemic settings, post-mortem rapid tests in dogs increasingly support Integrated Bite Case Management (IBCM), which links human and animal health services to assess every bite patient, investigate the biting animal, conduct animal observation and/or testing, coordinate post-exposure prophylaxis (PEP), and ensure follow-up. IBCM improves patient safety and surveillance while optimizing resources. However, robust assessments of rapid test accuracy under field conditions remain limited, and the Bionote Rabies Rapid Ag Canine Test has not yet been evaluated or validated in Uganda. This lack of evaluation data hampers implementation of Bionote rapid testing and, consequently, IBCM. The aim of this study was to assess the diagnostic performance in field conditions of the Bionote rapid test and the World Organisation for Animal Health (WOAH) reference test, the direct fluorescent antibody test (dFAT), using data available from rabies-endemic countries.

Methods: We conducted a Bayesian latent class analysis (no gold-standard assumed) using data from Kimitsuki et al. (2020), Yale et al. (2019), and Léchenne (2016) to estimate the diagnostic performance of the WOAH reference test (dFAT) and the Bionote rapid test. We applied the Hui--Walter model with two tests and three populations (referring to the three publications), assuming conditional independence, and also ran models allowing covariance between sensitivities and specificities. The `autohuiwalter` function from the `runjags` package was used to generate the model in R (R Core Team (2025)). Convergence was assessed by inspection of trace plots, PSRF (<1.1), and effective sample size ($SS_{eff} > 15,000$).

Results: In the conditional independence model, the estimated sensitivities and specificities (95% credible intervals) were: dFAT sensitivity 99.5% (98.2--100), dFAT specificity 97.8% (93.8--100), Bionote sensitivity 96.5% (93.3--100), and Bionote specificity 99.4% (98.0--100).

Conclusion: These estimates support careful incorporation of the Bionote test into dog post-mortem rapid testing within IBCM in Uganda, paired with confirmatory dFAT when feasible. We recommend piloting IBCM with standardized protocols, training, external quality assurance, and data systems for rapid feedback, alongside prospective evaluation of test performance and program impact on timely PEP, reduction of unnecessary PEP, and targeted dog vaccination.

Poster

POSTER PRESENTATION · ABSTRACT NO 50

'Monitoring wildlife matters': study on the presence of *Cryptosporidium spp.* in Portuguese wild boars and related hygiene risk factors

Poster Session · Thursday, 3 September 2026

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Key words: *gastrointestinal protozoa; hunters; parasitic diarrhea; zoonoses*

Social media message: *Monitoring wildlife matters: our findings highlight the presence of *Cryptosporidium spp.* in Portuguese wild boars and reinforce the need for vigilance, hygiene, and surveillance to reduce zoonotic risks.*

Background: *Cryptosporidium spp.* is a widely distributed gastrointestinal protozoan pathogen affecting a broad range of vertebrate hosts, including the European wild boar (*Sus scrofa*). Transmission occurs primarily through the fecal-oral route, either by direct contact or through the consumption of contaminated food and water. The presence of this parasite in wild boar populations raises concerns regarding its zoonotic potential, particularly for hunting stakeholders who are exposed to infected animals and carcasses during hunting activities.

Methods: This study aimed to investigate the occurrence of *Cryptosporidium spp.* in wild boars from ten hunting areas located in Northern and Central Portugal and to conduct a preliminary assessment of factors that may contribute to zoonotic transmission. Fecal samples collected from wild boars were analyzed using an immunochromatographic assay, which confirmed the presence of *Cryptosporidium spp.* antigens in four of the ten hunting areas surveyed, including one area in Northern Portugal and three areas in the southeastern region of Central Portugal.

Results: In addition to detecting the parasite, a qualitative assessment was conducted to identify factors associated with the persistence of infection within wild boar populations and to evaluate zoonotic risk factors related to carcass handling practices and hygiene procedures adopted during and after hunting activities. Identifying the presence of the parasite and assessing these contributing factors are essential steps in evaluating and managing the associated risks, as well as determining whether critical control points exist within the wild boar meat production chain.

Conclusion: The findings provide preliminary evidence of the circulation of zoonotic protozoa such as *Cryptosporidium spp.* in Portuguese hunting areas and highlight several practices that may facilitate the transmission of pathogenic agents to hunters and other individuals involved in game processing. Given the zoonotic significance of this parasite, it is essential to raise awareness among hunting stakeholders and to establish surveillance networks focused on game species. Furthermore, veterinarians, hunters, and consumers should adopt strict hygiene and biosecurity measures to minimize the risk of infection. Continuous monitoring of wild species such as wild boar is crucial for protecting public health and ensuring food safety, as these animals may act as reservoirs of zoonotic parasites capable of entering the food chain.

Poster

POSTER PRESENTATION · ABSTRACT NO 51

Gastric lesions in pig stomachs: An exploratory study

Poster Session · Thursday, 3 September 2026

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Key words: *By-products; edible viscera; gastric ulcer; swine production*

Social media message: *Gastric lesions in pig stomachs remain an important area of study within edible by-product quality control. In a swine slaughterhouse, 1,383 stomachs were evaluated. While 97.9% showed at least one gastric lesion, only 5.86% presented gastric ulcers. These findings highlight the importance of monitoring gastrointestinal by-products to ensure food safety, maintain product quality, and support sustainable use of animal resources. Further research is needed to better understand the causes and risk factors associated with gastric lesions.*

Background: Controlling the quality of gastrointestinal by-products in slaughterhouses is essential to ensure food safety, consumer health, and regulatory compliance. Edible by-products intended for commercialization must be carefully inspected, cleaned, and handled to prevent contamination by pathogens, foreign materials, or residues.

Methods: The study took place at a large-capacity slaughterhouse located in the Netherlands that processes around 90,000 animals per week. The main goal was to study the prevalence of gastric ulcers in stomachs from randomized pigs over a specific period. Using different scales adapted from the literature, the study was based on two distinct phases: first, the analysis of each stomach for the presence of any gastric lesions; and second, the presence or absence of any kind of ulcer and its distribution in the stomach. Four privileged locations in the stomach were catalogued (locations A, B, C, and D), and the analysis of ulcer presence data was associated with one of these locations.

Results: In total, 1,383 stomachs were analyzed and scored, all under the same sampling and evaluation conditions. 97.54% of stomachs revealed the presence of at least one gastric lesion in their mucosa (n=1,349). Regarding the second phase of the study, 5.86% of the 1,383 stomachs (n=81) revealed ulcers. Of the ulcers observed, 66.3% were located in location A (n=53), 30% in location C (n=24), and 8.8% in location D (n=7); nothing was detected in location B.

Conclusion: These results reveal that the percentage of stomachs with ulcers is low; however, gastric lesions are not limited to ulcer-like lesions, and there is therefore a need to investigate and catalog more data in this area of edible by-products, namely regarding causes, epidemiological predispositions, and risk factors. Effective quality control preserves product integrity, extends shelf life, and maintains market value. It also strengthens consumer confidence, reduces food waste by maximizing the use of animal resources, and supports sustainable and responsible meat industry practices worldwide.

Poster

POSTER PRESENTATION · ABSTRACT NO 52

Veterinary career preferences in Europe: Determinants of sector choice among students and early-career veterinarians

Poster Session · Thursday, 3 September 2026

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Key words: career choice; livestock practice; veterinary public health; Veterinary workforce

Background: A growing imbalance challenges the veterinary profession, with increasing demand for companion animal practice and declining demand in strategically important livestock, veterinary public health (VPH), and official veterinary (OV) roles for food security and animal health. Despite institutional efforts such as financial incentives and rural internships, limited evidence exists on the underlying motivations guiding career choices. This study aimed to identify factors influencing veterinary students' and recent graduates' career preferences and to explore barriers to entering underrepresented sectors, particularly livestock and VPH.

Methods: A cross-sectional, anonymous digital survey comprising 94 questions was distributed via social media with support from International Veterinary Students' Association (IVSA) member organizations across Europe. The questionnaire covered demographics, career intentions, education and preparedness, perceptions of veterinary fields, and strategies to improve sector attractiveness. The study population included veterinary students and recent graduates within five years of qualification. A total of 1,317 valid responses from 55 nationalities and 63 universities were analysed using descriptive statistics to summarise trends and associations across variables.

Results: Respondents were predominantly female (80%). Nearly 45% expressed intent to work in companion animal practice, compared to 23% in livestock and 10% in OV/VPH roles. Among recent graduates (n=156), 7% worked in livestock and 3% in OV/VPH. Perceived training exposure was uneven: companion animal medicine received extensive curricular focus, whereas industry, VPH, and research were reported as having limited or no exposure by a majority of respondents. Preparedness mirrored this disparity, with most participants feeling moderately to strongly prepared for companion animal practice but poorly prepared for VPH roles. Key factors influencing livestock career choice included lack of interest (65%), conflicting personal values (25%) and poor work-life balance. Conversely, societal perceptions of livestock farming had minimal importance. Potential solutions identified included improved working conditions (67%) and higher salaries (63%), alongside increased exposure during training, curriculum reform, mentorship opportunities, and greater visibility of these fields. Flexible work arrangements and team-based practice models were also perceived as attractive innovations.

Conclusion: Veterinary career choices in Europe are strongly shaped by perceived lifestyle, work conditions, and educational exposure. Imbalance of livestock and VPH career choices was driven by low perceived attractiveness, and misalignment with preferred work-life balance. Addressing these gaps through targeted exposure, improved working conditions, and enhanced visibility of these sectors is essential to rebalance the veterinary workforce and ensure sustainability in strategically important areas of VPH and animal health.

Poster

POSTER PRESENTATION · ABSTRACT NO 53

Evaluation of the public health risks from broiler carcasses rejected with localised perihepatitis during post-mortem inspection

Poster Session · Thursday, 3 September 2026

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2. University of Liverpool

3. St. David's Poultry Team

4. Pilgrim's Europe

Key words: Broilers; Localised perihepatitis; Meat inspection

Social media message: Broilers with localised perihepatitis detected at post-mortem inspection are fit for human consumption

Background: Post-mortem inspection (PMI) of carcasses in abattoirs is an official control stipulated in the Regulation (EU) 2019/627. In generalised conditions, the whole carcass must be rejected as unfit for human consumption (total rejection), while in localised conditions only the affected parts or organs are rejected. In PMI, a condition is considered generalised when macroscopic changes are detected in more than one body locations. Microscopically, increased presence of infectious agents in body parts that are normally sterile, e.g. bone marrow, spleen and deep muscle tissue usually confirms the generalised condition. Perihepatitis is the inflammation of the liver capsule and in broilers it can be a localised or part of a generalised condition (e.g. septicaemia). Following PMI rules, if only localised perihepatitis is detected on a carcass, it must be considered a localised condition (LPH) and the carcass considered fit for human consumption. However, in the UK, any sign of perihepatitis is considered generalised, and even carcasses with LPH are totally rejected, resulting in a loss of ~1.1 million carcasses annually. The aim of this study was to assess whether the rejection of the whole carcass is justified in cases of LPH in broilers in terms of risk to public health by comparing microbiologically carcasses with LPH to carcasses that have passed PMI inspection and carcasses rejected for generalised disease.

Methods: Samples of deep breast muscle were collected aseptically from 300 broiler carcasses in 3 different UK abattoirs over six days. Carcasses were divided into three groups: Control (CON), i.e. passed PMI (n= 106), LPH (n=107) and generalised disease (GEN), i.e. carcasses rejected at PMI for obvious, generalised conditions (n= 87). Samples were analysed for counts of ACC, Enterobacteriaceae (EBC) and generic *E. coli* (ECC) and for presence of *Salmonella* and avian pathogenic *E. coli* (APEC).

Results: Overall, levels of ACC, EBC and ECC and prevalences of APEC were found to be very similar and with no statistically significant difference in LPH and CON carcasses. They were significantly lower from GEN carcasses. Morphologically, no obvious differences were seen between LPH and CON carcasses.

Conclusion: Based on these results and other observations related to the lack of significant pathological findings associated with LPH and control carcasses, we conclude that there is no difference in risk to public health from carcasses with LPH relative to the carcasses that have passed PMI as fit for human consumption. Therefore, there is no reason for LPH carcasses to be rejected at PMI as unfit for human consumption. The results indicate that the change in policy is needed to align with risk-based principles in meat inspection.

Poster

POSTER PRESENTATION · ABSTRACT NO 54

Assessing pathogen surveillance in swine barn sedimentation dust via metagenomic profiling of environmental RNA

Poster Session · Thursday, 3 September 2026

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Key words: eNA, metagenomics, swine

Social media message: Metagenomic detection of swine pathogens in sedimentation dust: Our study detected bacterial and viral agents (e.g., Salmonella, Influenza A) in 22 pig farms using Oxford Nanopore sequencing.

Background: Recent advancements in metagenomic analysis of environmental nucleic acids have significantly improved the feasibility of laboratory procedures, reduced sequencing costs, and streamlined bioinformatic workflows. These developments have facilitated the broader adoption of this minimally invasive method. In the context of livestock monitoring, this approach enables diagnostic coverage of entire herds through the analysis of a limited number of samples. In conventional pig farms, sedimentation dust might be a particularly suitable material for investigation, as it can be easily collected and accumulates over the entire housing period. Unlike airborne dust or direct animal sampling, sedimentation dust potentially provides a cumulative record of the associated microbial and pathogen communities. To explore the potential of sedimentation dust as an investigative matrix, dust from 22 conventional pig-fattening farms in Lower Saxony was subjected to metagenomic analysis.

Methods: In preparation for sequencing, the samples underwent a dsDNA digestion step following nucleic acid extraction. The remaining RNA was then subjected to reverse transcription and second-strand synthesis. To enhance sensitivity for the detection of pathogens in low concentrations, the resulting cDNA was non-specifically amplified using SISPA-PCR. Sequencing was performed on the Oxford Nanopore MinION platform. The generated reads were classified using Kraken2, referencing the NCBI database. Sample comparisons and diversity calculations were conducted using the Pavian tool in R.

Results: On average, 1,407,513 reads per sample (min. = 671,262; max. = 1,922,531) with a mean read length of 400--600 base pairs were obtained. Using Kraken2 classification, an average of 89.3% of the reads were successfully classified. Over 99% of the classified reads were assigned to bacterial taxa. A range of swine-specific pathogens were detected, including bacterial agents such as *Actinobacillus pleuropneumoniae*, *Mycoplasma hyopneumoniae*, *Glaesserella parasuis*, *Brachyspira hyodysenteriae*, and *Lawsonia intracellularis*, as well as viral pathogens such as Transmissible Gastroenteritis Virus, Swine Enteric Coronavirus, and Porcine Circovirus 2. Additionally, zoonotic pathogens such as *Salmonella spp.*, Influenza A viruses, and Rotavirus A and C were identified.

Conclusion: Since the method requires further analysis and validation, particularly regarding post-sequencing classification, only preliminary data can be presented at this stage. The detection of the individual pathogens listed was, however, verified at sequence level and can therefore be considered valid. Particularly in the context of bacterial pathogens, the results strongly support the value of sedimentation dust analysis under the given conditions.

Poster

POSTER PRESENTATION · ABSTRACT NO 55

Relevance of cattle as source of resistant *E. coli* in Cameroon

Poster Session · Thursday, 3 September 2026

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Key words: Antimicrobial resistance; VTEC; EPEC

Social media message: A One Health approach to antimicrobial resistance surveillance, integrating data from human, veterinary, and environmental sectors, with coordinated monitoring and education programs are essential to mitigate the spread of resistance and safeguard both public and animal health.

Background: The One Health approach recognizes the interconnectedness of human, animal, and environmental health and promotes multidisciplinary collaboration to address complex public health challenges. *Escherichia coli* is an important example of a zoonotic pathogen that can circulate between cattle, humans, and the environment; transmission may occur through direct contact with livestock, contamination of food products, water sources, or environmental surfaces and cattle is recognized as a major reservoir for pathogenic *E. coli* including Shiga toxin-producing *E. coli* (STEC). The emergence and spread of antimicrobial-resistant *E. coli* further highlight the need for integrated surveillance and control strategies. The aim of this research is to investigate the prevalence of antimicrobial resistant *E. coli* isolates in cattle, farmers and slaughterhouse environment in Cameroon.

Methods: A total of 380 samples were collected from farmers (80), cattle (100) and the environment of the slaughterhouse (200) in Yaoundé, Cameroon. After a preselection in CHROM agar medium and confirmation by MALDI-TOFF, a total of 117 *E. coli* isolates from farmers (17, 14.5%), cattle (41, 35%) and environment (59, 50.4%) were available for further characterization. Antimicrobial resistance against 14 antibiotics from 8 different families, beta-lactamases (4), fluoroquinolones (2), aminoglycosides (2), macrolides (1), polypeptides (1), tetracycline (2), phenicol (1) and sulfonamides (1), was determined using disk diffusion.

Results: For all the antimicrobials tested, resistance was more common in *E. coli* isolates from farmers as compared with cattle and slaughterhouse environment. Among cattle, resistance against antimicrobials included in D category such as ampicillin or tetracycline were the most common, 56.09% and 36.59% respectively, although a high prevalence of resistance against colistin was also observed (43.9%). Multiresistance, defined as resistance to antimicrobials from three or more different families, was also very common, being reported in 94.12%, 34.15% and 52.54% of the isolates from farmers, cattle and slaughterhouse environment respectively.

Conclusion: These findings suggest that antimicrobial use and associated selective pressures in human populations may play a more prominent role in the emergence and persistence of resistant *E. coli* strains within the studied setting. Nevertheless, the detection of relevant antimicrobial resistant profiles in both bovines and the slaughterhouse environment highlights the potential for the exchange of resistant bacteria and resistance genes across human, animal, and environmental interfaces.

Poster

POSTER PRESENTATION · ABSTRACT NO 57

Report of control and surveillance measures against enzootic bovine leukosis in French Reunion Island over a 10-year period

Poster Session · Thursday, 3 September 2026

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Key words: Enzootic bovine leukosis (EBL), Bovine Leukemia Virus (BLV), Disease control program

Social media message: From endemic to control: a 10-year longitudinal analysis of a control program against bovine leukemia virus in French La Réunion Island showed a strong decline in prevalence and incidence following surveillance, movement control and herd management measures.

Background: Several European countries, including France, eradicated bovine leukemia virus (BLV) in the 90's. However, the French Outermost region (OR) of La Réunion, a southwestern Indian Ocean Island, combines a significant cattle industry with a long-lasting enzootic circulation of BLV. A mandatory control programme led by governmental authorities and professional organisations has been implemented since 2020, first targeting suckler herds---historically less affected---and subsequently dairy herds. This study aimed to evaluate BLV control and surveillance measures using data collected over a ten-year period. Specifically, the evolution of BLV epidemiology was characterized through a longitudinal analysis of prevalence and incidence at both herd and animal levels.

Methods: The control programme was conducted on a population of approximately 30,000 cattle distributed across 65 dairy herds and 1,000 suckler herds. Individual data from 103,310 animals, spanning birth to death, were extracted from the national cattle database and linked to corresponding BLV screening test results. Control strategies included generalised surveillance, movement restrictions with compulsory testing, and within-herd management measures such as hygiene practices and removal or segregation of infected animals. Analyses relied on descriptive epidemiology to identify temporal trends in key epidemiological indicators.

Results: Between 2014 and 2025, three major categories of interventions structured the control programme: (i) the establishment of widespread surveillance, (ii) the implementation of movement restrictions and peri-movement testing, and (iii) control measures within infected herds, including culling or segregation of infected animals. All cattle older than 12 months were subject to mandatory testing by ELISA. The plan initially targeted herds with prevalence up to 50%, and was then gradually expanded to all herds. Different control strategies were applied, including testing and culling or segregating seropositive animals. The selective removal of super-shedders detected by quantitative PCR test was used in some highly infected dairy herds. Concomitantly, several measures were implemented to prevent viral spread, including hygienic practices targeting iatrogenic transmission, the control of insect vectors (Stomoxys) and movement restrictions between herds. A marked decreasing trend in disease dynamics was observed across the study period. Significant reductions were recorded in both individual and herd-level prevalence and incidence. Concomitantly, the bovine population encountered a steep decline, both in head count and in number of herds. However, this decline began prior to the implementation of the formal control programme.

Conclusion: Altogether, these findings indicated a marked decline in BLV indicators in French OR La Réunion, suggesting a shift from high endemicity towards progressive control. However, herd-level heterogeneity remained, with uneven attainment of disease-free status, highlighting the influence of baseline conditions and local production systems.



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