UNIVERSITY OF LIVERPOOL

ECVPH
EUROPEAN COLLEGE OF
VETERINARY PUBLIC HEALTH

Getting ahead of the risks:
Strategies to avoid known and unknown hazards

ECVPH Annual Conference and AGM

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CONFERENCE PROCEEDINGS

Session 1

When the Dust Settles: Applying a disaster recovery lens to veterinary public health

Prof Lucy Easthope – University of Bath

In this presentation, Lucy Easthope will set the scene for Getting ahead of the risks: strategies to avoid known and unknown risks. As one of the country's leading advisers on disaster planning she will provide an insight into what the future holds for veterinary professionals as we enter our permacrisis era.

Health Protection response to zoonotic hazards

Dr David Edwards – UK Health Security Agency

Public Health is defined as 'the science and art of preventing disease, prolonging life and promoting health through organized efforts of society' (Acheson 1988). This recognises that the causes of ill health and solutions for improving population health are multifactorial, involving society and the wider environment beyond individual disease-causing organisms or risk factors.

Health Protection forms one of three domains of public health, categorised by the UK Faculty of Public Health (Griffiths, et al, 2005). The working definition for which is, the protection of individuals, groups and populations through expert advice and effective collaboration to identify, prevent and mitigate the impacts of infectious disease, and environmental, chemical and radiological threats (Ghebrehewet, et al, 2016).

Health Protection Teams deliver the health protection function at local level across England and the UK devolved administrations. Receiving daily statutory notifications of cases of communicable disease, potential outbreaks, or environmental exposures, which are risk assessed and acted upon to protect public health. This practice is underpinned by national guidance and is enabled by close working partnership with health and public health system colleagues in the National Health Service (NHS), local authorities and other agencies and stakeholders.

This includes identification of the public health risk resulting from zoonoses exposures, whether from companion animals, livestock or other events. Drawing on the subject matter expertise available from colleagues in the UK Animal and Plant Health Agency (APHA) and within UKHSA.

This presentation will provide examples of health protection response to such zoonotic exposures, their challenges, uncertainties and wider considerations for ensuring protection of public health in an ethical and proportionate manner.

References:

Acheson D (1988). Committee of Inquiry into the Future Development of the Public Health Function. Public health in England: The Report of the Committee of Inquiry into the Future Development to the Public Health Function. Faculty of Public Health https://www.fph.org.uk/media/3475/acheson-1988.pdf. Accessed 30/08/2024.

Ghebrehewet A, Stewart A, Baxter D, Shears P, Conrad D, Kliner M. (2016). Health Protection: principles and practice. Oxford University Press.

Griffiths S, Jewell T, Donnelly P. (2005). Public health in practice: the three domains of public health. Public Health;119: 907–913.

Session 2

Understanding human behaviour to mitigate zoonotic risks

Dr Charlotte Robin – UK Health Security Agency

Behavioural science is a fundamental part of Health Protection; it enables us to understand behaviour, how people are likely to respond to public health advice and identify barriers and facilitators to engaging with and implementing advice.

In the context of infectious diseases, behavioural science approaches can help us understand experiences of health and illness in the context of everyday lives. For zoonotic infections, this includes understanding our relationships with animals and the role they have in our society. As most emerging infections are zoonotic, recognising and understanding behaviour to reduce risk of zoonotic disease transmission is an essential part of Health Protection.

This presentation will discuss examples of how human behaviour can increase risk of zoonotic infections and how these risks can be mitigated. Using examples from farms and companion animals, we will explore the different ways in which risk is understood and conceptualised and the impact this has on behaviour. The case studies highlight that across the contrasting contexts of animal encounters, there are consistent concepts that influence behaviour; how people define and understand human-animal relationships and the role of different animal species in society.

This presentation highlights the importance of recognising how animals as vectors are understood from different perspectives and the impact of these on behaviour. Specifically, when we elevate the status of an animal to a pet, bring it within the boundary of the home or other safe space, different meanings are attributed to them. These meanings negate risk of transmission of zoonotic infections. Framing public health advice to incorporate a One Health approach would encourage and support adherence to infection prevention advice for zoonoses.

Tackling the public health risks associated with raw meat diets for dogs

Dr Genever Morgan – University of Liverpool

Raw meat diets (RMD) remain a popular and important alternative pet food choice for dog owners in the UK. However, these RMDs for pets have been demonstrated to be contaminated with potentially pathogenic bacteria with zoonotic potential, such as E. coli, Salmonella spp., Campylobacter spp., Listeria spp., and Mycobacterium spp. There is growing evidence to suggest that RMD can be contaminated with antimicrobial-resistant (AMR) bacteria, including bacteria demonstrating resistance to highest-priority critically important antibiotics, and that dogs fed RMD are more likely to shed these AMR-bacteria within their faeces than dogs fed conventional cooked diets. Therefore, RMDs, and the dogs fed them, may present an important and potentially previously overlooked public health concern.

Within this talk, I will present the findings of recent research from the University of Liverpool which highlights some of these AMR and zoonotic disease risks associated with commercially available pre-prepared RMD and dried treats for dogs in the UK. I will also discuss the findings of recent studies which have compared the carriage of AMR-E. coli by dogs fed RMD compared to those fed a cooked diet and will touch briefly on some of the reasons and beliefs discussed by dog owners for their pet diet choice.

Translating uncertainty and risk to policy makers

Prof Chris Jewel – Lancaster University

ABSTRACT TO FOLLOW

Session 3 – Residents' Presentations

These abstracts will all be found in the poster abstract section, later in the proceedings. The poster number is provided after each author's name.

Lore Heyvaert – F5

Michal Majewski – F1

Yvette de Guess – F6

Keli Gerken – P2

Davide Pagnossin – P9

Sarah Seery – P3

Session 4

Emerging and neglected bacterial foodborne hazards.

Prof Kurt Houf, Lore Heyvaert, and Muhammad Zafar Zeeshan

Department of Veterinary and Biosciences, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, 9820 Merelbeke, Belgium

The World Health Organization reports that more than 70% of the characterized emerging infectious agents have a zoonotic transmission. For emerging, as well as for neglected bacterial pathogens, transmission via food of animal origin must be taken into account. However, their assessment is inconsistent with the current analytical methods and human, veterinary, and food microbiological analysis strategies. Among the reasons are the increased selectivity and specificity of culture-dependent methods, such as the application of selective normalized methods, and the use of chromogenic agar media. Furthermore, the implementation of culture-independent methods, such as sample screening by genus or species-specific PCR assays, limits the detection and identification to predefined pathogens. Also, the more recently developed and applied amplicon and shotgun sequencing approaches have insufficient taxonomic identification depth and are unable to detect low numbers of pathogens. As a result, screening is only successful for already known pathogens, and (phenotypically) divergent isolates are no longer isolated, detected, or identified. Examples of neglected foodborne bacterial pathogens that will be presented are *Arcobacter* species, non-thermophilic *Campylobacter* species, and *Escherichia albertii*. Scientific data justify their urgency as causative agents of gastroenteritis, as well as their potential impact in patients with chronic gastrointestinal diseases showing dysbiosis. However, the sources of infection and their transmission routes have not been studied sufficiently, and data on the presence on food of animal origin are very limited to non-existent. At present, research, supported by the Belgian Federal Public Service of Health, Food Chain Safety, and Environment*, is being performed, to elucidate the knowledge gaps of poultry meat, pork, and beef contamination at retail level, and to establish a framework for the risk evaluation of upcoming and neglected bacterial foodborne pathogens.

* Belgian Federal Public Service of Health, Food Chain Safety, and Environment through the contract FOD RF22/6358 Camprotesch.

Development of the Oyster Risk Profile

Ms Chloe Thomas – Food Standards Agency

The oyster risk profile was produced by the Exposure Assessment and Trade (EAT) Team at the Food Standards Agency (FSA), commissioned by the UK Office for Sanitary and Phytosanitary Trade Assurance (UKOSPSTA) at Department for Environment Food and Rural Affairs (Defra), to inform the potential risks associated with importing oysters into the UK from any trading partner. Risks associated with importing oysters into the UK can be defined as any potential hazards identified within the specified commodity (oysters) which may pose a public health risk. These may occur naturally (for example marine biotoxins or naturally present microorganisms) or through anthropogenic sources (human interaction with the commodity) either via introduction of the hazard into the environment (for example agricultural or sewage waste entering marine systems resulting in the presence of certain chemicals or microorganisms) and/ or during the processing (including transit and storage) of the commodity (for example poor storage conditions or insufficient processing leading to microbial growth or poor hygiene leading to introduction of microbes).

The scope also includes the provision of a summary of key risk mitigation measures, production methods and management processes from international standards and guidelines. Additionally, relevant domestic import controls, UK consumption patterns and information on key global producers and international trade. This is intended to provide information for auditors within the process of market access requests.

A risk profile is not an import risk assessment in that a final risk output is not provided.

This talk provides some of the background information around the risk profile project, with focus on the known and unknown aspects of the risks associated with oysters and consideration of the mitigation measures available to control them, future considerations and some learnings from the first iteration of the risk profile project.

Understanding food hygiene behaviours in kitchens

Prof Gulbanu Kaptan – University of Leeds

Behaviours in household and food business kitchens sometimes do not adhere to recommended practices and regulations due to established habits, lack of time, insufficient knowledge, and physical environment. Non-compliance with recommendations and regulations may lead to foodborne illnesses, negatively impacting people’s quality of life and the medical system. Furthermore, there is a significant variability between self-report and observational studies on kitchen behaviours, suggesting that the rates of positive behaviours are over-estimated in self-report studies. Kitchen Life 2 project, commissioned by the Food Standards Agency aimed to identify the key food safety behaviours in household (N=31) and food business kitchens (N=70) through an observational study by filming participants in their kitchens with motion-sensitive cameras for five days. The footage was coded and analysed. The results show that (1) the five most frequently observed behaviours in household and business kitchens were licking fingers or touching face, washing hands without soap or product, improperly drying hands, using mobile phones, and leaving the fridge door open for an extended period; (2) the risky behaviours in food businesses occurred more frequently at dinner times on Fridays and Saturdays and during the day on Sundays; (3) male participants in household kitchens engaged risky behaviours more frequently than females. For example, compared to females, males were significantly more likely to dry/wipe their hands improperly and reuse unwashed utensils for other purposes. The Kitchen Life 2 project has allowed unprecedented access to real-life behaviours in kitchens. Data analysis is ongoing as a PhD project to identify the discrepancies and similarities between observed and self-reported behaviours.

Posters

F1 - Development of a risk-based code set for post-mortem inspection of broilers

Michał Majewski[a,b], Lis Alban[c,d], Désirée S. Jansson[e], Thomai Lazou[f], Nina Langkabel[g], Dragan Antic[j], Eija Kaukonen[h], Helena Wall[i], Madalena Vieira Pinto[k], Laila Østergaard[l], Ole Gyvelgaard Nielsen[l], Sergio Ghidini[m], Marianne Sandberg[a]

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

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m Department of Veterinary Medicine and Animal Sciences, Milan University, Lodi, Italy

Background: In Europe, broilers are inspected after slaughter by official veterinarians or official auxiliaries. Macroscopically visible lesions and contaminations are recorded, and unfit carcasses are removed from the food chain. Information about the reason for the condemnation is valuable for various stakeholders. However, procedures vary extensively between European countries, and the lack of uniform ways of reporting meat inspection findings makes it a challenge to analyse and compare data.

Objective: The objective was to develop a new harmonised and risk-based code set for post-mortem inspection of broilers, which would enable a detailed analysis of the data as well as implementation of computer vision systems in the future.

Materials and Methods: Information about national code sets used to registrate poultry condemnations in nine European countries was collected. Based on the most frequently recorded findings in the countries included in the study and considering harmonised epidemiological indicators for poultry meat and broiler welfare indicators, we developed a new harmonised risk-based code set for broiler carcasses.

Results: The resulting code set consists of 10 codes, which were the most frequently used reasons for condemnations in the countries included in the study, as well as three additional codes of importance for broiler welfare. These 13 codes can be assigned to the following areas of impact: health, welfare, quality and food safety.

Discussion and Conclusion

Harmonisation of the code list and the associated decision criteria would allow for conducting post-mortem inspection in the same way in all abattoirs and countries. Such a standardisation would enable a detailed analysis of the results. The next step will be to develop harmonised decision criteria defining the thresholds for condemnation based on lesion severity.

Perspectives: A harmonised code set, and associated decision criteria will favour implementation of computer vision systems in the future.

F2 - Attribution of human infections with Listeria monocytogenes to food sources and identification of source-specific risk factors thereof

Lapo Mughini-Gras[1,2], Julian A. Paganini[2], Ruoshui Guo[2], Claudia E. Coipan[1], Ingrid H.M. Friesema[1], Angela H.A.M. van Hoek[1], Maaike van den Beld[1], Sjoerd Kuiling[1], Indra Bergval[1], Bart Wullings[3], Menno van der Voort[3], Eelco Franz[1], Timothy J. Dallman[2]

(1) National Institute for Public Health and the Environment (RIVM), the Netherlands. (2) Utrecht University, the Netherlands. (3) Wageningen Food Safety Research (WFSR), the Netherlands.

Background: *Listeria monocytogenes* (*Lm*) can contaminate various food products due to its ability to form biofilms in food-processing environments and replicate at low temperatures, leading to foodborne disease. Tracing the sources of *Lm* is important to inform food safety policy.

Objective: To determine the contributions of different food sources of human listeriosis and identify risk factors at the point of exposure for human *Lm* infection of cattle, chicken or seafood origin.

Materials and Methods: *Lm* isolates from human cases (n=756) and different food sources (n=950) from national surveillance systems in the Netherlands (2010-2020) were whole genome sequenced. Questionnaire-based exposure data for human cases was also collected. Source attribution was performed using Random Forest models based on core-genome multi-locus sequence typing (cgMLST) data. Source-specific risk factors for human listeriosis were determined using beta-regression analysis on cgMLST-based attribution estimates.

Results: Human cases were mainly attributed to cattle (62.3%), chicken (19.4%), and seafood (16.9%). Specifically fresh meat (86.2%), including fresh bovine meat (43.7%) and fresh chicken meat (39.3%), accounted for most cases. Attributions derived from *Lm* contamination of either food products or their production environments as sources. Consuming steak tartare and smoked salmon increased the risk for cattle- and seafood-associated human *Lm* infections, respectively. No specific risk factors for chicken-associated human listeriosis were identified.

Discussion and Conclusion: *Lm* of cattle origin, specifically from fresh bovine meat, was estimated as the primary cause of human listeriosis in the Netherlands. This concurred with other European studies on *Lm*. Moreover, identified risk factors at human exposure level (i.e., steak tartare and smoked salmon) clearly pointed to cattle and seafood as attributable sources.

Perspectives: Joint analyses of core-genome and epidemiological data provide insights into the origins and transmission routes of human listeriosis, which guide prioritization and assessment of control activities in the food supply chain.

F3 - Unravelling the Genetic Determinants behind the resilience of Salmonella enterica on ready-to-eat Melon

Irene Esteban-Cuesta[1], Laura Führer[1], Steffen Prowollik[2], Weiping Chu[2], Michael McClelland[2], Claudia Guldimann[1]

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Background: *Salmonella enterica* is one of the most important foodborne pathogens worldwide. In 2022, *S. enterica* remained the second most commonly reported zoonosis and the most frequently reported causative agent for foodborne outbreaks in the EU. Infection mainly results from the consumption of contaminated food. To cause disease, *S. enterica* needs to survive and, in many cases, grow in the food matrix. Therefore, understanding the molecular mechanisms behind its resilience towards the stress conditions in different food matrices is crucial, not only for developing highly targeted methods to reduce pathogen fitness in various foods but also to better assess food safety risks.

Objective: In this study we aim to better understand the genomic basis underlying the interaction of *S. enterica* with ready-to-eat melon acknowledging the full complexity of the matrix.

Materials and Methods: Barcoded transposon mutant Libraries of *S. enterica* serovars Typhimurium, Enteritidis and Newport were screened on ready-to-eat melon to analyze genome-wide fitness effects of individual genes and the associated metabolic pathways. Analyses were performed at room (22 °C) and storage (8 °C) temperatures for 24 hours and 5 days, respectively. The aggregated abundances of the input and output libraries were statistically analyzed using DESeq2.

Results and Discussion: Representative genes showing a fitness effect during the interaction with ready-to-eat melon were selected for further competition assays between the wildtype and single gene deletion mutants of *S.* Typhimurium 14028s. Genes for which deletion was deleterious for growth on melon were involved in metabolism, cell surface structure and oligonucleotide binding. Positive selection occured in mutants with deletions in genes encoding several regulatory proteins and enzymes, as well as the DNA-binding transcriptional regulator *oxyR*.

Perspectives: These results could lead to highly targeted science-driven control measures, that may help reducing the burden of Salmonella in public health.

F4 - Presence of Campylobacter spp. on meat at retail

Lore Heyvaert[1], Muhammad Zeeshan Zafar[1], and Kurt Houf[1]

[1]University of Ghent, Belgium

Background: Current isolation methods for *Campylobacter spp.* in human and food microbiology focus on the isolation of the thermophilic species *Campylobacter jejuni* and *Campylobacter coli*. These methods hamper, or even do not allow the isolation of more fastidious or non-thermophilic *Campylobacter spp.,* resulting in the underestimation of their prevalence. Multiple studies have reported that applying less selective culture methods on human diarrheic samples results in the isolation of a wide range of *Campylobacter* species, other than *C. jejuni* and *C. coli,* with *Campylobacter concisus* and *Campylobacter upsaliensis* showing a high prevalence, enhancing their potential clinical relevance. Up until now, only one study has reported the recovery of these fastidious *Campylobacter* species in meat at retail.

Objective: Aims of this study are to apply a non-selective isolation method for *Campylobacter* on retail meat samples in parallel with the 10272-1 ISO procedure.

Materials and Methods: In the present study, a total of 293 retail meat samples including pork(n=106), chicken(n=88) and beef(n=61) were collected from supermarkets and butcher shops. An optimized filter method was used in parallel with a selective isolation protocol for thermophilic *Campylobacter spp.* in meat.

Results: Using the filter method, *Campylobacters* were isolated in 19,3% of chicken samples(n=17), 16% of pork samples(n=17) and 1,3% of beef samples(n=1). Isolates were identified as *C. concisus*(n=18), *C. jejuni*(n=13), *C. coli* (n=3) and *C. lari*(n=1). Using the ISO 10272-1 29.5% of chicken samples was positive, including only *C. jejuni*(n=20) and *C. coli*(n=5) and *C. lari*(n=1).

Discussion and Conclusion: Results of the study show that retail meat samples are contaminated with a greater diversity of *Campylobacter spp.* than is currently detected using the ISO 10272-1. The study confirms the association of *C. jejuni* with chicken meat samples(29.5%) and indicates an association between pork meat and the clinically relevant *C. concisus*(16%).

F5 - Genomic diversity of Arcobacter spp. in pigs

Lore Heyvaert[1] Charlotte Peeters[1] , Davide Buzzanca[2], Peter Vandamme[1] and Kurt Houf[1]

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[2]University of Turin

Background: Members of the genus *Arcobacter* are considered potential hazards to human health. *Arcobacter butzleri* and *Arcobacter cryaerophilus* are the main species associated with human gastro-intestinal illness. They are often isolated from food of animal origin, including pork products and are also frequently present in healthy pigs, suggesting pigs can function as asymptomatic carriers. Elucidating the transmission routes from animal reservoirs to humans has been challenging due to the extensive diversity of *Arcobacter*. At present, this diversity has only been studied using conventional typing methods such as Pulsed Field Gel Electrophoresis (PFGE) and Enterobacterial Repetitive Intergenic Consensus Polymerase Chain Reaction (ERIC-PCR).

Objective: In order to elucidate transmission routes and to identify animal reservoirs, a first aim is to assess the possible additional contribution of whole genome sequencing (WGS) as a method for strain characterization within *Arcobacter spp.* by comparing ERIC-PCR with phylogenomic analysis on a collection of closely related *Arcobacter* isolates. Additionally, the underlying mechanisms of genomic variations present are explored in a subset of relevant isolates to evaluate genomic mechanisms and drivers.

Materials and Methods: For these purposes, the gastro-intestinal tract of a pig was subdivided in 17 different sections from which both content and mucus were sampled. Using an *Arcobacter* selective protocol, a total of 135 isolates including 5 different species and 77 different ERIC types were retrieved from 11 different sections. Sixty-four isolates were selected based on genotype and gastro-intestinal section and sent for Illumina sequencing.

Results: Results confirmed the high genomic diversity within *Arcobacter* species, even within closely related isolates, but showed also discrepancies between strain delineation based on ERIC and different WGS tools.

Discussion and Conclusion: WGS resulted a promising tool to track *Arcobacter spp.* contaminations, to be taken into consideration in studies related to its transmission in farming and food handling environments.

F6 - Goat milk and fecal microbiome around parturition: a longitudinal study.

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Background: Total bacterial count in bulk milk (BMTBC) is an important quality parameter in goat milk. High bacterial counts can shorten shelf life, negatively impact cheese production, and result in milk price penalties for dairy goat farmers. Knowing the bacterial composition of milk, along with the role of fecal contamination on the milk microbiome, might allow farmers to implement preventive measures to control total bacterial count (TBC) in both individual goats and bulk milk.

Objective: We quantified the variations in size, composition, and diversity of the bacterial microbiome of bulk milk, individual goat milk and feces around kidding. Milk samples were analyzed using culturing, MALDI-TOF MS, 16S-qPCR, and 16S-rRNA. Fecal samples were analyzed with 16S-qPCR and 16S-rRNA.

Materials and Methods: In a longitudinal study on four Dutch dairy goat farms, we collected milk and fecal samples from 67 goats, along with 16 bulk milk samples around kidding.

Results: The farm where the goats were housed significantly influenced the composition and diversity of the bulk milk and the fecal bacterial microbiome. The bacterial microbiome composition of bulk milk originated from environmental, or goat related bacteria (*Staphyloccus spp., Streptococcus spp.*) or a combination of both sources. Individual milk samples were low biomass.

Discussion and Conclusion: Analyzing the bulk milk microbiome might help to identify the source of bacteria contributing to BMTBC, facilitating the implementation of preventive measures for controlling BMTBC. Although around kidding the individual goat milk samples can be regarded as low biomass samples, we found bulk milk samples which had a high relative abundance of goat related bacteria. Whether these bacteria were excreted by goats with intramammary infections in other stages of the lactation should be further investigated.

Perspectives: Analyzing the microbiome of bulk milk can help dairy goat farmers identify the source of bacteria contributing to the BMTBC.

F7 - Prevalence of Yersinia spp in the tonsils of pigs slaughtered in the UK

Rita Papoula-Pereira, Lottie Hay, Ruari O'Carroll, Marta Kis*, Dragan Antic

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* University of Zagreb, Faculty of Veterinary Medicine

Background: Yersiniosis, is the 3rd most common zoonotic disease in the EU. It is highly infectious and self-isolation for 48h due to acute gastroenteritis is often recommended. Infection is mainly through the consumption of undercooked pork or contaminated water.

Objective: Disease incidence in the UK, is much lower than the rest of Europe but this is suspected to be due to massive underreporting. Very few studies have investigated prevalence of Yersinia spp. in British food. In this study, we aim to partly address this gap and present data related to pork slaughtered in a large-scale abattoir.

Materials and Methods: We sampled 300 tonsils of pigs slaughtered. On all isolates confirmed to be *Yersinia spp*. we performed: direct plating for quantification; MALDI-TOFF for species identification and disc diffusion tests for antimicrobial susceptibility. Yersinia enterocolitica isolates were biotyped via indole, esculin, xylose trehalose reactions and serotyped via slide agglutination test for O3/O8/O9/O5.

Results: Out of the 300 samples, 133 were assumed to be positive for yersinia spp. MALDI-TOFF confirmed 122 samples as Yersinia enterocolitica or pseudotuberculosis. The remaining tests have been performed but are at analysis stage and will be ready for the conference.

Discussion and Conclusion: This study is the first to characterise the prevalence of Yersinia spp. in pigs slaughtered in the UK. The study shows a relatively high prevalence and is consistent with a recent study that has found a high prevalence of Yersinia in samples of pork taken at retail.

Perspectives: This study supports the hypothesis that the low prevalence of Yersiniosis is thought to be much lower in the UK compared to the rest of Europe due to underreporting. Further studies into the real prevalence of this pathogen should be instated so that food safety can be better managed, and the societal impacts of this infection mitigated.

F8 - Online gamification used in Undergraduate One Health teaching

Rita Papoula-Pereira

University of Liverpool, Institute of Infection, Veterinary and Ecological Sciences

Background: Due to Avian Influenza/ COVID, it was uncertain if physical samples for practical teaching would be possible for all sessions. To prevent different students having different experiences, a face-to-face meat inspection class in the BVSc, was replaced by a facilitated online virtual escape room. Students were surveyed on their experience

Objective:
1. Investigate engagement/ attendance of virtual escape room designed to replace a face-to-face session vs face to face sessions
2. Assess student's perception of the benefits of face-to-face vs virtual teaching vs online formative assessment (FA)
3.Assess correlation between teaching-approach preference, study behaviour and achievement?
4. Gage if student's perception of teaching sessions has any association with their perception of the teaching subject

Materials and Methods: The escape room was run on Microsoft Teams and students were divided into breakout rooms. All students were provided to links to OneNote workbooks with password protected sections that represented several scenarios. The session was facilitated. Following the session all students had access to an anonymous survey on the activity.

Results: Data is still at analysis stage and will be presented at the conference but the in-session student feedback and engagement with activity was mostly positive.

Discussion and Conclusion: The current and future generations are mostly composed of digital natives and more and more we are aware of different learning styles. If we develop different formats of teaching, there is scope to get more engagement from all students. In addition, it allows for "worldwide" teaching where experts can teach from anywhere enhancing the learning experience.

Perspectives: This format was used in the context of a pandemic where logistical issues led to the adaptation of teaching. However, the design has proven itself such a useful tool for students learning and logistical reasons that it has been continued beyond its intended use.

F9 - Occurrence and characterization of β-lactam-resistant Escherichia coli and Klebsiella pneumoniae in poultry farms and slaughterhouses in Greece

Anestis Tsitsos[1], Alexandros Damianos[1], Konstantinos Kiskinis[1],
Tilemachos Mantzios[1], Vasilios Tsiouris[1], Nikolaos Soultos[1], Anna Papa[2], Ilias Tyrodimos[2], Vangelis Economou[1]

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Background: Extended-spectrum-β-lactamase (ESBL) and carbapenemase-producing *Escherichia coli* and *Klebsiella pneumoniae* are associated with hospital-acquired infections and are commonly isolated across the poultry food production chain. However, there is scarce comprehensive data regarding the prevalence, spatiotemporal fluctuations and characterization of β-lactam-resistant bacteria in poultry farms and slaughterhouses.

Objective: To assess the occurrence, seasonal and regional variations and to characterize the β-lactam-resistant *E. coli* and *K. pneumoniae* in poultry farms and slaughterhouses in Greece.

Materials and Methods: A total of 224 environmental samples were gathered from poultry farms and slaughterhouses located in different geographical regions in Greece on a seasonal basis. Strains were selectively isolated using β-lactams and identified via MALDI-TOF MS. Antimicrobial susceptibility and presence of β-lactamase genes were evaluated. Protein profiles were analyzed to determine strain relationships, whereas the *E. coli* isolates were further classified into phylogenetic groups.

Results: The prevalence of β-lactam-resistant strains in farm and slaughterhouse environments was 15.0%/57.3% for *E. coli* and 11.0%/1.6% for *K. pneumoniae,* respectively. Significantly higher *E. coli* isolation rates were observed in warmer seasons. All strains were multidrug-resistant and phenotypically confirmed as ESBL/AmpC producers. Most strains carried ESBL/AmpC genes. Most *E. coli* isolates belonged to phylogroups A and B1. Proteomic analysis indicated relatedness among strains isolated from different regions and seasons.

Discussion and Conclusion: The poultry farm and slaughterhouse environment is a significant reservoir of β-lactam-resistant *E. coli* and *K. pneumoniae*. The selective isolation using β-lactams offered a more accurate representation of the prevalence of resistant bacteria in the environment.

Perspectives: Further studies are needed to assess the potential transmission risk of resistant strains or resistance genes from the farm and slaughterhouse environment to poultry meat.

The research work was supported by the Hellenic Foundation for Research and Innovation (HFRI) under the 3rd Call for HFRI PhD Fellowships (Fellowship Number: 6054).

F10 - Prevalence and characterization of β-lactamase-producing Escherichia coli and Klebsiella pneumoniae in poultry meat at the abattoir level in Greece

Anestis Tsitsos[1], Alexandros Damianos[1], Konstantinos Kiskinis[1], Tilemachos Mantzios[1], Vasilios Tsiouris[1], Elias Papapanagiotou[1], Nikolaos Soultos[1], Anna Papa[2], Ilias Tyrodimos[2], Vangelis Economou[1]

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Background: Extended-spectrum-β-lactamase (ESBL) and carbapenemase-producing *Escherichia coli* and *Klebsiella pneumoniae* are significant nosocomial pathogens frequently isolated from food matrices and patients. However, comprehensive data on the occurrence, spatiotemporal fluctuations, and characterization of β-lactam-resistant bacteria in poultry meat is limited.

Objective: To assess the prevalence, seasonal and regional variations and to characterize the β-lactam-resistant *E. coli* and *K. pneumoniae* in poultry meat at the abattoir level in Greece.

Materials and Methods: A total of 600 neck skin samples were collected from two poultry slaughterhouses located in different geographical regions in Greece on a seasonal basis. Strains were selectively isolated using β-lactams and identified via MALDI-TOF MS. Antimicrobial susceptibility, presence of β-lactamase genes and proteomic relationship of the isolated strains were evaluated. The *E. coli* isolates were further classified into phylogenetic groups, whereas one ertapenem-resistant *K. pneumoniae* isolate underwent whole-genome sequencing.

Results: The prevalence of β-lactam-resistant *E. coli* and *K. pneumoniae* was 40.8% and 3.3%, respectively. Most strains were multidrug-resistant. All *E. coli* and *K. pneumoniae* strains were phenotypically confirmed as ESBL/AmpC producers. One *K. pneumoniae* strain showed additional resistance to ertapenem. Most strains carried ESBL/AmpC genes, but no carbapenemase genes were detected. Most *E. coli* isolates belonged to phylogroups A and B1. Proteomic analysis indicated relatedness among strains isolated from different regions and seasons.

Discussion and Conclusion: Poultry meat remains a significant reservoir of β-lactam-resistant strains of *E. coli* and *K. pneumoniae*. The selective isolation using β-lactams provided a more precise depiction of the actual prevalence rates of resistant bacteria in poultry meat.

Perspectives: Further studies are needed to assess the potential transmission risk of resistant strains or resistance genes from poultry meat to humans.

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F11 - Antimicrobial resistance of Salmonella spp. to EU-Licensed Veterinary antibiotics in large and small ruminants: a meta-analysis

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Background: *Salmonella* spp. is the second leading cause of foodborne outbreaks, with antimicrobial resistance (AMR) in these bacteria posing significant treatment challenges and increasing the risk of severe infections

Objective: the objective of this study is to verify, through meta-analysis, the prevalence of *Salmonella* spp. in carcasses and/or organs of cattle, sheep and goats as well as their AMR against EU-Licensed Veterinary antibiotics

Materials and Methods: A total of 49 studies were selected troughtout booleams terms in Google Scholar, Scopus, and PubMed. The systematic review was performed in accordance to the PRISMA guidelines. The study assess the prevalence of *Salmonella* spp. in slaughterhouses. Based on the prevalence of the AMR of *Salmonella* spp. isolated from cattle, goat and sheep at slaughterhouses against the different antimicrobials, they are classified into three categories: low (≤5), high (>5-10≤) and very (high >10).

Results: The results of the meta-analysis found an 8.01% prevalence of *Salmonella* spp. in large and small ruminants (8.31% in cattle, 7.04% in goats, and 6.12% in sheep). Among 28 antimicrobials, 9 showed low, 8 showed high, and 11 showed very high resistance rates. *Salmonella* spp. displayed the highest resistance to penicillins, sulphonamides, quinolones, and aminoglycosides. Resistance to cephalosporins, important for treating human salmonellosis, was moderate, with cefazolin showing low resistance and ceftiofur being a veterinary-exclusive antibiotic. Quinolones like enrofloxacin (veterinary use) and ofloxacin (used for dogs and cats) showed increased resistance but posed no significant public health threat. High resistance to penicillins, such as ampicillin, may be linked to genes encoding extended-spectrum β-lactamases (ESBLs), with a 40% resistance rate observed in the meta-analysis.

Discussion and Conclusion: Despite these resistance concerns, the overall contribution of cattle, sheep, and goats to the AMR of *Salmonella* spp. and its public health impact is relatively low due to their low prevalence in carcasses and organs.

F12 - Antimicrobial resistance of Salmonella spp. isolated from cattle, sheep, and goats in slaughterhouses to the main antibiotics recommended for the treatment of salmonellosis: a meta-analysis

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Background: Salmonellosis is the second leading cause of foodborne illness in the EU. The infection ranges from mild to severe and can be life-threatening, especially for high-risk groups. Treatment is generally symptomatic, but antibiotics may be necessary in certain cases. The increasing antibiotic resistance of *Salmonella* spp. poses a public health threat.

Objective: The objective is to verify, through meta-analysis, the prevalence of *Salmonella* spp. in carcasses and organs of cattle, sheep, and goats, as well as their antimicrobial resistance (AMR) to antibiotics recommended for treating human salmonellosis.

Materials and Methods: Forty-nine studies were selected using Boolean terms in Google Scholar, Scopus, and PubMed, according to PRISMA guidelines. The study assessed the prevalence of *Salmonella* spp. in slaughterhouses. Based on the prevalence of AMR in *Salmonella* spp. isolated from cattle, goats, and sheep at slaughterhouses, antibiotics were categorized as having low (≤5%), moderate (>5-10%), or high (>10%) resistance.

Results: The meta-analysis showed an 8.01% prevalence of *Salmonella* spp. in large and small ruminants (8.31% in cattle, 7.04% in goats, and 6.12% in sheep). Resistance prevalence was ≤5% for 10 antibiotics, >5-10% for 4 antibiotics, and >10% for 6 antibiotics. The highest resistance was observed for cefixime (75.21%), ampicillin (30.49%), amoxicillin (14.55%), trimethoprim-sulfamethoxazole (13.70%), and chloramphenicol (12.23%). Scarce resistance was noted against cephalosporins and carbapenems.

Discussion and Conclusion: Generally, *Salmonella* spp. show low resistance to cephalosporins and azithromycin, ensuring satisfactory treatment outcomes when antibiotics are required.

Severe infections and/or more resistant strains remain susceptible to last-line antibiotics like carbapenems. However, increasing resistance to quinolones, first-line antibiotics for treating salmonellosis, poses a public health concern due to mutations in specific genes. The contribution of cattle, sheep, and goats to the increase in AMR of *Salmonella* spp. appears low given their low prevalence in slaughterhouses and low resistance to primary treatment antibiotics.

F13 - Status of biosecurity measures on family small ruminants farms in Portugal

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Background: Livestock production of small ruminants is a longstanding tradition in Portugal, primarily conducted on family farms with few animals. The emergence of infectious diseases can threaten the economic viability of these farms, making the implementation of biosecurity plans essential.

Objective: This study aimed to identify the types of biosecurity measures applied on small ruminant farms in Portugal.

Materials and Methods: A cross-sectional study was conducted on biosecurity knowledge and practices using a checklist of 88 questions, based on the biosecurity checklist from the Confederation of Portuguese Farmers.

Results: Farm limits and fencing: 53.3% of farms indicated possible contact with other animals, and 74.7% had incomplete fencing. Cleaning and disinfection: 85.3% of farms lacked plans for cleaning and disinfecting materials, equipment, and infrastructures. Premises Design: 82.7% of respondents believed their premises were appropriately designed for the number of animals. However, 69.3% lacked a maternity area, 48% lacked a kids' area, and 54.7% lacked a quarantine area. Feed traceability and storage**: Only 13.3% of producers ensured feed traceability, and 42.7% could not guarantee contamination-free storage. Welfare and health management: 44% of producers were unfamiliar with prophylaxis plans, though 98.7% dewormed their animals. Only 30% used vaccine prophylaxis programs, and 45.3% acquired animals without quarantining them, with 81% neglecting quarantine. Additionally, 86.7% lacked an emergency disease outbreak plan, and 34.7% did not isolate sick or suspected animals. Manure and carcass management: These were satisfactorily managed by 86.7% and 97.3% of farms, respectively.

Discussion: Unlike large, highly technical farms, small ruminant farms often lack basic biosecurity measures. Issues such as inadequate hygiene, acquiring animals from other farms, poor prophylaxis implementation, improper feed storage, and contact with other herds or wildlife compromise herd health and economic sustainability. Livestock family farms are crucial for sustainable agriculture, economic stability, cultural heritage, environmental health, and social cohesion. Supporting these farms and implementing tailored biosecurity measures is vital for their economic viability.

F14 - Microbiological Quality of Poultry Meat in Portuguese Retail

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Background: Contamination of poultry meat by spoilage and pathogenic agents often occurs during slaughter and processing. Typically, 1-day-old broiler chicks are sourced from hatcheries and transported to grow-out facilities, where they are raised for 4 to 8 weeks before slaughter. Following slaughter, broiler carcasses and viscera undergo further processing before being distributed to retail facilities, where they are sold as whole carcasses, fresh meat portions, or processed chicken products.

Objective: The main aim was to assess the level of microbiological contamination (deteriorative) of broiler meat (*Gallus gallus*) products, namely viscera (liver, heart, gizzard) and feet and neck purchased from retail markets and supermarkets.

Materials and Methods: Seventy-two samples of poultry meat purchased from local markets and supermarkets in North Portugal were analyzed for selected foodborne and spoilage microorganisms (Enterobacteriaceae, *Pseudomonas* spp., *E. coli*, moulds and yeasts, and total mesophilic and psychrotrophic bacteria). Respective ISO methods were applied and after incubation, typical colonies were enumerated and results were expressed in log cfu/g.

Results: The microbiological evaluation of spoilage microorganisms in the food samples showed that total viable count at 7ºC and 30ºC, *Enterobacteriaceae*, *Pseudomonas* spp., and yeasts were present in all samples. *E. coli* was present in 87.5% of samples and at least one mould specie was isolated from 30.6% samples. Microbiological counts (mean±SD) of different broiler meat are presented in Table 1.

Table 1. Microbiological counts (mean±SD) of different broiler products (log cfu/g).

Sample (N)	Total (72)	Feet (16)	Gizzard (14)	Heart (16)	Liver (14)	Neck (12)	p
Moulds and yeasts	0.38±0.6	0.49±0.70	0.48±0.797	0.13±0.342	0.43±0.745	0.38±0.57	NS
Enterobacteriaceae	4.39±0.1	4.24±1.02	4.40±1.26	4.64±1.10	4.13±0.779	4.56±0.69	NS
Psychrotrophic	6.03±1.2	6.94±0.91a	5.73±1.54b	5.79±1.20b	5.59±0.86b	6.01±0.9b	P<0.01
Mesophilic	6.12±1.0	6.93±0.79a	5.55±1.23b	6.05±0.10a	5.77±0.66b	6.20±0.7a	P<0.001
Pseudomonas spp.	4.07±1.2	4.61±0.79a	3.74±1.01a	4.00±0.82a	3.64±0.32b	4.14±1.03a	P<0.001
E. coli	2.36±1.3	1.78±1.28a	1.24±1.08ab	2.52±1.02ad	2.83±0.85ac	3.68±0.77d	P<0.001

NS: not significant

Discussion and Conclusion: Rearing on-farms, transport to slaughter, slaughter process, and retail market are all stages of food production with implications in hygiene and quality, where contamination can occur. Contact with equipment, food handlers, and exposure to various environmental sources pose significant hazards.

Perspectives: The potential routes of microbial contamination of products throughout the poultry production and supply chain are challenging for the food industry worldwide. To address the challenges, several measures can be reinforced such as stringent hygiene protocols at every stage from farm to processing facilities to retail outlets, training and education of farm workers and handlers, implementation of biosecurity measures and strict temperature control.

F15 - Measuring emotions by high-pitched vocalizations in a slaughterhouse of fattening pigs

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Background: The movement from the lairage pen to the stunning area constitutes one of the key points regarding animal welfare in pig slaughterhouses. When pigs are moved from the lairage to the stunning point, they can experience impeded movement which corresponds to a difficulty of movement of the pigs resulting in slipping and falling. High-pitched vocalizations (squealing or screaming) indicate both pain and fear since pigs are very prone to vocalize.

Objective: The human-animal relationship in a slaughterhouse of fattening pigs using CO_2 for stunning was assessed by registering high-pitched vocalizations (HPV).

Materials and Methods: The observations were conducted three times a day to assess three different farm batches in a total of 31 observation days. Two types of measures were taken while two individuals from the slaughterhouse staff moved groups of 10-15 pigs from the lairage pens to the beginning of a ramp where the pigs were moved as a group to the gas stunning system by hydraulic push gates. Investigators recorded whether any of the observed group of animals vocalized during each 20-second interval (focal sampling) and whether any pig vocalized just at the end of the 20-second interval (scan sampling). The 20-second evaluation periods and focal scanning were carried out during locomotion 12 times per batch.

Results: This study evaluated the human-animal relationship through the record of pig vocalizations. Higher counts of HPV are associated with more focal scanning vocalization, indicating a more stressful phase. Additionally, the use of automatic doors to move animals to the stunning area seems to reduce human-animal interaction. The present study also found a low occurrence of HPV and lower vocalization assessments before stunning.

Perspectives: HPV appears particularly useful in evaluating human-animal contact in a slaughterhouse of fattening pigs.

F16 - Tuberculosis in wild large game: food safety or occupational hazard?

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Background: Over time, it has been known that the zoonotic transmission of Tuberculosis (TB) to humans is closely linked to food issues, namely unpasteurized milk. However, the occupational character of zoonotic transmission, is in recent years the one that is most concerns, due to the transmission directly from animals to humans. And contact with large game species is no exception since there is a direct exposure of hunters and game managers to animals and carcasses infected by this zoonosis.

Objective: The study presented has as its main objective to highlight which the main sources of zoonotic TB infection related to the wild large game species.

Materials and Methods: During 7 hunting periods, diverse risk practices for the transmission of TB were directly observed at evisceration spots of carcasses in an epidemiological area at risk of TB in large game in Portugal: direct contact with carcasses without gloves or mask, evisceration procedure without personal protective equipment, final washing of contaminated carcasses and the place of evisceration, not properly destroying contaminated carcasses, among others risk practices.

Results: On several occasions, several incorrect procedures for carcasses' handling and evisceration, lack of biosecurity measures and personal protective equipment have been observed. It was also not observed extra care at evisceration spots with the handling of contaminated carcasses.

Discussion and Conclusion: It should be noted that the potential zoonotic occupational transmission of TB among the hunting stakeholders is an obvious risk. The successive use of the same non-hygienic equipment, the handling of potentially contaminated carcasses without safety and protective methods, and the formation of hazardous aerosols when handling and washing contaminated carcasses are the main risk practices to be highlighted.

Perspectives: Prevention, updated information, and training are the best tools to mitigate the risk practices for occupational zoonotic exposure to TB in this hunting-related population

F17 - Comparative assessment of pigs' ante-mortem inspection at three different lairage sites

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Background: Before animals are slaughtered, Official Veterinarians must carry out ante-mortem inspections which involve checking documents/identification and evaluating animal health and welfare requirements. During the visual inspection of pigs at a slaughterhouse (risk-based meat inspection), the findings of the ante-mortem inspection are essential for the official veterinarian to decide on the additional measures required for the post-slaughter inspection. Therefore, it is important to ensure the effectiveness of the ante-mortem examination.

Objective: Evaluate if the location of the ante-mortem inspection could impact its effectiveness.

Materials and Methods: Ante-mortem inspection was conducted, and data was recorded in three different locations: during unloading, outside and inside the pen. The batches used for the study were chosen randomly, and all data were collected by the same person.

Results: 9542 animals were observed in a total of 62 batches. The comparison of these three locations showed that there was indeed a very significant loss of information between the inspection conducted outside the pen and the other two locations. Furthermore, comparing unloading with inside the pen observations, the last recorded more observations.

Discussion and Conclusion: The way ante-mortem inspection is currently conducted, outside the pen, results in significant information loss. While inspection inside the pens may not be feasible for all pens in a slaughterhouse, it highlights the need to revise the methodology used to effectively utilize ante-mortem inspection as a tool to support risk-based meat inspection.

Perspectives: Implementing overhead walkways above the pens and entering high-risk batches can enhance the accuracy of ante-mortem inspections. Exploring remote inspection technologies can optimize resources and improve efficiency. Further research and policy updates are necessary to validate and integrate these new methodologies into standard practices.

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F18 - Ante-mortem inspection of pigs at the slaughterhouse: Procedures and relevance in risk-based meat inspection

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Background: Risk-based meat inspection (RBMI) was introduced in Europe in 2014, involving the evaluation of each batch's risk to determine its suitability for visual inspection or, if deemed unsuitable, the need for additional procedures. According to Regulation (EU) 2019/627, the official veterinarian shall carry out additional post-mortem inspection procedures whenever a possible risk to human health, animal health or animal welfare is present, which can be detected by the result of the ante-mortem inspection.

Objective: Evaluate the effectiveness of ante-mortem inspection as a tool for assessing the risk of batches: Can ante-mortem conditions act as predictors of post-mortem lesions?

Materials and Methods: Ante and post-mortem conditions were collected to establish correlations through a case-control study involving 245 animals. For the case group, animals presenting conditions were selected, while apparently healthy animals formed the control group. Selected animals were properly marked ante and post-mortem. Correlation and Odds ratios were calculated to assess ante-mortem conditions as predictors of post-mortem lesions

Results: Significant correlations ($p < 0.05$) were observed between variables, such us coughing and pneumonia (OR = 6.7); delayed growth and arthritis (OR = 5.1), enteritis (OR = 14.5); lameness and arthritis (OR = 14.9); non-ambulatory status and bone trauma (OR = 546); abscesses and arthritis (OR = 15).

Discussion and Conclusion: Ante-mortem inspection correlates with post-mortem lesions, affirming its potential as a risk assessment tool in slaughterhouses. Further studies are essential to validate findings and enhance inspection methodologies for improved risk assessment accuracy.

Perspectives: Implementing enhanced ante-mortem inspection protocols could optimize RBMI in slaughterhouses, fostering safer meat production practices and public health.

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F19 - Presence of foodborne pathogens and hygiene indicators on surfaces and self-reported food safety knowledge of food-handlers in Greek university cafeterias

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Background: Approximately 40% of foodborne outbreaks in the EU occur in cafeterias or restaurants within workplaces and education institutions. (1) Three key factors at consumption are associated with foodborne diseases: food safety knowledge, behavior, and handling practices. (2,3,4) Food handlers are often unaware of key food hygiene aspects (e.g., foodborne pathogens; temperature control). (2,3,4)

Objective: The aim was to collect data on food hygiene knowledge of food handlers, and the presence of foodborne pathogens and hygiene indicators in the environment of university canteens in Thessaloniki, Greece.

Materials and Methods: The self-reported food hygiene knowledge of employees in 15 university cafeterias was surveyed via an anonymous questionnaire with 15 multiple-choice questions. One kitchen sponge and cloth, and swabs (refrigerator door handle, food tray, refrigerator shelf, kitchen counter, table) were collected per canteen and analysed for *Campylobacter*, *L. monocytogenes*, and *Salmonella*, *S. aureus, E. coli* and coliforms (culture-based methods). Overall, 105 samples and 25 questionnaires were analysed.

Results: Most food handlers correctly replied to general food hygiene and temperature control questions (57.7 – 100%). Enrolment in food hygiene training in the past was statistically significantly correlated ($p < 0.05$) with recognising sanitizers as potential chemical hazards (53.8%). Except for *Salmonella*, food vehicles most likely associated with other foodborne pathogens were recognised only by approximately 30% of respondents. *S. aureus* was detected in the kitchen sponge and cloth of one canteen, and coliforms in 13 – 20% of the tested environmental samples.

Discussion and Conclusion: Though the minority of respondents was aware of specific foodstuffs being most likely associated with foodborne pathogens other than *Salmonella,* such pathogens were not detected in the environmental samples apart from *S. aureus* in one cafeteria, and the overall level of hygiene was satisfactory.

Perspectives: The detected food hygiene knowledge gaps revealed food safety educational needs of food-handlers in Greek university cafeterias.

F20 - Wild boar as brucellosis spillover to Bísaro pig, an autochthonous Portuguese breed

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Background: Brucellosis caused by *Brucella* spp. is a disease with public health importance that affects vertebrates, and it is one of the most important zoonoses in the Mediterranean region, which includes Portugal. Although it is widespread in all vertebrates, brucellosis is increasing in wildlife and constitutes a growing risk of spillback to livestock and human.

Objective: The aim of this study was to investigate the presence of antibodies against *Brucella* spp. in sympatric wild boar and Bísaro pigs (traditionally raised outdoors), in Vinhais county (Northeast of Portugal).

Materials and Methods: From November 2022 to June 2023, blood samples, using convenience sampling, were collected from the endocranial venous sinuses of the 66 hunted wild boars. Blood samples from 66 Bísaro pig were taken during bleeding procedure at abattoir. All blood samples were centrifuged immediately after receipt and serum were stored at -20°C until tested by indirect enzyme-linked immunosorbent assay (i-ELISA), using a commercial ELISA kit (ID Screen® Brucellosis Serum Indirect Multi-species, ID.vet Innovative Diagnostics, Grabels, France).

Results: It was observed that 27 wild boar and 8 domestic pigs were exposed to *Brucella* spp. pointing to a seroprevalence of 40.9% (95% CI: 29.1% – 52.8%) and 12.1% (95% CI: 4.3% – 20.0%), respectively.

Discussion and Conclusion: The results raise awareness of the importance that wild boar may have in the dynamics of this zoonotic disease in the region and its potential role as spillover to Bísaro pigs, an autochthonous breed with social an economic relevance in Vinhais county.

Perspectives: The results of this work emphasise the need to carry out further studies to better understand the epidemiology of the disease between sympatric wildlife/livestock/human from a One Health perspective.

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F21 - Studies on the contamination and fate of pyrrolizidine alkaloids and pyrrolizidine alkaloid N-oxides in milk and dairy products (yogurt, cheese)

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The spread of ragworts has been observed with concern by food and feed control authorities. They contain liver-toxic and carcinogenic pyrrolizidine alkaloids (PA) and their N-oxides (PANO). Farmland or extensively managed pastures in Germany are often infested with PA/PANO-containing weeds, leading to PA/PANO exposure of animals through feeding of contaminated preserved feed (silage, hay) or during grazing. Additionally, a PA/PANO transfer from feed into milk has been reported[1,2]. Mulder et al. (2018) already found traces of PA in milk from retail (n=187)[3]. PA/PANO exposure poses a potential risk to human and animal health and needs to be further investigated.

Milk monitoring was carried out to describe current PA/PANO contaminations in milk from individual farms in two model regions in Germany (Bavaria, Schleswig-Holstein). In total, 228 samples were analyzed. We hypothesized that milk from single farms is potentially higher contaminated than retail milk from large dairies. The results showed that 11% of the milk samples were contaminated with PA/PANO. The sum concentrations of PA/PANO in the contaminated samples were between 0,007 µg/L and 5,6 µg/L (median 0,024 µg/L).

Next, the fate of PA/PANO from contaminated milk into dairy products (yogurt and cheese) was investigated by tracking PA/PANO along the production process. We assumed that processing steps like microbial fermentation and separation of material flows (e.g. whey) alter the PA/PANO concentrations in the dairy products compared to the initial milk[4]. We found that during cheese production, the PA/PANO are likely to follow the aqueous phases since whey or the brine solution (in case of feta production) were contaminated. Microbial fermentation during yogurt and cheese production can lead to changes in the PA/PANO-profile as PANO were reduced to their corresponding PA. Within the investigated production processes, there was no level of PA/PANO degradation that would equal a detoxification of the final products.

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F22 - Impact of an extended bleed-to-evisceration interval on the microbiological quality of on-farm slaughtered cattle carcasses

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Background: In the 2021 revision of Annex III of regulation 853/2004, the European Commission allows slaughter of cattle at the holding of provenance outside the emergency slaughter context. There is a lack of knowledge about the microbiological risk involved in extending the time between bleeding and evisceration, when bleeding takes place on the farm and evisceration at the abattoir.

Objective: This study aimed to obtain relevant, currently lacking, data regarding the microbiological consequences of extending the evisceration delay in cattle up to 4 hours *post-mortem*.

Materials and Methods: Five Holstein dairy cattle were slaughtered at the experimental farm of the University of Liège. A laparotomy of the paralumbar fossa was performed to expose the visceral peritoneum of the large intestine. Non-destructive sampling technique was used. Deep abdominal muscles were swabbed every 45 minutes thereafter, up to 3 hours and 45 minutes after the first sampling. Samples were suspended in saline solution and spread on Plate Count Agar (PCA), Violet Red Bile Glucose (VRBG), and Tryptone-bile-glucoronate (TBX) culture media and incubated. The enumeration results were analyzed as "individual data points", and "compiled data points" and subsequently converted to log CFU.

Results: Only two samples on TBX and two samples on VRBG showed minor colony growth on the culture media. All the results for ACC, *Enterobacteriaceae*, and *E. coli* were below the more severe threshold prescribed by the Belgian health authority.

Discussion and Conclusion: All these observations were consistent with those made by other authors, who reported no significant bacterial growth on samples of muscle from sheep carcasses for 24 hours at 20 °C.
The various results obtained suggest that consuming meat from cattle slaughtered on the farm should not pose an increased risk to human health.

Perspectives: The experiment should be replicated with more diverse animal profiles and in warmer temperatures.

P1 - The Burden of Disease in Swiss Pork Production

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Background: Animal diseases significantly impact economic efficiency and productivity of food systems. Within the Global Burden of Animal Diseases (GBADs) programme the Animal Health Loss Envelope (AHLE) metric was developed to consider economic losses due to all possible causes of disease burden.

Objective: Within the GBADs programme, this study's aim was to estimate the AHLE, biomass and economic value of Swiss swine production.

Materials and Methods: Production and economic data from national databases, industry and literature were used to estimate biomass, capital value and AHLE. We developed production models for most common farm types and performed gross margin analyses. The input levels required to produce a target number of slaughter pigs in a disease-free scenario were determined through backward calculation. Farm-level estimates were extrapolated to population level. Based on these values, the AHLE was estimated as the gross margin difference between baseline production and the 'ideal' disease-free scenario. This 'ideal' scenario was based on AHLE definitions and empirical data from top-performing farms.

Results: For the Swiss pig population, total biomass for 2021 was estimated at 83'395 tonnes liveweight (58'483 tonnes for fattening pigs, 24'912 tonnes for breeding pigs), and total capital value at CHF 247 million, (CHF 210 million attributable to fattening pigs, CHF 37 million attributable to breeding pigs). Preliminary AHLE estimates are currently being validated with industry data. Final results will be available and presented at the conference.

Discussion and Conclusion: Our capital value estimate highlights the significance of pork production within the Swiss agri-food system. The AHLE demonstrates that scenarios with lower disease burden require lower input levels to produce the same number of slaughter pigs, with implications for sustainable food production and economic efficiency.

Perspectives: Our model can be adapted to other countries and livestock categories. Biomass, capital value and AHLE estimates for livestock production are useful for optimal resource prioritisation and allocation.

P2 - First, do no harm: Field evaluation of an independent Rift Valley fever vaccination campaign and the impact on pregnant livestock in a semi-pastoral area in Kenya

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Background: Rift Valley fever (RVF) is a devastating zoonotic and livestock disease causing abortion and death of young animals. Without human vaccines, livestock vaccination is key to protect public health and livelihoods. The effectiveness of RVF livestock vaccination is complicated by reactive strategies following early warnings and limited coverage.

Objective: This study assessed an independent vaccine event in Loitokitok sub-county, southern Kenya.

Materials and Methods: We sampled vaccinated animals and had a unique opportunity to understand the impact of the live-attenuated Smithburn vaccine on pregnancy in a field setting. Vaccinated pregnant dams were prioritized for sampling.

Results: We sampled 150 animals including 123 females (76 sheep, 47 goats) and 23 males (6 sheep, 17 goats) across two herds in Imbirikani and Risa villages, with 41 and 47 days between vaccination and sampling. Over this time, farmers reported 23 sheep abortions and nine goat abortions and at sampling, we counted 289 sheep and 79 goats in total. Yet, anti-RVFV IgG antibodies were detected only in 43.3% (65/150) of adult animals, and we did not find a statistical association with the animals' village, sex, species, or age. We sampled 108 dams and matched them to 74 offspring. Seroprevalence was higher in the aborted dams sampled (75%, 6/8) compared to all adults ($p=0.08$). Abortions occurred between 18-32 (median: 24.5) days post-vaccination, and dams vaccinated earlier in gestation were more likely to abort ($p=0.001$). Offspring had low seroprevalence (21.6%, 16/74), and seropositivity was associated with having a seropositive mother ($p=0.05$).

Discussion and Conclusion: Abortions associated with vaccination is concerning, particularly given the low seroprevalence achieved, but this design does not allow for determination of causation.

Perspectives: Nonetheless, these results highlight the need to improve livestock vaccination strategies, including safe vaccines for pregnant animals, to reduce vaccine hesitancy in vulnerable livestock-owning populations. Models are useful to assess strategies to maximize efficacy with limited vaccine stocks.

P3 - Trends in *Mycobacterium bovis* prevalence in badgers across Wales, 2017-2023

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Background: Bovine tuberculosis (bTB) is one of the most important animal health issues facing Wales. Wildlife reservoirs, for example the European badger, are a known barrier to eradication of bTB. Passive surveillance of bTB in badgers has been in place across the whole of Wales since September 2014.

Objective: This study examines estimated prevalence of *Mycobacterium bovis* infection in badgers from 2017-2023 and compares them with 2014-2016 survey results[1].

Materials and Methods: Badger carcasses found dead are collected and undergo post-mortem examination, sampling, and laboratory culture for *Mycobacterium bovis,* the causative organism of bTB. The badgers found may have died following road traffic accidents or other causes.

Results: From 2017 to the end of 2023 the apparent bTB prevalence in badgers was 7.1% (136/1905), similar to the findings from the 2014-2016 survey (7.3%)[1]. The worst affected area in 2014-2016 (High TB Area East) saw a reduction in prevalence in 2017-2023 to 16.6%.

High TB Area West increased in prevalence to 9.1% in 2017-2023, compared with 7.4% previously[1]. Results in the first half of the reporting period were responsible for this (2017-2020 = 11.1%); from 2021-2023 the prevalence was 6.5%.

Intermediate TB Areas of Wales saw increases in apparent badger bTB prevalence during 2017-2023 compared with 2014-2016. In 2021-2023 prevalence in the Intermediate TB Area North more than tripled (4.4%) compared with 2014-2016 (1.4%).

Discussion and Conclusion: BTB prevalence estimates in badgers across Wales as a whole have remained stable over a 10-year period (2014-2023). However, regional differences exist within this, with some areas showing deterioration in recent years. Considerable work is needed to achieve Officially TB-Free status in Wales by the target year of 2041.

Perspectives: Monitoring the bTB status of badgers in Wales provides valuable information on environmental levels of disease in the country. Active surveillance would provide more certainty around prevalence estimates which may aid eradication efforts.

P4 - Automated detection of wing fractures in broiler chickens using computed tomography and artificial intelligence

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Background: The prevalence of wing fractures is a reliable animal welfare indicator routinely monitored in broiler chicken slaughterhouses. However, the current practice consisting of human visual inspection and manual counting has some significant limitations including subjectivism and high variability among inspectors. Possibly new imaging techniques like Computed Tomography (CT) scanning combined with Artificial Intelligence can help to standardize the inspection and consequently provide closer animal welfare monitoring.

Objective: To develop a deep learning model categorizing isolated wing samples as broken (BRO) or healthy (HEAL) based on their CT scan.

Materials and Methods: In total 306 chicken wings have been collected in the chicken slaughterhouse and labelled as BRO (n=134) or HEAL (n=172). All the wings have been CT scanned in veterinary clinic in Utrecht. The binary classification model (BRO or HEAL) based on CT scan was implemented in PyTorch using custom 3D convolutional neural network architecture.

Results: The model performance assessed on the test dataset (never seen before data) was: Accuracy: 95.23%, Precision: 100%, Recall: 89.29%, AUC: 97.24%.

Discussion and Conclusion: This model provides high accuracy and precision (more than 95%) for detecting wing fractures based on the CT scans. Recall reaches almost 90%, so there is potentially a room for improvement by e.g. adding more samples. However, the model is not able to detect soft tissues injuries (e.g. bruises or haematomas), which was already proven by our earlier research.

Perspectives: The automated detection of wing fractures based on CT scans can contribute to more accurate, standardized and reliable animal welfare monitoring in poultry slaughterhouses. Challenges as CT scanner investment cost, scanning time and radiological safety need also to be taken under consideration. However, these are the limitations, which might be overcome in the future due to rapid development of technologies.

P5 - Toxigenic *Corynebacterium Ulcerans* infections in animals in England and Wales

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Background: Toxigenic *Corynebacterium ulcerans* (*C. ulcerans*) is a zoonotic bacterium capable of causing human diphtheria. Its natural history in animals is not well understood. We have observed increasing reports of the bacterium from animals in England and Wales since 2018. UKHSA and APHA developed collaborative guidance for management of positive animals and their human contacts.

Objective: Describe toxigenic *C. ulcerans* infections in in animal index cases reported to APHA from 2018 to 2023.

Materials and Methods: UKHSA notifies APHA of toxigenic *C. ulcerans* animal isolations. APHA liaises with the animals' veterinarian and Health Protection teams, providing advice on management of the animal. We describe animal index cases reported.

Results: Between 2018 to 2023, 60 unrelated animal cases were identified. Clinical presentation varied. Bacteriological clearance was unsuccessful following initial treatment for nine cases. One animal never cleared infection despite successive treatment. 48 contact animals were swabbed for 23/33 cases with close animal contacts; from seven cases, nine contacts were positive. All contact positives cleared infection after one treatment. Swabbing human contacts of animal index cases has not identified any cases. A limited number of animals have been identified following detection of human index cases.

Discussion and Conclusion: Animal infection is not reportable and index cases arise from clinical investigation. Asymptomatic animals may remain undetected. Reported cases likely underrepresent true prevalence. Reasons for increasing detections are unclear. Co-morbidities can complicate clearance. Animal-animal transmission can occur, but risk factors for this need further investigation. Metaphylactic treatment of animal contacts may be challenged given low positivity rate of contact animals. Zoonotic transmission is evidenced, although directionality cannot be determined. Further work is needed to understand infection dynamics and zoonotic implications of positive animals.

Perspectives: Toxigenic *C. ulcerans* animal infection can be controlled to protect human and animal health through a proportionate One Health approach.

P6 - Association between antimicrobial use in livestock and antimicrobial resistance in *Salmonella* and *Campylobacter* from human gastrointestinal infections, and *Escherichia coli* from urinary tract infections

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Background: Antimicrobial use (AMU) promotes antimicrobial resistance (AMR) in bacteria. Since 2009, the Netherlands has substantially reduced AMU in livestock. However, to which extent this reduction influenced AMR among human infections remains unclear.

Objective: To assess associations between AMU in livestock and AMR in *Salmonella* and *Campylobacter* isolates from human gastrointestinal infections, and *Escherichia coli* from urinary tract infections (UTI).

Materials and Methods: A registry-based ecological study was conducted using AMU and AMR data in livestock and humans from different national surveillance programmes in the Netherlands (2008-2019). Associations between livestock AMU and human AMR were assessed per homologous antimicrobial-class using multivariable regression models, accounting for potential co-selection. The commonest *Salmonella* serotypes (Enteritidis and Typhimurium), and the *Campylobacter* species *jejuni* and *coli*, were included. Associations were studied per every animal reservoir-serotype/species combination. For *E. coli* UTI, besides AMU in livestock, also age, gender and AMU in humans were accounted for. A 1-year lag was assumed for an effect of livestock AMU on human AMR.

Results: Positive associations were found mainly between livestock AMU and AMR among human *S.* Typhimurium infections. Livestock AMU was negatively associated with AMR among human *Campylobacter* infections. For AMR in *E. coli* UTI, both positive and negative associations with livestock AMU were observed. Associations were generally stronger within human or animal populations than between them.

Discussion and Conclusion: Potential effects of livestock AMU on AMR among human zoonotic infections are not always unambiguous, varying according to pathogen subtype and animal reservoir in question. Confounding concerns mainly infections from imported foods and international travel. Non-significant associations for *E. coli* UTI provide further evidence for their limited zoonotic origin.

Perspectives: The occasionally unclear potential effects of livestock AMU reduction on human AMR levels stress the need for additional efforts to mitigate public health risks from AMR emergence and spread.

P7 - Leveraging Data Visualization for Effective Avian Influenza Surveillance

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Background: The Italian surveillance programme for avian influenza (AI) viruses is tailored for poultry and wild birds, following Annex II of Delegated Regulation (EU) 2020/689 guidelines, encompassing both passive and active components. Data on surveillance activities are systematically collected, collated, and analyzed to timely inform decision-makers and health authorities. Advances in web-based technologies now enable creating user-friendly interfaces that present complex data graphically, highlighting critical information like disease trends, spatial distribution, and other pivotal surveillance metrics.

Objective(s): Building an interactive dashboard with the following objectives:
Monitor: Keep track of current disease status and trends.
Respond: Take timely actions to prevent and control outbreaks.
Educate: Provide relevant information to farmers and veterinarians.
Collaborate: Facilitate data sharing and collaboration among public health officials, researchers, and policymakers.

Materials and Methods: Raw surveillance data collected since 2016 were integrated with the national poultry registry, prepared and analysed to feed maps and graphs in an interactive dashboard, which was developed in R Shiny and deployed on a cloud service.

Results: The dashboard interface includes three tabs, allowing users to visualize and filter data on maps and time series bar charts:
Overview: Displays the number of poultry holdings and wild birds tested in selected regions and provinces;
Poultry: Contains details about poultry species and productive types sampled and tested, categorized by results, activity type (active or passive), and date;
Wild Birds: Contains details about wild bird species and productive types sampled and tested, categorized by results, activity type (active or passive), and date.

Discussion and Conclusion: By leveraging health intelligence and dashboards, stakeholders gain an up-to-date comprehensive view of avian influenza surveillance in Italy. This approach supports timely decision-making, effective resource allocation, transparent public communication, and expert evaluation of disease trends.

Perspectives: Designed for reusability, the AI surveillance dashboard serves as template for diverse applications, with future plans to integrate metrics guiding prompt risk mitigation measures implementation.

P8 - The Effect of Animal Welfare Levels on Economic Performance in Dairy Cattle Farms

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Background: The relationship between animal welfare and economic impact is a critical area of study, as improvements in animal welfare practices can lead to significant economic benefits for the dairy sector.

Objective: The aim of this study is to investigate the impact of animal welfare on the economic performance of dairy cattle farms in Karaman Province in Türkiye.

Materials and Methods: Economic data were obtained through face-to-face interviews from 91 farms and the welfare of dairy cows was assessed using the ANI 35L/2000 method. The farms were categorized based on rearing methods (tie-stall and free-stall system) and on scale (small, medium and large). According to ANI scores, the farms were classified into five groups: poor, average, acceptable, good, and very good.

Results: The study's findings indicate that the cost/revenue ratio was 1.21 for small-scale farms, 1.25 for medium-scale farms, and 1.28 for large-scale farms. For tie-stall farms, this ratio was 1.17, and for free-stall farms, it was 1.26. According to ANI score groups, the cost/revenue ratio was 1.17 in the poor group, 1.19 in the average group, 1.25 in the acceptable group, 1.30 in the good group, and 1.29 in the very good group. The profitability factor was 14.65 in the poor group, 16.04 in the average group, 19.86 in the acceptable group, 22.70 in the good group, and 22.18 in the very good group. By ANI score groups, the marginal profit increased from 57.63 TL in the poor group to 392.23 TL in the acceptable group.

Discussion and Conclusion: The findings strengthen the view that higher levels of animal welfare are associated with better economic performance indicators in dairy farming.

Perspectives: Future research may explore long-term trends and investigate other factors influencing economic performance in dairy farming, including environmental and social aspects.

P9 - **Carcass collection in outbreaks of highly pathogenic avian influenza in wild birds: does it make a difference?**

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Background: Highly pathogenic avian influenza (HPAI) has affected wild birds globally in recent years, often resulting in extensive mortality. Where mass mortality occurrs, mitigation options to prevent onward transmission of the virus are limited. The main strategy proposed is carcase collection.

Objective: A veterinary risk assessment (VRA) was commissioned by a governmental department to assess the risk of onward transmission of HPAI H5N1 to other wild birds, wild mammals, and captive birds, and how carcase collection may influence the likelihood of transmission.

Materials and Methods: A qualitative VRA was conducted, based on extant literature and expert opinion, and has been reviewed by relevant expert groups. A quantitative framework to estimate the impact of carcase removal on HPAI spread in wild birds was also developed.

Results: Carcase collection reduced the likelihood of onward transmission to other wild birds in areas of low bird density because in such areas carcasses represented the main source of infection. Collecting carcasses was not considered to alter the likelihood of transmission in areas of high bird density, where contact with live, infected birds and environmental contamination with faeces are the main sources of infection. However, the uncertainty around these estimates is high. The mathematical model supported the qualitative findings that carcase collection has a limited impact on onward disease spread in wild birds.

Discussion and Conclusion: The VRA has informed Scottish policy around HPAI control in wild birds, as well as operational decisions at local level, and the VRA has also identified keys areas for further empirical research, such as the relative contribution of wild bird carcasses vs. live birds to transmission.

Perspectives: Although this VRA does not provide definitive conclusions, it represents a robust and transparent approach to support decision-making on a subject that can be extremely challenging to address due to the scarcity of available evidence.

P10 - Investigating the impact of various emissions reduction strategies on the resilience and economic viability of the Danish livestock supply chain

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Background: Livestock farming is a considerable contributor to global greenhouse gas emissions and is associated with climate change. Reduction strategies of emissions are therefore needed and are being proposed by governments worldwide.

Objective: This study aims to analyze the impact of various emissions reduction strategies on the Danish livestock sector, taking into account the potential disruptions of the supply chain and the economic viability.

Materials and Methods: A modeling framework will be developed for typical Danish livestock farms, including cattle, pigs, small ruminants, and mixed farms. The framework considers the input-output flows of goods, such as feed used per kilogram of meat produced, and estimated average emissions (e.g., CH_4, NH_3, N_2O, CO_2) across different production types, health statuses and feed compositions. We will explore the impact of different emission reduction strategies on the livestock sector through the following scenarios:
i. 30% reduction of animal production by randomly removing livestock farms from production.
ii. Targeted removal of farms based on their input-output emission values to maximize emissions reduction.
iii. Removal of farms to minimize the negative economic impact on the livestock industry.
iv. Using a generic optimization algorithm to find the best combination of maximizing emissions reduction and minimizing the negative economic impact by re-arranging livestock production.
v. Following the optimization, we will introduce a highly contagious animal infectious disease outbreak to determine the stress resistance threshold for the Danish livestock sector.

Results: The study will introduce an input-output framework that incorporates emission estimations and interventions designed to obtain a sustainable livestock production in Denmark, across species, production systems, feed compositions and different health status of Danish farms.

Discussion, Conclusion and Perspectives: A target analysis of the consequences of emission reduction strategies is needed to minimize emissions while maintaining supply chain and economic stability.

P11 - Insect-mediated Transmission of Pathogens in Domestic Pigs: A Systematic review

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Background: Flies and beetles are ubiquitous insects in pig farms, raising concerns about their potential role in pathogen transmission. Effective biosecurity measures on farms require a clear understanding of these transmission pathways.

Objective. The present study aims to investigate the existing evidence for pathogen transmission by flies and beetles to domestic pigs.

Materials and Methods. Following the PRISMA guidelines, a comprehensive search of PubMed®, Scopus, and Web of Science databases was conducted with a focus on peer-reviewed literature published between 2007 and 2023, specifically from Europe and North America. The search identified 1062 initial records, of which 39 articles met the inclusion criteria after screening and evaluation.

Results. Among the selected studies, 87.2% (34/39) focused exclusively on flies, 2.6% (1/39) focused solely on beetles, and 10.3% (4/39) included both flies and beetles. Overall, only four studies provided conclusive evidence of the transmission of pathogens. Among them, three studies included viruses, namely, ASFV, PRRSV, and VSNJV (transmitted by flies), and one study described canthariasis caused by beetle larvae. For 18 pathogens (17 through flies and one through beetles) the transmission evidence is considered as “likely”, and for eight pathogens the literature analyses suggested that flies or beetles may “potentially” play a role. Contrary to the expectation, two studies concluded that the transmission of ASFV by blow fly larvae and PRRSV by stable fly is “unlikely”.

Discussion and Conclusion. Through a systematic review, adult flies emerged as potential contributors to the transmission of 27 pathogenic agents to pigs within and between farms. However, there is a notable scarcity of studies that have convincingly demonstrated conclusive evidence of the role of insects, particularly flies and beetles, in pathogen transmission.

Perspectives. Further large-scale field investigations should aim to explore the role of insects in the transmission of pathogenic agents to domestic pigs.

P12 - A preliminary analysis of antimicrobial use in cats in a Veterinary Hospital

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Background: In 2021 we initiated an antimicrobial stewardship program at the University of Porto Veterinary Teaching Hospital (UPVet). To prioritize interventions, information on current antimicrobial use (AMU) and prescription habits in companion animals was required. Despite the routine use of a clinical software by the clinical staff, this information was not readily available. Therefore, a pilot-study was designed, focussing on invoiced antibiotics for feline patients over a two-month period.

Objectives

- Assess the ease of data extraction and it´s quality
- Characterize the feline population at UPVet
- Characterize AMU in this population

Materials and Methods: A cross-sectional study included all feline patients invoiced between 1st January and 29th February 2024, at UPVet. Data were extracted from clinical software and paper-based files, and an Excel database was created with information on the cat population, visit types, and AMU.

Results: A total of 281 cats were seen in 385 visits. The sex distribution was similar, with 35% neutered cats. Most cats were European shorthair (77%) and from Porto Municipality (50%). Visits included 212 consultations, 51 hospitalizations and 24 surgeries, of which 15%, 57% and 8%, respectively, had antibiotics invoiced. Of the 42 cats with antibiotic invoices, 50% had more than one antibiotic. The most invoiced antibiotics were enrofloxacin (26%), amoxicillin+clavulanic acid (21%), ampicillin (18%), and metronidazole (13%). Administration routes were primarily oral (29%) and intravenous (31%).

Discussion and Conclusion: Major difficulties were encountered during data extraction of the clinical software, requiring manual consultation of patient files. Important information on diagnosis and prescribed antimicrobials was often lacking. The highest AMU was observed for hospitalized cats, and this area could be prioritised regarding antimicrobial stewardship.

Perspectives

- To improve data entry within the clinical software by the clinical staff
- To develop a better system to monitor and review AMU patterns for improvements, as the current method was too time-consuming

P13 - An international disease monitoring tool to estimate the likelihood of entry of animal health hazards from legal trade of live animals and products of animal origin imported from different countries (IDM+)

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Background: Trade of live animals and products of animal origin (POAO) carries an inherent risk of spreading pathogens.

Objective: To provide biosecurity assurances for imports of live animals and POAO into Great Britain, the International Disease Monitoring Plus (IDM+) model assesses the likelihood of disease entry from an animal health perspective from legal, commercial imports.

Materials and Methods: The IDM+ tool is a semi-quantitative risk assessment tool that combines prevalence data, import volumes, and expert opinion on country- and commodity-specific mitigation measures to derive an entry risk score for each country, commodity, and pathogen combination. Overall, the model includes more than 550 commodity types, 125 pathogens, and 55 countries. The model utilises publicly available data on the prevalence of pathogens in countries and volumes of commodities imported into the UK.

Results: Examples of the model output are presented as comparisons of the aggregated risk likelihoods for representative commodity categories imported from hypothetical countries with different volumes of exported commodities and sanitary status.

Discussion and Conclusion: The model considers changes in global pathogen distribution and trade volumes to provide ongoing and rapid appraisal of the entry likelihood of hazards of interest, enabling efficient border control inspections. Moreover, the model is versatile in its presentation of results, allowing for trade volume weighting and required likelihood thresholds. This flexibility makes the model suitable for a variety of purposes, including prioritisation of border inspections and in-country audits, rapid output generation for emergency outbreak assessments, and assessing risk from specific imported consignments.

Perspectives: The IDM+ model can be utilised by any country to assess import risks of live animals or POAO. Data inputs can be easily updated and the model is quick to run with a largely automated process, highlighting it as a valuable tool that can be utilised in time-constrained environments.

P14 - Spatio-temporal distribution of European surveys on zoonosis in wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*)

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Background: Europe has a marked population of wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*). They can be a source of zoonotic infections for cohabiting humans.

Objective: This systematic review aimed to examine the spatiotemporal tendencies and sanitary profiles of surveys on zoonotic diseases of wild boars and red deer in Europe in 15 years (2006–2020).

Materials and Methods: Through the search strategy "((sus scrofa OR wild boar OR cervus elaphus OR red deer) AND (zoonosis OR zoonot* OR infectious disease))" in Pubmed and ScienceDirect databases. Pursuing the inclusion criteria: species of interest – wild boar and red deer, established zoonosis and presence of natural infection and the exclusion filters: European study, specified a timeline (2006–2020), printed in English and with open-access.

Results: 194 European surveys issued in indexed journals were included after revising all abstracts and eliminating unrepeated articles.
Geographically, there was a disparity in the survey distribution pattern across different geographic areas, but there is a predominance of studies on this subject in southern Europe.
Temporarily, it is observed an increasing tendency over 15 years under study.
The majority of attention is paid to zoonoses such as the Hepatitis E virus, Toxoplasmosis, Trichinellosis, Salmonellosis, and Tuberculosis while analysing the sanitary profile of the qualifying surveys.

Discussion and Conclusion: The main conclusions, it could be affirmed that most of the publications on large game zoonoses have increased over the years, and focusing on southern Europe. The zoonoses that stand out are mostly foodborne diseases such as Hepatitis E and Toxoplasmosis, instead of those mostly occupational transmission such as Tuberculosis.

Perspectives: The potential risk of these zoonoses is highlighted for veterinarians, game managers and hunters, therefore, in the future, more training in this area for these stakeholders should be provided.

P15 - EARS-Vet: A European network for surveillance of antimicrobial resistance in veterinary medicine

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Background: In the EU, surveillance of antimicrobial resistance (AMR) in animals primarily focuses on monitoring at slaughter and food thereof. An important gap is monitoring of AMR in diseased animals. This is critical to guide antimicrobial stewardship in veterinary medicine, and more generally to support evidence-based management of AMR in animals in Europe.

Objective: Paralleling EARS-Net in the human sector, the EARS-Vet network aims to monitor AMR in bacterial pathogens from livestock and companion animals. EARS-Vet also intends to act as a knowledge hub to strengthen and harmonize AMR surveillance in veterinary medicine across Europe.

Materials and Methods: EARS-Vet was initiated in 2018 as part of the EU Joint Action on AMR and healthcare-associated infections (EU-JAMRAI). Activities so far have consisted in reviewing national systems for surveillance of AMR in animal pathogens across Europe, as well as defining the objectives, scope and standards of EARS-Vet. In addition, a pilot study involving 9 countries was conducted in 2022.

Results: In 2020, 11 out of 27 EU/EEA countries had a national surveillance system of AMR in animal pathogens. However, these systems were highly diverse. Building on the existing monitoring activities, an initial common scope including six animal species and 11 bacterial species was defined. The pilot study gathered antimicrobial susceptibility testing (AST) data from 140,110 isolates, and demonstrated substantial variations of AMR levels, both among and within countries.

Discussion and Conclusion: We have built a network of European scientists with a strong interest to monitor AMR in veterinary medicine at the EU level. Key issues at this stage include the lack of data from many EU/EEA countries, harmonization of AST methods, and the absence of many AST interpretation criteria.

Perspectives: Further development of the network will occur as part of EU-JAMRAI2 (2024-2027) that aims to make EARS-Vet a full-scale and sustainable initiative.

P16 - Habitat suitability of *Ixodes ricinus* ticks carrying pathogens in North-East Italy

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Background *Ixodes ricinus* ticks are ubiquitous in Europe, including North-East Italy. These ticks are important vectors of several zoonotic pathogens of public health relevance. Information on pathogen circulation in a given area helps assessing the risk of exposure to these pathogens upon tick bites.

Objective To predict the habitat suitability range of *Ixodes ricinus* ticks carrying the zoonotic pathogens *Borrelia, Rickettsia* and/or *Anaplasma/Ehrlichia* spp. in North-East Italy, and to identify their relevant environmental predictors.

Materials and Methods From 2015 until 2021, ticks were repeatedly sampled at 26 sites in North-East Italy. Pathogens carried by the collected ticks were detected via PCR assays. Both separate and joint habitat suitability models were built for *Borrelia, Rickettsia* and *Anaplasma/Ehrlichia* spp., based on ecological niche modelling using Maxent; 25 environmental determinants potentially related to tick habitat suitability were used as input parameters.

Results The predicted suitable habitat distributions revealed several hotspots in the most central part of the study area in terms of probability of presence of the pathogens in the ticks. Key environmental predictors were temperature, rainfall and altitude, and vegetation index for specific pathogens (*Rickettsia* and *Anaplasma/Ehrlichia* spp.).

Discussion and Conclusion The study area provides widespread suitable habitats for *I. ricinus* carrying pathogens such as *Borrelia*, *Rickettsia* and *Anaplasma/Ehrlichia* spp. The identified hotspots allow for awareness campaigns amongst local communities to mitigate the health risks resulting from exposure to tick-borne pathogens.

Perspectives Future research should focus on risk mapping, determining tick bite incidence in the area as well as infection probability upon tick bite. This will further help identifying areas with increased disease risk.

P17 - Veterinarian assistance in Portuguese animal shelters

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Background: Shelter medicine is an emerging specialisation. Nevertheless, information about veterinarian assistance in Portuguese animal shelters is scarce.

Objective: The aim of this study was to characterise veterinarian assistance in Portuguese animal shelters.

Materials and Methods: An electronic questionnaire was sent to 65 associations (AS) and 97 municipal (MS) shelters. Questions focused on animals' frequency of observation, veterinary assistance (more than one option possible), and treatments lacking veterinary supervision. Descriptive statistical analysis was performed.

Results: Twenty five AS and 42 MS responded. Animals were observed daily in 76.2% MS and 80% AS, 4-6 times per week (AS 8%; MS 14.3%), 1-3 times per week (AS 8%; MS 4.8%), and less than 1 time per week (AS 4%; MS 4.8%). Veterinary assistance was reported to be performed by shelter veterinarians in 44% AS and 90.5% MS, by external veterinarians in external practices in 72% AS and 40.5% MS, and by external veterinarians in the shelter in 36% AS. Treatments lacking veterinarian supervision were reported by 16% AS but no MS.

Discussion and Conclusion: In the majority of both shelter types, animals were observed daily by a person qualified to recognize pain and/or disease. Clinical assistance by shelter veterinarians occurs more frequently in MS than in AS, because MS are public organisations where the presence of a veterinarian is mandatory. A high proportion of the MS still use external veterinarian assistance, suggesting that internal services are insufficient. Treatments without veterinarian supervision targeted emergency lesions caused by animal-animal aggressions. Animal observation should be guaranteed daily and supported by a manual of procedures, ensuring immediate medical treatment. The range of veterinarian services should be optimised.

Perspectives: Characterise animal shelters to understand their specificities and constraints.

P18 - Cross-sectional survey of anti-*Toxoplasma gondii* antibodies in feral cats from an urban area in Northwest of Spain

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Background: Feral or free-roaming cats living in colonies are tolerated and deliberately fed in certain urban and peri-urban areas although their proliferation is a matter of concern due to public nuisance, cat impact as opportunistic predator and their potential as source of infection of zoonotic diseases such as toxoplasmosis (McCarthy et al., 2013).

Objective: The aim of our research was to estimate the prevalence of seropositive cats to *Toxoplasma gondii* in feral cats from the city of León and to investigate associate risk factors.

Materials and Methods: A total of 160 serum samples were collected between January 2022 and March 2024 from feral cats captured within the trap-neuter-release programme implemented in León, a city located in the northwest of Spain (Castilla y León region). Anti-*T. gondii* antibodies were detected using a quantitative ELISA (VetLine Toxoplasma ELISA® NovaTec).

Results: Seroprevalence of toxoplasmosis among feral cats was 37.97% (95% CI 30,38-46,03) and mean concentration of specific IgG was 181.27 IU/mL (SD 52.56) among positive cats. The colony was the only risk factor identified. Indeed, results allowed to classify colonies in three categories: low, medium and high risk according to their seroprevalence ($Chi^2=24.94$; $p=0.071$) and mean concentration of specific antibodies ($F=2.49$; $p=0.002$).

Discussion and Conclusion: Our results confirm a high seroprevalence of anti-*T. gondii* antibodies, similar to previously described in other studies in the Iberian Peninsula (Gauss et al., 2003; Miró et al., 2004), and allow for the identification of hotspots with high pathogen exposure.

Perspectives: Monitoring and further studies to identify risk factors that favour *T. gondii* transmission in certain urban or peri-urban locations are highly recommended. Moreover, hygiene and sanitary measures together with sanitary education should be implemented to minimize risk of cat-human transmission.

P19 - Evaluation of the most common zoonotic diseases published by the medical community in Portugal in the last decade. Comparative analysis with EFSA/ECDC reports

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Background: Gathering and analyzing information from scientific publications about the occurrence of human zoonotic diseases, in addition to what is reported to EFSA/ECDC, can provide valuable insights into the epidemiology of these diseases. Moreover, these findings indicate the level of concern within the medical community. Both data sets are crucial for effectively supporting the development of surveillance and control programs tailored to each country.

Objective: In order to evaluate the significance of human zoonotic diseases in Portugal, an analysis of medical community's scientific publications over the past 10 years was conducted.

Materials and Methods: The literature review included original papers published in peer-reviewed journals between January 2012 and October 2023, concerning the top 5 human zoonotic diseases in Portugal described on EFSA/ECDC reports between 2012 and 2021: campylobacteriosis, salmonellosis, brucellosis, listeriosis and Q Fever.

Results: Regarding the top 5 human zoonotic diseases more prevalent in Portugal, out of a total of 301 scientific national publications in the past 10 years, 100 were on campylobacteriosis, 83 on brucellosis, 78 on salmonellosis, 20 on listeriosis and 20 on Q fever.

Discussion and Conclusion: In the past 10 years, the number of scientific publications in Portugal on the five most prevalent human zoonoses in the country has followed a similar ranking as that presented in the EFSA/ECDC reports. The only exception is brucellosis, for which there are more publications than for salmonellosis. It seems that brucellosis stills an important disease in Portugal, probably mostly related with consumption of contaminated food and contact with infected livestock. By understanding and mitigating risk behaviors, and implementing robust control measures, the incidence of brucellosis can be significantly reduced.

Perspectives: A prevalence assessment is necessary, with data on the geographic distribution of zoonotic diseases in Portugal, as well as an assessment of risk factors and sources of infection.