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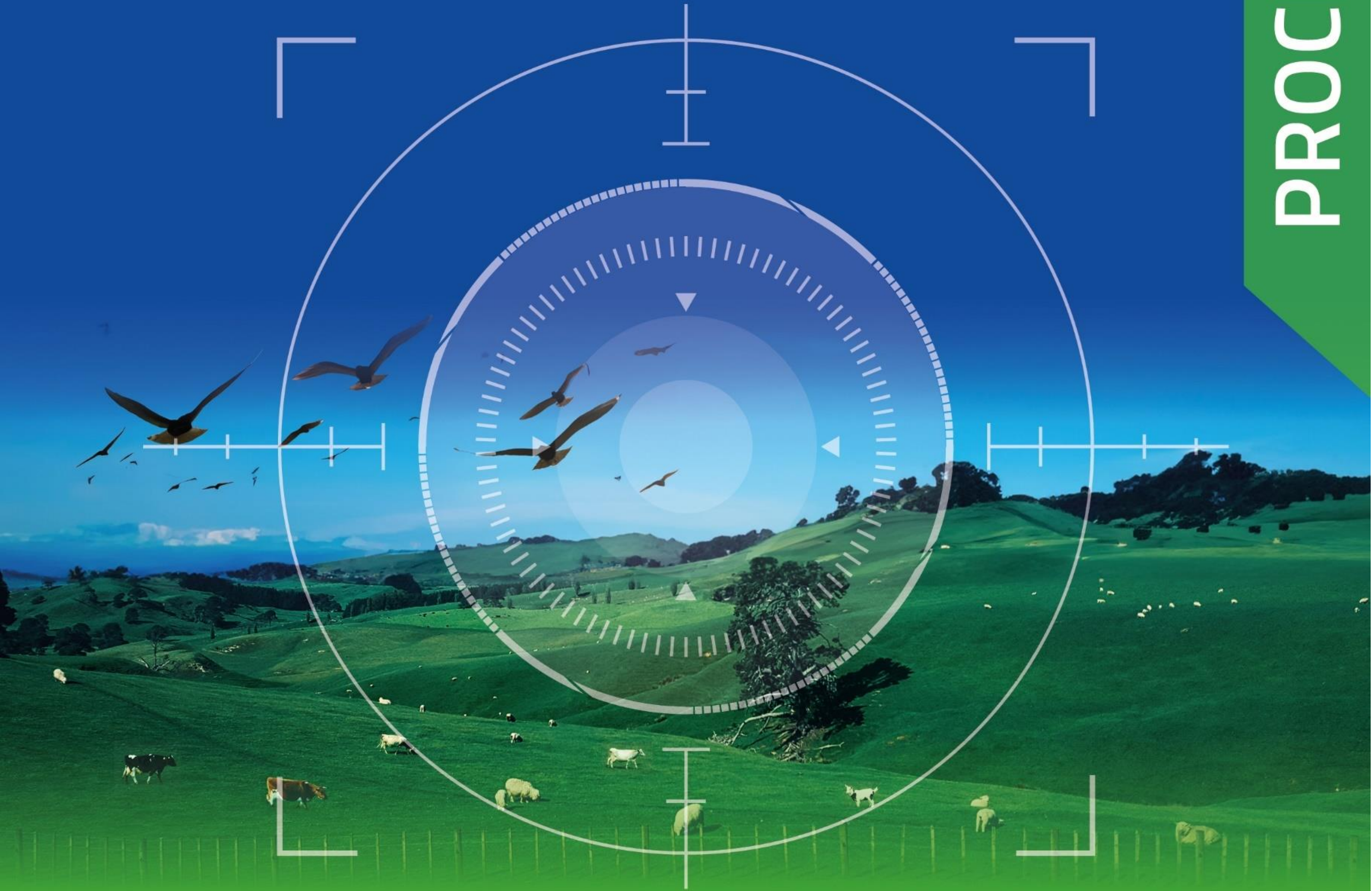

Horizon scanning
in veterinary epidemiology

17-19 April 2024
Château de Colonster, University of Liège
Allée des Érables 4000 Liège - Belgium

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HORIZON SCANNING IN VETERINARY EPIDEMIOLOGY

Welcome

to the AESA 33th anniversary International Symposium !

It is our pleasure to welcome you in Liege at the second international symposium in Animal Epidemiology of the Association of Epidemiology and Animal Health (in French, Association d'Epidémiologie et de Santé Animale, AESA). The AESA aims to enhance the interest and education and to stimulate research in the field of veterinary epidemiology and animal health, mainly by organizing workshops, conferences, and symposia and by providing scientific support in those matters.

Despite increased interest, research and some investment in veterinary epidemiology and animal health, the scale of the task for the future is considerable for epidemiologists and many challenges remain or new challenges will arise. This reason together with the 33th anniversary of our association are explaining the title of our international congress: **« Horizon scanning in veterinary epidemiology »**. With a look at the present, in order to anticipate the orientation of the future is the main idea of this topic. This big challenge needs sharing of information, exchange, brainstorming, interdisciplinary approach (e.g. social and economic sciences) and connectivity.

Considering these epidemiological challenges, do we need to adapt the epidemiological approach or not? Invited speakers with international appeal will try to find answers for the future in eleven different sessions concerning the Academia and Government work hand-in-hand to support wildlife conservation, protect public health and prevent the next pandemic, the one health veterinary drug resistance, the bee management practices including biosecurity and sustainability, the artificial intelligence assistance, video games and other digital tools in epidemiology, the participatory epidemiology, the emerging and vector-borne diseases, the one health integrated surveillance, the molecular biology and bio-informatics in epidemiology and finally the biological weapons and epidemiology.

In addition of this variety of interesting subjects, we will give young scientists the opportunity to present their work during different parallel sessions during the two days symposium (oral presentations and posters).

At the end of the symposium, five prizes will be attributed to the best presentation by AVIA-GIS, ARSIA, AMCRA, UREAR-ULiege and AESA.

We thank the Heliport brewery (Brasserie Héliport) for its hospitality in the splendid setting of Colonster Castle of the University of Liege.

A special thanks to the board members of the Scientific Committee and the AESA Organization Committee.

We appreciated all the work that had been fulfilled during the organization of this meeting as well during the evaluation of the submitted proceedings, abstracts and posters. We can be proud of the obtained results.

On behalf of the boards of the AESA we wish you a pleasant and stimulating and inspiring meeting.

Best regards,

Prof. Dr Claude Saegerman
E
AESA President

Organizing committee

Dr Géraldine Boseret, Dr Fabiana Dal Pozzo, Dr Laurent Delooz,
Dr Valérie De Waele, Dr Jean-Yves Houtain, Dr Mathieu Hubaux,
Dr Marie-France Humblet, Dr Ludovic Martinelle, Dr Axel Mauroy,
Prof. Claude Saegerman, Prof. Damien Thiry

Scientific committee

Member	Institution	Role
Prof. Claude Saegerman	University of Liège	President
Prof. Benoît Muylkens	University of Namur	Vice-president
Prof. Jean-Paul Dehoux	Catholic University of Louvain	Vice-president
Prof. Damien Thiry	University of Liège	Member
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Program

Wednesday, April 17, 2024

13:00	**17:00**	**Workshop**	**One Health Quantitative Risk Assessment**	*Prof. Claude Saegerman (ULiège)* *Prof. Maria Eleni Filippitzi (Aristotle University of Thessaloniki, GRC)*	**Salle Carpay**
13:00	**17:00**	**Workshop**	**Spatial visualization of health events: A hands-on practical with R**	*Prof. Timothée Vergne (ENVT, Toulouse - FRA))* *Dr. Brandon Hayes (ENVT, Toulouse - FRA))*	**Salle bleue**
18:00	**23:00**	**Ice breaking dinner**			**Salle Creative**

Thursday, April 18, 2024

8:00	**09:00**		**Registration**		***Hall***
09:00	**09:20**		**Opening ceremony and Introduction to the international symposium**	*Prof. Claude Saegerman - President of AESA*	***Salle de Lecture***
Session 1		**Wildlife**	Chairwoman:	***Dr V. De Waele***	***Salle de Lecture***
09:20	10:00	Keynote	**How can Academia and Government work hand-in-hand to support wildlife conservation, protect public health and prevent the next pandemic ? (video conference)**	***Dr. Anne-Lise Chaber*** *(University of Adelaide - AUS)*	
10:00	10:15	Selected oral presentations	Usutu virus circulation in wild birds, Wallonia 2023	*Laura Duran Ilán* *(ULiège-BEL)*	
10:15	10:30		In vitro and in vivo characterization of four bacteriophages targeting Aeromonas salmonicida	*Salomé Desmecht* *(ULiège-BEL)*	
10:30	10:45		An R-Shiny application to assess the risks of introduction of infectious animal diseases in Belgium	*Xavier Simons* *(Sciensano-BEL)*	
10:45	**11:15**		**Coffee Break**		***Péristyle***
Session 2A		**Veterinary Drug Resistance**	**Chairwoman:**	**Dr F. Dal Pozzo**	**Salle Bleue**
11:15	11:45	Keynote	**Veterinary Drug Resistance in a One Health Perspective**	***Dr Laeritia Lempereur*** *(FAO - One Health & Disease Control Group - BEL)*	
11:45	12:00	Selected oral presentations	A first One Health integrated analysis of antibiotic resistance surveillance data in France	*Lucie Collineau* *(ANSES - FRA)*	
12:00	12:15		The consumption of veterinary antibacterial products in Belgium in 2022 and its evolution since 2011	*Maries Lissens* *(AMCRA - BEL)*	
12:15	12:30		Challenges on data collection on antibiotic use in companion animals and horses	*Bénédicte Callens* *(AMCRA - BEL)*	
Session 2B		**Bee Health**	**Chairwoman:**	***J.S. Ocaña Cabrera***	***Salle de Lecture***
11:15	11:45	Keynote	**One Health, Bee Management practices including biosecurity & sustainable beekeeping**	***Dr. Giovanni Formato*** *(IZSLT– ITA)*	
11:45	12:00	Selected oral presentations	Sweet stingless beekeeping from the middle of the world	Joseline Sofia Ocaña Cabrera – *(ULiège- BEL)*	
12:00	12:15		BeeToxWax: real time tool for calculation of the toxicity risk of waxes that have been subjected to a pesticide analysis	Claude Saegerman *(ULiège - BEL)*	
12:30	**14:00**		**Lunch & Posters session**		***Péristyle***

SESSION 3A		MODELISATION IN EPIDEMIOLOGY	Chairman:	Prof. C. Saegerman	Salle Bleue

14:00	**14:30**	**Keynote**	**Modelisation in epidemiology : for which purpose ?**	***Prof. Timothée Vergne*** *(Université de Toulouse – FRA)*
14:30	**14:45**	**Selected oral presentations**	Modeling High Pathogenicity Avian Influenza: Integration of Sociological and Environmental Factors	*Maryem Ben Salem* *(ANSES – FRA)*
14:45	**15:00**		Predicting mosquito biodiversity and abundance using land use and climate changes (videoconference)	*Antoinette Ludwig* *(Public Health Agency – CAN)*
15:00	**15:15**		A highly efficient ELISA to specifically detect CCHFV antibodies in animals and humans	*Philippe Bevilacqua* *(ID-VET - FRA)*

SESSION 3B		SOCIO-ECO EPIDEMIOLOGY	Chairman:	*Dr L. Delooz*	*Salle de Lecture*

14:00	**14:30**	**Keynote**	**Socio-eco epidemiology**	***Prof. Niemi Jarkko*** *(NNRI - FIN)*
14:30	**14:45**	**Selected oral presentations**	Stability and lytic activity assessment in milk of bacteriophages targeting Escherichia coli causing bovine mastitis	*Jacob Diderich* *(ULiège – BEL)*
14:45	**15:00**		Antimicrobial resistance characterization of MRSA and MRSP isolated in dogs and cats in Belgium	*Suzanne Dewulf* *(UGent – BEL)*
15:00	**15:15**		Comparaison of herd mortality rates in Wallonia	*Julien Evrard* *(ARSIA – BEL)*

15:15	**15:45**	**Coffee Break**	***Péristyle***

SESSION 4A		DIGITAL TOOLS IN EPIDEMIOLOGY	Chairman:	Dr L. Martinelle	Salle Bleue

15:45	**16:15**	**Keynote**	**Artificial intelligence assistance, video games and other digital tools in Epidemiology**	***Ir. Sébastien Picault*** *(INRAe – FRA)*
16:15	**16:30**	**Selected oral presentations**	New real time biosecurity tool in your hands	*Claude Saegerman* *(ULiège – BEL)*
16:30	**16:45**		Horizon scanning for plant pests at EFSA : tools and methods	*Magali Larenaudie* *(EFSA – FRA)*
16:45	**17:00**		Optimizing surveillance strategies of highly pathogenic avian influenza in live bird markets across southeast Asia	*Brandon Hayes* *(ENVT – FRA)*

SESSION 4B		PARTICIPATORY EPIDEMIOLOGY	Chairman:	*Dr J.-Y. Houtain*	*Salle de Lecture*

15:45	**16:15**	**Keynote**	**The added-value of participatory epidemiology**	***Dr. Bryony Jones*** *(Animal &Plant Health Agency – UK)*
16:15	**16:30**	**Selected oral presentations**	Surveying tick control practices on dairy farms in subtropical areas of continental Ecuador	*Valeria Paucar* *(ULiège – BEL)*
16:30	**16:45**		Assessing acaricide treatment expenses on dairy farms in subtropical areas of Ecuador	*Valeria Paucar* *(ULiège – BEL)*
16:45	**17:00**		First Expert Elicitation of Knowledge on Drivers of Emergence of Bovine Besnoitiosis in Europe	*Claude Saegerman* *(ULiège – BEL)*

18:00	**19:00**	**Visit of the « Plants World Observatory » of University of Liège**	
19:00	**23:00**	**AESA 33rd anniversary gala dinner**	***Péristyle***

Friday, April 19, 2024

8:30	**09:00**		**Registration**		***Hall***
Session 5			**Emerging and Vector-borne diseases**	Chairman: ***Prof. D. Thiry***	***Salle de Lecture***
09:00	**09:40**	**Keynote**	**Emerging and Vector-borne viral diseases**		***Dr Gaëlle Gonzalez*** *(ANSES – FRA)*
09:40	**09:55**	**Selected oral presentations**	Forest dynamics and acari-borne diseases: lessons from a scoping review (videoconference)		*Nolwenn Blache* *(VetAgro Sup -FRA)*
09:55	**10:10**		Genetic diversity of Ehrlichia ruminantium strains in West Africa, Amblyomma variegatum, tick populations		*Tidjani Ayole Djiman* *(ULiège – BEL)*
10:10	**10:25**		Bovine besnoitiosis: A serious threat to animal health in Belgium		*Laurent Delooz* *(ARSIA – BEL)*
10:25	**10:55**		**Coffee Break**		***Péristyle***
Session 6A			**One Health**	**Chairman:** **Dr. A. Mauroy**	**Salle Bleue**
10:55	**11:25**	**Keynote**	One health integrated surveillance		***Dr Pascal Hendrikx*** *(CGAAER – FRA)*
11:25	**11:40**	**Selected oral presentations**	RAG-CA and RAG-V-EZ - two initiatives from the FASFC to sustain authorities facing emeging zoonoses		Axel Mauroy (FASFC – BEL)
11:40	**11:55**		Cross-sectional serosurvey of HEV in Belgian pig farms and identification of risk factors		Constance Wielick (ULiège – BEL)
Session 6B			**Molecular biology and bio-informatics**	**Chairman:** ***Prof. C. Saegerman***	***Salle de Lecture***
10:55	**11:25**	**Keynote**	**Added value of molecular biology and bio-informatics in epidemiology**		***Dr. Steven van Borm*** *(Sciensano – BEL)*
11:25	**11:40**	**Selected oral presentations**	Uncovering New Pathogens in Bovine Diseases through Comparative 16S rRNA sequencing		Fabien Grégoire (ARSIA -BEL)
11:40	**11:55**		A new pen-side test to confirm RVF clinical suspicions in the field		*Philippe Bevilacqua* *(ID-VET - FRA)*
11:55	**12:10**		Evaluation of the performances of a M. avium subsp. paratuberculosis Ab ELISA in young cattle		*Jean-Yves Houtain* (ARSIA -BEL)
12:10	**13:30**		**Lunch & Posters session**		***Péristyle***
Session 7			**Biological weapons**	**Chairwoman:** **Dr M.-F. Humblet**	**Salle Bleue**
13:30	**14:10**	**Keynote**	**Biological weapons and epidemiology**		***Prof. Maria J. Espona –*** *(Catholic University of Argentina)*
14:10	**14:25**	**Selected oral presentations**	Veterinary students' perception of zoonotic diseases and their prevention through an online survey in three Belgian universities		Marie-France Humblet (ULiège - BEL)
14:25	**14:40**		Synergistic approaches to gastrointestinal nematode control in sheep and goat flocks		François Claine (ARSIA – BEL)
15:00	**15:30**		**Oral presentations and posters awards (Avia-GIS, ARSIA, UREAR-ULiège, AESA, AMCRA)**	*Guy Hendrickx - AVIA-GIS*	***Salle de Lecture***
15:30	**16:00**		**Closing Ceremony**	Prof. Claude Saegerman - President of AESA	***Salle de Lecture***

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Workshops

Workshop 1 One Health Quantitative Risk Assessment

Prof. Claude Saegerman[1] , *Prof. Maria Eleni Filippitzi* [2]

[1] DVM, MSc, PhD, Dipl. ECVPH, Claude Saegerman is a full professor in Epidemiology, Quantitative Risk Assessment and Biosecurity. He is director of the Research Unit Epidemiology and Risk Analysis applied to veterinary sciences in the Faculty of Veterinary Medicine, University of Liège, Belgium

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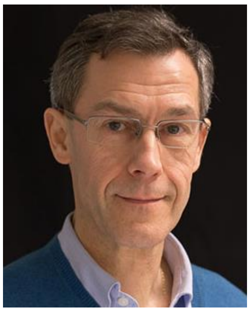
[2] DVM, MSc, PhD, Dipl. ECVPH, Maria Eleni Filippitzi is assistant professor at the Aristotle University of Thessaloniki, Greece. She is a specialist in Veterinary Epidemiology.

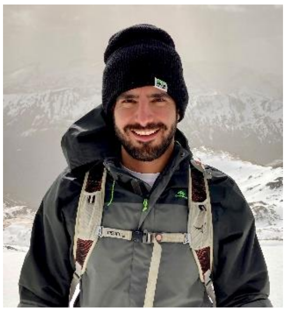


Workshop summary

The goal of this workshop is to provide attendees with the knowledge and tools needed to perform a One Health Quantitative Risk Assessment (OH-QRA). SARS-Cov-2 from an infected patient (human) to a cat will be the example followed. In practice, participants will construct the OH-QRA using a step-by-step process: (i) Drawing the risk pathway; (ii) Translation of event diagram; (iii) Probability estimation of each event; (iv) Data input search; (v) Modelling the risk and express the risk estimate; (vi) Introduction of mitigation measures in the model and estimation of their effect on the risk; (vii) Interactive exercise with participants to investigate certain mitigation measures, alone or in combination and; (viii) Critical discussion about the model and proposal of improvement.

Workshop 2: Spatial visualization of health events: A hands-on practical with R

Dr. Brandon Hayes [1]*, Prof. Timothée Vergne* [2]



[1] DVM MPH PhD Brandon Hayes is a veterinary epidemiologist and mathematical modeller with a passion for cartography and spatial modelling. Currently a research fellow in epidemiological modelling at the French National Research Institute for Agriculture, Food and the Environment (INRAE), he is involved in informing avian influenza biosecurity policy through mathematical modelling. His interests include spatial epidemiology, Bayesian statistics, spatiotemporal mechanistic models, and brachycephalic cats.

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[2] DVM, MSc, PhD, Dipl. ECVPH, Timothée Vergne is an associate professor of veterinary public health at the National Veterinary School of Toulouse, and leads the Epidesa group.

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Workshop summary

The goal of this workshop is to provide attendees with the knowledge and tools needed to visualize and manipulate spatial health data using R and RStudio. Theoretical learning objectives consist of gaining understandings of basic geocomputational theory (e.g. coordinate systems and projections), geocomputation in R (e.g. what are types of spatial objects), and where to find publicly-available spatial data sources. The practical learning objectives, achieved through a hands-on group practical, are how to explore and manipulate synthetic spatial data to generate thematic maps. Coding scripts will be provided to transform, subset and visualize a data set using boundary and base maps, dot maps, choropleth maps, and bubble maps. By the end of the workshop, participants will understand how to transform raw spatial data into publication-quality plots through using the sf, tmap, and ggplot2 packages.

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Keynote lectures

Keynote lectures

How can Academia and Government by working together increase their impact to support wildlife conservation, protect public health, and prevent the next pandemic?

Dr Anne-Lise Chaber

School of Animal and Veterinary Sciences, Faculty of Medical Sciences, University of Adelaide, Australia

Anne-Lise Chaber is a practitioner-academic in the field of One Health, dedicated to comprehending and addressing the interconnectedness between human, animal, and environmental health, particularly in the context of anthropogenic activities precipitating health crises.

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Catastrophic fires, flooding, chemical pollution, and pandemics are all symptoms of the disruption of the earth's ecosystem balance due to anthropogenic activities. The direct link between zoonotic disease, human activities and demographic population growth has been demonstrated. Land use modification for urbanization, food production and agricultural change have been linked to around 50% of all zoonotic Emerging Infectious Diseases (EIDs) [1].

To address these challenges a One Health perspective that recognizes the interconnectedness between human, animal, and environmental health, has been adopted. Academia and governments are promoting an interdisciplinary research and policy approach to face these complex issues.

Research institutions and governments collaborate on projects related to wildlife conservation, protecting public health, and preventing future pandemics in the following ways:

Scientific research: Academia conducts pivotal research in wildlife ecology, zoonotic diseases, and public health to gain a better understanding on disease transmission between animals and humans. This research could serve as the cornerstone for informed policy decisions by government agencies. Notable projects include the Global Virome Project and the PREDICT Project, which conduct global surveillance of emerging infectious diseases.

Monitoring and Surveillance: Effective monitoring and surveillance systems are essential for identifying and mitigating threats to wildlife populations and public health. Government agencies collaborate with academia to establish robust systems, leveraging academic expertise in data collection, analysis, and interpretation. Initiatives like Gorilla Doctors and EUROBATS exemplify such successful collaborations by monitoring wildlife populations and combating threats such as habitat loss and disease transmission.

Policy Development: Academic research informs evidence-based policy development, ensuring that decisions are grounded in scientific understanding. Collaboration between academia and government agencies leads to the formulation of policies aimed at environment preservation. Examples include the Global Forest Watch and the European Union Timber Regulation, which leverage scientific expertise to inform policy decisions related to forest conservation and trade regulation.

Capacity Building: Government support for academic programs is vital for building capacity in wildlife conservation, ecology, and public health. Through funding and training opportunities, academia prepares the next generation of professionals to tackle complex challenges. Projects like APCOVE and the Field Epidemiology Training Program (FETP) facilitate collaboration between academia and government agencies to strengthen field epidemiology capacity and wildlife conservation efforts.

Public Outreach and Education: Collaborative efforts between academia and government raise public awareness about the interconnectedness of wildlife conservation, public health, and pandemic prevention. Initiatives like the Wildlife Conservation Society’s “Health & Ecosystems: Analysis of Linkages” (HEAL) Program engage communities to understand the links between wildlife conservation and human health, fostering a culture of conservation and responsibility.

International Collaboration: Recognizing that global challenges require international cooperation, academia, and government collaborate on various international initiatives. Efforts like the Global Avian Influenza Network for Surveillance (GAINS) and the World Health Organization (WHO) Global Outbreak Alert and Response Network (GOARN) facilitate collaboration between countries to monitor and respond to disease outbreaks effectively.
Nevertheless, these positive initiatives, focus on crisis and pandemic, preparedness and response.

When it comes to prevention, a true cross-sectoral approach that goes beyond a purely transdisciplinary approach, is urgently needed. This must include the driving forces that shape human activities and movement, namely trade. It is only by offsetting and limiting the environmental and social costs of extraction, production, and trade, that our world can will become more sustainable and continue to be liveable for future generations. Academia can by utilising their expertise in transdisciplinary and cross-sectoral collaboration to support the integration of trade and economy in the global health picture. Integration of trade organisations and policy makers in the One Health realm is necessity that will require the involvement of all.

Reference

[1]. Chaber AL. (2020). The Era of Human-Induced Diseases. Ecohealth.15(1): 8–11. doi: 10.1007/s10393-017-1299-9.

Veterinary Drug Resistance in a One Health Perspective

Laetitia Lempereur, DVM, PhD, EVPC

Food and Agriculture organization of the United Nations (FAO)

Laetitia Lempereur is AMR- Parasite Resistance Specialist from the One Health & Disease Control Group (NSAH-CJW) of the Food and Agriculture Organization of the United Nations.

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The global market for animal health products was approaching €30 billion per year in 2019, with an annual growth rate (6-9%) which will at least double this figure by 2030. Products include biologicals (e.g., vaccines), parasiticides, anti-infectives (e.g., antibiotics, antifungals), other pharmaceuticals (e.g., antihypertensives, antidiabetics), and medical feed additives. The current animal health market is understood to be driven primarily by three factors: (i) Pet owners, farmers, and veterinarians prefer more technically advanced and more convenient treatments. (ii) The growing world population increasingly demands affordable sources of protein from food animals and animal products, requiring improvements in livestock health care. (iii) The development of resistance requires new resistance-breaking preventatives and treatments [1].

Antimicrobials, such as antibiotics, antivirals, antifungals and antiparasitics, play a crucial role in preventing and treating infections and diseases in humans, animals and plants. Over 60% of antimicrobials used in aquatic and terrestrial food-producing animals and crops are classed as either critically or highly important to human medicine and up to 80 percent of antibiotics consumed by animals are released into the environment unmetabolized.

European data show a considerable decrease (53%) in overall veterinary antibiotic sales between 2011 and 2022 [2]. Additionally, in 2021, for the first time, the population-weighted mean antimicrobial use (AMU) in food-producing animals was lower than in humans in the EU/EEA [3]. This reduction of AMU in food-producing animals could be explained by policies and stewardship efforts. However, while the availability of data on global AMU has gradually improved, there is still no publicly available country-level reports of veterinary AMU in the majority of countries of the world. Based on current trends, antimicrobial usage is projected to increase globally by 8.0% by 2030. Hotspots of antimicrobial use were overwhelmingly in Asia (67%), while <1% were in Africa [4]. Their over-use and misuse in people, animals and plants is the main driver of antimicrobial resistance (AMR). Poor sanitation, inadequate infection prevention and control practices, as well as a lack of access to clean water are aggravating the issue by facilitating the spread of treatment-resistant microbes. As a result, AMR threatens global public health, food safety, food security and economic prosperity, as well as planetary biodiversity and ecosystems.

Most of animal health management is also supported by antiparasitic drugs representing the second largest market segments in the global animal health industry (23% of the market share), accounting for €7 billion in sales, a third of which are intended for livestock. Drug and multidrug resistance are increasingly common across all parasites. Resistance to products used to control parasites is considered to be a serious challenge in livestock parasites. In dogs and cats, drug resistance is as yet less serious. Worms, ticks and trypanosomes are the top disease agents globally ranked according to their impact especially on small-scale producers [5]. Approximately 70 percent of production animals especially in developing countries are estimated to experience severe parasite transmission. The impact of these diseases in different geographical regions of the world varies hugely depending on many factors but both livestock producers from developed and developing countries set aside a considerable budget to control these parasitic diseases. However, the rapid emergence and spread of drug resistant parasite strains such as ticks and worms are alarming. Overuse, misuse and use of substandard medicinal products are main factors which contribute to the antiparasitic drug resistance with an impact not only on animal, but also on public health and environment. Compared with the development of antibiotic resistance in bacteria, resistance to antiparasitics has been relatively slow to develop under field conditions. However, resistance is becoming widespread because relatively few chemically dissimilar groups have been introduced over recent decades. Thus, resistance to one particular compound may be accompanied by resistance to other members of this compound class. While methods for successful parasite control change over time; parasite susceptibility to chemotherapeutics shifts, new management strategies are introduced, and parasite epidemiology fluctuates in particular under the effects of climate change and animal movements, the global access to integrated and diversified parasite control methods should be ensured at regional, national and local level.

The Veterinary Drug Resistance issue underscores the need to ensure their prudent and responsible use under a One Health approach, and making global agrifood systems more resilient, sustainable, and capable of meeting the relevant Sustainable Development Goals (SDGs). This would also need engagement of all stakeholders to collectively develop economically, socially, and environmentally sustainable solutions with the ultimate goal to improve living standards for everyone, with a particular focus on supporting the most vulnerable populations.

References

[1]. Selzer PM, Epe C. (2021). Antiparasitics in Animal Health: Quo Vadis? Trends Parasitol. 37(1), 77-89. doi: 10.1016/j.pt.2020.09.004.

[2]. ESVAC (2023). European Surveillance of Veterinary Antimicrobial Consumption (ESVAC): 2009 – 2023. URL address: https://www.ema.europa.eu/en/veterinary-regulatory-overview/antimicrobial-resistance-veterinary-medicine/european-surveillance-veterinary-antimicrobial-consumption-esvac-2009-2023

[3]. European Medicines Agency, European Surveillance of Veterinary Antimicrobial Consumption (2022). Sales of veterinary antimicrobial agents in 31 European countries in 2022 (EMA/299538/2023). URL address: https://www.ema.europa.eu/en/documents/report/sales-veterinary-antimicrobial-agents-31-european-countries-2022-trends-2010-2022-thirteenth-esvac-report_en.pdf

[4]. Mulchandani R, Wang Y, Gilbert M, Van Boeckel TP. (2023). Global trends in antimicrobial use in food-producing animals: 2020 to 2030. PLOS Glob Public Health., 3(2), e0001305. doi: 10.1371/journal.pgph.0001305.

[5]. Rist C.L., Garchitorena A., Ngonghala CA., Gillespie T.R., Bonds M.H. (2015). The Burden of Livestock Parasites on the Poor, Trends in Parasitology, 31(11), 527-530, https://doi.org/10.1016/j.pt.2015.09.005.

One Health, Bee Management Practices Including Biosecurity and Sustainable Beekeeping

Dr Giovanni Formato DVM

ITZER - IT; FAO and WAOH Reference Centre for Apiculture, Health and Biosecurity

Giovanni Formato is a veterinarian (DVM), specialized in "Food inspection of animal products", expert on "bee disease management". He collaborates with Government Institutions, Universities, other laboratories and International Organizations (FAO, WOAH).

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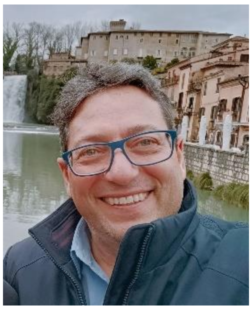

Introduction

One Health is the forefront of public health and agri-food chain concerns. The increasingly complex health challenges interconnect issues related to animal welfare, biosecurity, and drug management in farming. The challenges faced by the public health are complex and include addressing animal welfare, regulation of drugs usage, evidence at the slaughterhouse (acting as an epidemiological observatory), biosecurity measures, and health risk assessment primarily from a preventive perspective.

The CLASSYFARM system

In Italy, the Ministry of Health, in collaboration with the National Center of Animal Welfare at IZSLER (Istituto Zooprofilattico Sperimentale Emilia Romagna) developed a system to address complex issues concerning human and animal health and welfare, named ClassyFarm. This innovative system categorizes farms by risk through an integrated approach, aligning with European regulations such as the Animal Health Law, the European Food Safety Authority (EFSA) evidences and Risk Assessment methodology. ClassyFarm provides tools and standardized protocols for assessing and improving animal health and welfare in farming. ClassyFarm serves as a comprehensive platform integrating information on Biosecurity, Animal Welfare, antimicrobial consumption, production, feeding, and nutrition. In the same time, it offers manuals, checklists, and protocols tailored to specific species and categories to stakeholders and veterinarians. The system enables veterinarians to conduct standardized, recordable, repeatable, reproductible and integrable on-field observations. These observations are complemented by data sourced from: official controls (e.g. inspections at slaughterhouses, national diagnostic laboratories like Zooprophylactic Institutes and other official laboratories, etc.), the National Register of Farms, and drug information from the Electronic Veterinary Prescription Register, Regional Epidemiological Observatories, other National Databases. In this way, it is possible to perform an accurate risk identification, categorization, and prevention in animal farming. This integration allows the monitoring of animal welfare, biosecurity, and antimicrobial use, facilitating the comparison of vast amounts of data altogether, rather than singularly, widening the perspective around prediction and prevention of specific risks. This, in turn, enables the simultaneous observation of multiple stressors for the first time, fostering collaboration among farmers, veterinarians, and competent authorities.

The system operates on a voluntary basis. Farm operators voluntarily adhere and sign to the protocol that includes voluntary control (by farm veterinarians) and official control (by official veterinarians). It functions at two levels: firstly, on singular farms, using checklist-guided inspections (made by farm veterinarians) highlight the critical points for every farm within each thematic area. Such evidences are registered in the centralized veterinary portal (www.vetinfo.it) by farm veterinarians. Secondly, on national level, where data are integrated with other institutional databases and finally merged into a specific and centralized section, encompassing all farms nationwide. A final judgment is automatically generated by the Classyfarm System, which can be compared with national medians for the specific risk category, as well as with farms of the same type and category. Results may even serve as an effective tool in disease prevention and combating antimicrobial resistance or may be useful to officers in planning their controls based on relative risk per farm. An informative dashboard categorizes data alongside each operator’s personalized page, accessible only with authorization from the Ministry.

The Classyfarm operational framework facilitates the optimization of livestock management, prioritizing actions concerning safety and sustainability, in agri-farming, while minimizing the impact of the farmers on the animals and of animals on the environment. It embraces the One Health perspective and safeguards consumer health, while also controlling antimicrobial resistance and zoonosis through epidemiological surveillance practices and biosecurity measures. This is achievable through the categorization of risk into three classes, which not only enables the monitoring of farms in poor conditions on any level (from structural to managemental to strictly animal related) but also promotes those in better conditions. It encourages the adoption of virtuous practices endorsed by the Common Agricultural Policy (CAP) and the European Green Deal in a holistic manner.

Currently, activities by certification institutions are underway to implement the voluntary ClassyFarm labelling system, enhancing the supply chain.

Risk categorization:

To categorize the risk, on farm observations are carried out following official checklists provided by ClassyFarm. These checklists are classified according EFSA, into 5 thematic areas:

A. concerning “person and corporate management” environmental hazards (based on indirect measurement methods);
B. concerning “facilities and equipment” environmental hazards (based on indirect measurement methods);
C. concerning “animal-based measures” (ABM) that are issues strictly related to animal welfare, based on direct measurements;
D. “Biosafety and Biosecurity”, that are environmental hazards (based on indirect measurement methods) and include antimicrobial resistance risk assessment;
E. “Great risks and Alarm systems”, that are environmental hazards (based on indirect measurement methods).

In Area A, **managerial and administrative specifics** are determined through structure-based management measures, including training, staff numbers, education of operators, presence of specific premises, preventive measures, load, discharge, and movement registers, emergency slaughter procedures, as well as feeding and housing protocols. Area B oversees equipment, surfaces, and materials, space utilization, and environmental parameters. Area C involves sampling a proportional number of animals and directly evaluating welfare by observing physical, pathological, or behavioural phenomena associated with poor welfare, such as manifestations of fear and aggression, nutritional status, and movement patterns. The Great Risks and Alarm Systems area monitors factors impacting welfare and safety, such as lighting, water quality, noise levels, automatic equipment functionality, ventilation systems, and operator safety measures.

Biosafety and Biosecurity area ensures the application of the four principles aimed at disease containment (prevention, prophylaxis, control, and eradication) by evaluating the health condition of animals based on type, category, number, position, hygienic status, prophylactic measures, or other measures aimed at countering the introduction of new contagious agents on the farm.

Scores classify farms as:

- “Unacceptable” (or high risk): not meeting legal parameters, non-compliant conditions or distressed state; risk of a disease to entry or spread;
- “Acceptable” (or controlled risk): compliant with the law and the Five Freedoms;
- “Optimal” (or low risk): enrichment condition, positive states, eustress, risk prevented.

Above mentioned scores are grouped under 3 different thematic areas: animal welfare, animal health/biosecurity, and drug management/biomass.
The final score is obtained by the different level of risk above mentioned.

Every final score is comparable with average national reference data and with other farms, serving institutions to plan subsequent control intensities according to risk assessment and aiding operators in improving their business practices. To support operators and veterinarians, checklists, and manuals for biosecurity and animal welfare are available on the official ClassyFarm website.

So far, the system is already applied to dairy cow, calves, beef cattle, dairy buffaloes, sheep and goats for milk, laying hens, turkeys, broilers, and pigs, with continuous updates.

The CLASSYALV project

An ongoing integration within ClassyFarm involves the ClassyALV project, which is dedicated to the honey bee health and welfare in a sustainable beekeeping approach. ClassyALV is developed by IZSLER (National Reference Centre for Animal Welfare), in collaboration with IZSLT. The project, funded by the Italian Ministry of Health, is still ongoing.

Beekeeping plays a central role in the supply chain in terms of productivity and ecosystem services but faces increasing colony mortality. Therefore, an integrated approach like ClassyALV, appears to be a valuable addition for the beekeeping sector. Main issues affecting honey bee health in Italy are: *Varroa destructor*, *Aethina tumida*, AFB (American Foulbrood), *Nosema ceranae*, and invasive predators like *Vespa velutina*, along with climate change, improper apiary management and poisoning by plant protection products.

With the aim of implementing the ClassyFarm system in the beekeeping sector, we are developing dedicated checklists for welfare and biosecurity. The application of unique and nationally comparable monitoring protocols holds promise in sustainable beekeeping. In this regard, planned phases include evaluation via checklists concerning observations in the apiary, registrations done by beekeepers at the apiary level and hive inspections. Data from check-list will be integrated with other obtained from Italian National Database (e.g. the Beekeeping Register database, honey bee notification of diseases and poisonings, results of official controls or prescriptions, traceability systems concerning honey bees' movements, etc.). The quantitative evaluation system will consider even the adoption of good management practices and biosecurity measures, including type of treatments and productivity. ClassyALV pinpoints practices linked to higher risks of colony depopulation and mortality. Manuals for operators and officers are under development. A coordinated data-driven approach is envisioned through collaboration among beekeepers, veterinarians, and competent authorities.

ClassyALV, as well as Classyfarm, is a potent sustainability tool orienting on best farming, operating through Risk Reduction to curb disease outbreaks and preserve bee health by minimizing conventional acaricide use. Of course, ClassyALV should consider factors that are strongly related to the environment-mediated factors (e.g. the use pesticides, presence of plant producing alcaloids or allergenics) and should need of other kind or registers not needed for other farming species. Guidelines will be accessible to all officers and beekeeping operators. The objective is to promote a sustainable beekeeping advancing the concept of One Health.

In conclusion, ClassyFarm and ClassyALV integrate biosecurity and biosafety into sustainable farming practices through comprehensive risk assessment protocols, standardized (direct or indirect) observations, and data integration from national databases. Utilizing checklists, manuals, and inspections, these tools can be considered potent sustainability tools aimed at achieving sustainable management and ensuring the One Health status.

Suggested readings

[1]. Aderinto Y., Azagbaekwe A., Bamigbola O., Oke M., Obayomi A., Salaudeen L., Aliu, T. (2020). Optimization of Honey Bee Production. International Journal of Mathematical Models and Methods in Applied Sciences, 14, 54-60.

[2]. Blokhuis H., Miele M., Veissier I., Jones, B. (2013). Improving farm animal welfare: science and society working together: the Welfare Quality approach. Cardiff: Wageningen Academic.

[3]. Blokhuis H., Veissier I., Miele, Jones B. (2010). The Welfare Quality® project and beyond: Safeguarding farm animal well-being. Acta Agriculturae Scandinavica, Section A, 60, 129-140.

[4]. Brodschneider R., Gratzer K. (2021). The FAO Guideline on Good Beekeeping Practices for Sustainable Apiculture. Bee World, 98(4), 144-144.

[5]. Broom D. (1991). Animal welfare Concepts and measurements. Journal of Animal Science, 69(10), 4167-4175.

[6]. Buoio E., Cialini C.C.A. (2023). Air Quality Assessment in Pig Farming: The Italian Classyfarm. Animals, 13(14), 2297.

[7]. De Lucia V. (2023). The CAP 2023-2027 and the role of ClassyFarm. Campania Region.

[8]. EFSA. (2012). Scientific Opinion on the use of animal-based measures to assess welfare of dairy cows. EFSA Journal, 10(1), 2254.

[9]. EFSA. (2021). EFSA Strategy 2027 – Science, safe food, sustainability. [Online]. Available: https://www.efsa.europa.eu/en/corporate-pubs/efsa-strategy-2027-science-safe-food-sustainability.

[10]. EFSA-AHAW. (2022). Methodological guidance for the development of animal welfare mandates in the context of the Farm to Fork Strategy. EFSA Journal, 20(7).

[11]. El Agrebi N., Steinhauer N.R.V., de Graaf D., Saegerman C. (2021). Beekeepers perception of risks affecting colony loss: A pilot survey. Transboundary and Emerging Diseases, 69(2), 579-590.

[12]. El Agrebi N., Tosi S., Leinarts L., de Graaf D., Saegerman C. (2021). Risk and protective indicators of beekeeping management practices. Science of the Total Environment, 799, 149381.

[13]. European Commission. (2016). Regulation (EU) 2016/429 on transmissible animal diseases. [Online]. Available: https://www.classyfarm.it/index.php/en/.

[14]. European Union. (2018). The CAP 2023-2027. [Online]. Available: https://op.europa.eu/webpub/eca/special-reports/animal-welfare-31-2018/en/The CAP 2023-2027.

[15]. European Union. (2019). Farm to Fork strategy for a fair, healthy, environmentally-friendly food system.

[16]. Italian Official Bulletin. (2001). Legislative Decree 146 of March 26, 2001: implementation of directive 98/58 EC on the protection of animals kept for farming purposes.

[17]. Johnson R. (2010). Honey Bee Colony Collapse Disorder. In Congressional Research Service.

[18]. Miele M., Lever, J. (2013). Civilizing the market for welfare friendly products in Europe? The techno-ethics of the Welfare Quality® assessment. Geoforum, 48, 63-72.

[19]. Miele M., Pérez C., Parra M. I. (2022). Predicting internal conditions of beehives using precision beekeeping. Biosystems Engineering, 221, 19-29.

[20]. Robustillo M.C., Pérez C., Parra M.I. (2022). Predicting internal conditions of beehives using precision beekeeping. Biosystems Engineering, 221, 19-29.

[21]. Smith K.M., Loh E., Rostal M., Zambrana-Torrelio C., Mendiola L., Daszak, P. (2013). Economics: Drivers of Honey Bee Colony Declines and Losses. EcoHealth, 10(434-445), 434-445.

Mechanistic modelling of infectious disease transmission: for which purposes?

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A model is just a simplified representation of reality. It is particularly useful when the phenomenon under study is complex, difficult, or expensive to study or present critical ethical considerations. Under this logic, infectious diseases are obvious subjects for modelling [1]. In general, two modelling paradigms are used in mathematical modelling: statistical and mechanistic models. Statistical models aim at quantifying a hypothesised relationship between the variables in a dataset, where the relationship seeks only to best describe the data. Alternatively, mechanistic models aim at identifying a hypothesised relationship between the variables in a dataset where the nature of the relationship is specified in terms of biological processes that are thought to have given rise to the data. In this presentation, I will focus on mechanistic modelling approaches and illustrate how they can be used in the field of the transmission of infectious diseases in animals in order to analyse historical epidemics or provide evidence-based policy recommendations.

One of the most important objectives of mechanistic modelling of infectious disease transmission is to unravel infectious disease transmission patterns that occurred in the past. To reach this objective, the approach generally consists in confronting a mechanistic model to observed epidemic data. This is usually done by developing mechanistic models, defined by a set of processes and parameters (some of which are unknown), and adjusting them to historical epidemics in order to estimate the value of the unknown parameters and reproduce the epidemic trends as accurately and precisely as possible. In doing so, mechanistic models can quantify the relative contribution of different hosts in the propagation of a pathogen. As an example, using a multi-host mechanistic model of highly pathogenic avian influenza adjusted to the French epidemic (2016-2017), Andronico et al. [2] estimated that duck farms were 2.5 times more infectious and 5 times more susceptible than chicken farms, and therefore played a substantial role in the circulation of the pathogen. Mechanistic models of infectious diseases that investigate past epidemics can also be valuable for estimating the relative contribution of different transmission routes. As an illustration, Lambert et al. [3] modelled the transmission of brucellosis in Alpine ibex and demonstrated that horizontal transmissions through infectious abortions and births were responsible for almost 60% of new cases, followed by vertical transmission and veneral transmission. Finally, the adjustment of mechanistic models to historical epidemics can be used to estimate retrospectively the effectiveness of management strategies that were implemented to control the epidemics. This is usually done by integrating into the model structure a process related to the management strategy that was implemented (e.g. the preventive culling of flocks around outbreaks), fitting the model to the historical epidemic, and running epidemic simulations using the fitted model after having discarded the process related to the management strategy. This allows a comparison of the epidemic development with and without the management strategy under scrutiny. As an example, Andronico et al. [2] estimated that the preventive culling strategy of poultry flocks that was implemented in France during the winter 2016-2017 to curb the HPAI epidemic, halved the total number of outbreaks that would have occurred should no preventive culls had been put in place.

Mechanistic modelling of infectious diseases can also be extremely valuable to predict the development of infectious disease epidemics under different hypothetical scenario for which there is no option to run in vivo or in vitro experiments. This is usually done by using models that have been calibrated to reproduce realistic epidemics and to run in silico simulations. The simplest application of this objective is to forecast the development of the epidemic on the short term and anticipate the disease burden to plan the needs. This was particularly salient during the COVID-19 pandemic during which a number of international modelling groups developed mathematical models to predict excess demand for hospital services and timing of deaths due to COVID-19 (as in [4]), or to predict international spread of COVID-19 (as in [5]). These short-term forecasts, that can provide evidence-based support to anticipate the needs, are only relevant if made available as the epidemic develops. Finally, in silico simulations of mechanistic models can be used to compare different scenarios of disease management and answer “what if” questions. This type of use of mechanistic models is probably one of the most popular, as it provides a very direct and tangible outcome to feed infectious disease management decision-making processes. As an example, Probert et al. [6] used a mechanistic model of FMD transmission calibrated to historical epidemics from the UK and Japan to run in silico simulations allowing the comparison of the expected total number of outbreaks under several alternative management strategies, including culling of infected premises only, culling all flocks within 3 or 10 km around outbreaks, vaccinating all flocks within 4 or 10 km around outbreaks, etc.

As exemplified in this presentation, mechanistic modelling in a powerful tool to analyse infectious disease spread. It allows the testing of assumptions, the estimation of key parameters, the prediction of epidemic development and the comparison of management scenarios. In the field of animal health, I think that the greatest room for improvement lies in their ability to be used in (almost) real-time to provide relevant policy support. To valorise this exceptional potential, I argue that there is the need to improve the level of preparedness of modelling teams, the access to relevant epidemiological data in real time and the stabilisation of human resources.

References

[1]. Vynnycky, E., White, R., Vynnycky, E., White, R. (2010). An Introduction to Infectious Disease Modelling. Oxford University Press, Oxford, New York.

[2]. Andronico, A., Courcoul, A., Bronner, A., Scoizec, A., Lebouquin-Leneveu, S., Guinat, C., Paul, M.C., Durand, B., Cauchemez, S. (2019). Highly pathogenic avian influenza H5N8 in south-west France 2016-2017: A modeling study of control strategies. Epidemics 28, 100340. https://doi.org/10.1016/j.epidem.2019.03.006

[3]. Lambert, S., Gilot-Fromont, E., Toïgo, C., Marchand, P., Petit, E., Garin-Bastuji, B., Gauthier, D., Gaillard, J.-M., Rossi, S., Thébault, A. (2020). An individual-based model to assess the spatial and individual heterogeneity of Brucella melitensis transmission in Alpine ibex. Ecological Modelling 425, 109009. https://doi.org/10.1016/j.ecolmodel.2020.109009

[4]. Roosa, K., Lee, Y., Luo, R., Kirpich, A., Rothenberg, R., Hyman, J.M., Yan, P., Chowell, G. (2020). Short-term Forecasts of the COVID-19 Epidemic in Guangdong and Zhejiang, China: February 13–23, 2020. Journal of Clinical Medicine 9, 596. https://doi.org/10.3390/jcm9020596

[5]. Wu, J.T., Leung, K., Leung, G.M. (2020). Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. The Lancet 395, 689–697. https://doi.org/10.1016/S0140-6736(20)30260-9

[6]. Probert, W.J.M., Jewell, C.P., Werkman, M., Fonnesbeck, C.J., Goto, Y., Runge, M.C., Sekiguchi, S., Shea, K., Keeling, M.J., Ferrari, M.J., Tildesley, M.J (2018). Real-time decision-making during emergency disease outbreaks. PLOS Computational Biology 14, e1006202. https://doi.org/10.1371/journal.pcbi.1006202

Socio-economics and epidemiology

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Professor Niemi has contributed several EU-funded research and development projects, which have focused on animal health and welfare issues. Currently he is coordinating Horizon Europe project Digi4Live and contributing to Horizon 2020 projects PPILOW and HoloRuminant, COST action BETTER and to development project Z4ABC.

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This abstract examines the role of economics and social sciences in animal health issues. It will provide a short overview of diseases and their financial impacts and then focus on the role of economics and social sciences in analyzing disease prevention measures. Economics studies how economic actors allocate scarce resources to satisfy their unlimited needs. Biosecurity is a key measure to mitigate animal diseases and economic issues related to farm animal biosecurity can have significant implications for farmers, agricultural industries, and the broader economy.

The economic costs of disease are caused by the additional costs and foregone revenue because of disease and preventive measures. By contrast, the benefits of improved disease risk management are obtained as the reduced economic burden of diseases (i.e. fewer and/or less impactful disease incidents that are causing economic loss). The incidence, severity and costs of disease can vary by case and therefore also the benefits depend on how much the risk of disease losses can be mitigated by preventive measures. Different diseases have different economic impacts. For example, highly contagious animal diseases, such as highly pathogenic avian influenza or foot and mouth disease can cause substantial one-time losses through costly disease eradication measures and distortions that they can cause to individual businesses and to the agricultural sector both through disease-related restrictions and disruptions in the international trade of animals and animal-based products. Production diseases by contrast often lead to a continuous cost burden which increase production costs per unit of produce and impair the cost-competitiveness of production. The financial impacts of disease do not concern only effects which emerge after an infection has taken place. Rather they include also the costs of preventive and mitigative measures which are taken irrespective whether an infection occurs. Moreover, studies covering different types of disease risk illustrate that increased risk of disease that the farmers face can reduce the quantity they are willing to produce.

In general, perceived benefits of measures affect farmers' decision to a adopt new disease prevention measures. Hence, farmers will adopt a biosecurity practice if the expected net economic benefits from adoption are greater compared to not adopting the practice. The risk perceived by the farmer contributes to this decision, and the more costly a biosecurity measure is, the less likely the farmer is to adopt it. Moreover, while the costs of disease prevention, such as additional labor, materials and consequences to farm operations are incurred with a fairly high degree of certainty, the benefits of biosecurity are not known beforehand. For example, lower veterinary and medication costs, improved yield and reduced variation of production results are observed only if the disease is not manifested. This uncertainty about the benefits may affect the adoption decision if the benefits are unclear.

Although financial aspects are strong drivers for the adoption of new practices, endogenous factors such as perceived impact of disease, lack of knowledge, previous experiences on disease control and diseases and farmer's technical skills can be barriers for adoption. Hence, having a strong scientific and localized evidence that the practice is affordable and that it affects favorably production, workload, animal health, product quality and safety, the environment and sustainability of ecosystem increases the implementability of measure. The socio-economic barriers and enabling factors for adopting biosecurity practices will be elaborated by using results from a European study. One of the approaches to promote good disease management practices in practice is to use nudges. Nudging is a concept used in behavioral economics and it refers to designing the choice situations so that there are features – for example details related to the positioning of items – which stimulate the person to take preferred actions.

The final part of the presentation will discuss about economic benefits that enhanced biosecurity can provide to the producers, consumers and the society by using modelling results. Studies provide mixed evidence of biosecurity practices on economic outcomes. While some measures are seen to provide even substantial economic net benefits (e.g. [1]: benefit of improved hygiene to pig fattening farms was around 50% of the gross margin), there is evidence (e.g. [2,3]) that not all measures may lead to favorable economic outcomes.

Overall, effective farm animal biosecurity measures are essential for safeguarding animal health, ensuring food safety, maintaining market access, and protecting the economic viability of agricultural enterprises. By addressing these economic issues, policymakers, farmers, and industry stakeholders can work together to promote sustainable livestock production and mitigate the risks associated with infectious diseases.

References

[1]. Niemi J, Bennett R, Clark B, Frewer L, Jones P, Rimmler T, Tranter R. (2020) A value chain analysis of interventions to control production diseases in the intensive pig production sector. PLOS ONE 15(4): e0231338. https://doi.org/10.1371/journal.pone.0231338

[2]. Osawe W, Läpple D, Mee JF. (2022). Economic analysis of biosecurity adoption in dairy farming: evidence from Ireland. Journal of Animal Science 100: 1-10. https://doi.org/10.1093/jas/skac218

[3]. De Roest K, Montanari C, Ferrari P, Fourichon C, Levallois P, Kefalas G, Schreuder J, Papasolomontos S, Simitopolou M, Angastiniotis K, Scollo A. (2023). Costs and benefits of the improvement of biosecurity on pig and broiler farms. HSOA Journal of Animal Research and Veterinary Science 7: 0.41.

Artificial intelligence assistance, video games and other digital tools in Epidemiology

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Sébastien Picault is a researcher in artificial intelligence, currently working in the Animal Health division of INRAE (the French National Research Institute for Agriculture, Food and Environment) in the BIOEPAR research unit in Nantes. He obtained a Ph.D. in computer science from the Sorbonne University in 2001 and became an assistant professor at Lille University in 2002. He has developed multi-agent modelling methods to better separate simulation algorithms from model description through an interaction-oriented approach. He extended these methods to tackle the design of multi-level agent-based simulations, with applications to serious games, transport, retailing and cartography. He joined BIOEPAR in 2016 to develop new methods at the crossroads between AI and software engineering, to facilitate the co-design of mechanistic epidemiological models together with non-modellers (e.g., other scientists or stakeholders). This approach, which resulted in an open-source software (EMULSION), helps increase model readability, evolvability and assessment, without the need to write simulation code. Sébastien Picault also co-organized the first international modelling challenge in animal health. His current work focuses on automating the production of decision-support tools based on mechanistic models, and on integrating sensor data with mechanistic model scenarios and predictions.

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The integration of artificial intelligence (AI) and other digital tools, such as sensor data and video games, in epidemiology, particularly within the context of livestock farming, is initiating a transformative shift towards more informed, efficient, and effective animal health management practices [1]. This evolution is characterized by the growing use of connected devices to collect data and new analysis methods, which can feed mechanistic models and foster the development of advanced decision-support tools for animal health management, innovative applications in veterinary medicine, and advances in education through serious games.

AI [2] is as old as computing itself, but the simultaneous increase in the computing power of machines and the mass of data available since the mid-2000s led to spectacular advances in machine learning methods, especially with the emergence of deep learning. These data analysis methods are particularly effective for pattern recognition or classification tasks [3]. Precision farming is developing rapidly, based on the adoption of machine learning technologies to optimise herd management and performance, and to improve animal welfare while reducing environmental impact. The collection and analysis of real-time sensor data by machine learning methods enable farmers to make more informed decision regarding the physiological needs of their animals, such as diet [4]. It also allows for highly accurate detection of events such as heats or farrowing.

Hence, it is quite natural to expect the same methods to provide a substantial assistance in the detection and management of infectious diseases. However, machine learning methods face several limitations. First, they are based on observed data, which means their capability to extrapolate to unobserved scenarios, as with any statistical method, is highly questionable. Especially, even assuming that early detection can be achieved properly, making relevant intervention recommendations based solely on these detections is risky. Second, while they are very effective in identifying patterns within a short time window, infectious disease transmission spans broader time periods and involves interactions among multiple individuals, complicating detection and prediction efforts. Third, many clinical signs (e.g. hyperthermia) lack specificity, which can lead to false positives if the detection of diseases relies solely on alert events.

To overcome such limitations, mechanistic epidemiological models are very valuable as they can be used to understand, predict and control disease transmission in complex pathosystems and at various scales. Mechanistic models rely on explicit processes reflecting existing knowledge or assumptions regarding biological aspects of the pathosystem (such as the diversity of transmission pathways), but can also incorporate farm management practices, surveillance and control methods, and treatments. Thus, they are very effective in comparing contrasted scenarios, even counterfactual ones, to support decision making [5].

One challenge in incorporating all these components is a high development cost. Fortunately, AI also provides methods to assist mechanistic model design, precisely because AI also deals with knowledge representation and management methods, and also with simulation architectures which help making model entities interact in accordance with knowledge and assumptions (e.g. agent-based models). This capability to handle explicit knowledge enables to describe mechanistic epidemiological models as structured texts rather than code [6]. Thus, the development and revision of models is made faster as it does not require to write code, and models can be co-constructed through iterative interactions between modellers and animal health stakeholders (farmers, veterinarians, public policymakers…). In the same way, decision support tools can be co-designed from mechanistic models and the specification of relevant scenarios, input parameters, and simulation outputs, resulting in code generation to build a web application [7].

Another interest of mechanistic models lies in their capability to incorporate a broad diversity of scenarios. Indeed, these scenarios can be designed for educational purposes and the simulation turned into a serious game [8], helping students actively apply their knowledge in realistic and engaging situations. These models can also be used to simulate an outbreak, generate synthetic data, and feed a modelling challenge, where participants attempt to predict and manage epidemic scenarios, suggesting or assessing mitigation strategies [9, 10].

However, feeding mechanistic models with field data makes them more accurate, more specific and more reliable. So, perhaps, one of the most transformative applications of connected tools in the field of epidemiology is the development of decision-support tools where the vast amounts of data generated by sensors are processed first by machine learning models, which themselves are used to provide information and scenarios to mechanistic models.

An example of this innovative approach is the SEPTIME project, which aims to leverage AI and software engineering to create web-based decision-support tools based on mechanistic models and fed by real-time sensor data. This project illustrates the potential of combining sensor data with advanced modelling techniques to predict and manage bovine respiratory diseases. By automating the process of updating decision-support tools in line with evolving biological knowledge, the SEPTIME project represents a significant step forward in the application of AI in veterinary science and livestock management.

While the promise of AI and decision-support tools is vast, their development and implementation are not without challenges. The accuracy of these tools depends heavily on the quality and comprehensiveness of the data collected, necessitating robust sensors and data management systems. Additionally, mechanistic models, while powerful in their predictive capabilities, require extensive expertise to develop and interpret. Despite these obstacles, the benefits of mechanistic modelling in understanding complex biological processes and informing decision-making processes are undeniable.

Despite these advancements, the path forward is not without its challenges. The financial and environmental costs associated with implementing and maintaining digital technologies, coupled with the need for ongoing training and adaptation among farmers and veterinarians, present considerable hurdles. Moreover, issues related to data privacy, security, and the digital divide between "high-tech" and "traditional" farming practices require thoughtful navigation [11]. Nevertheless, the opportunities presented by these digital tools - including enhanced disease prevention, improved animal welfare, and the democratization of expert veterinary knowledge - should outweigh these challenges. Continued advancements in AI, machine learning, and sensor technologies promise to further refine decision-support tools, making them more accessible, accurate, and user-friendly.

References

[1]. Ezanno P, Picault S, Beaunée G, Bailly X, Muñoz F, Duboz R, Monod H, Guégan J-F (2021) Research perspectives on animal health in the era of artificial intelligence. Vet Res 52:40. https://doi.org/10.1186/s13567-021-00902-4

[2]. Russell SJ, Norvig P (2010) Artificial Intelligence. A Modern Approach, 3rd edition. Upper Saddle River, New Jersey

[3]. Hastie T, Tibshirani R, Friedman J (2009) The Elements of Statistical Learning. Data Mining, Inference, and Prediction, 2nd edition. Springer

[4]. Durand M, Largouët C, De Beaufort LB, Dourmad JY, Gaillard C (2023) Prediction of the daily nutrient requirements of gestating sows based on sensor data and machine-learning algorithms. J Anim Sci 101:skad337. https://doi.org/10.1093/jas/skad337

[5]. Ezanno P, Andraud M, Beaunée G, Hoch T, Krebs S, Rault A, Touzeau S, Vergu E, Widgren S (2020) How mechanistic modelling supports decision making for the control of enzootic infectious diseases. Epidemics 100398. https://doi.org/10.1016/j.epidem.2020.100398

[6]. Picault S, Huang Y-L, Sicard V, Arnoux S, Beaunée G, Ezanno P (2019) EMULSION: Transparent and flexible multiscale stochastic models in human, animal and plant epidemiology. PLOS Comput Biol 15:e1007342. https://doi.org/10.1371/journal.pcbi.1007342

[7]. Picault S, Niang G, Sicard V, Sorin-Dupont B, Assié S, Ezanno P (2023) Leveraging artificial intelligence and software engineering methods in epidemiology for the co-creation of decision-support tools based on mechanistic models. bioRxiv

[8]. Messina A, Schyns M, Dozo B-O, Denoël V, Van Hulle R, Etienne A-M, Delroisse S, Bruyère O, D'Orio V, Fontaine S, Guillaume M, Lange A-C, Louppe G, Michel F, Nyssen A-S, Bureau F, Haubruge E, Donneau A-F, Gillet L, Saegerman C (2023) Developing a Video Game as an Awareness and Research Tool Based on SARS-CoV-2 Epidemiological Dynamics and Motivational Perspectives. Transbound Emerg Dis 2023:1–11. https://doi.org/10.1155/2023/8205408

[9]. Picault S, Vergne T, Mancini M, Bareille S, Ezanno P (2022) The African swine fever modelling challenge: Objectives, model description and synthetic data generation. Epidemics 40:100616. https://doi.org/10.1016/j.epidem.2022.100616

[10]. Ezanno P, Picault S, Bareille S, Beaunée B, Jan Boender G, Dankwa EA, Deslandes F, Donnelly CA, Hagenaars TJ, Hayes S, Jori F, Lambert S, Mancini M, Munoz F, Pleydell DRJ, Thompson RN, Vergu E, Vignes M, Vergne T (2022) The African swine fever modelling challenge: model comparison and lessons learnt. Epidemics 100615. https://doi.org/10.1016/j.epidem.2022.100615

[11]. Bellon-Maurel V, Lutton E, Bisquert P, Brossard L, Chambaron-Ginhac S, Labarthe P, Lagacherie P, Martignac F, Molenat J, Parisey N, Picault S, Piot-Lepetit I, Veissier I (2022) Digital revolution for the agroecological transition of food systems: A responsible research and innovation perspective. Agric Syst 203:103524. https://doi.org/10.1016/j.agsy.2022.103524

Participatory epidemiology

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Participatory epidemiology (PE) has been defined as the systematic use of participatory approaches and methods to improve the understanding of diseases and options for animal disease control [1]. The origins of PE lie with the development of participatory appraisal in the 1980s by people involved in international development projects, to address weaknesses in conventional methods for data collection in rural communities [2]. Participatory appraisal was adapted and applied by veterinarians in community-based animal health programmes in Africa and Asia, which aimed to address gaps in animal health services delivery in marginalised populations, such as pastoralist, agro-pastoralist and small-holder livestock keepers. Participatory methods were incorporated into all stages of the project cycle: assessment, project design, monitoring and evaluation. The methods included community meetings, semi-structured interviews, ranking and scoring tools, and visualisation tools such as mapping, timelines, and seasonal calendars. The training of community-based animal health workers used participatory training methods.

Participatory methods were subsequently applied in field research on specific disease problems, and in participatory surveillance – active surveillance for specific diseases or syndromes. These applications of participatory methods became known as participatory epidemiology [3]. Fundamental to the methods were the exploration of local knowledge, perceptions, and attitudes.

The main participatory methods that were used were group discussions with livestock keepers and animal health personnel, that incorporated a variety of tools to promote discussion, include diverse knowledge and opinions, and encourage all to contribute. Key tools were maps of livestock resources and movements, and areas of disease risk, timelines to visualise the occurrence of important livestock events such as outbreaks and droughts, seasonal calendars to visualise the seasonal livestock-related activities and occurrence of different disease problems, and proportional piling to visualise the relative importance of disease problems. It was important that the veterinarians facilitating the discussions were open-minded and flexible, ready to set aside their biomedical knowledge to learn from the livestock keepers who had valuable expertise in livestock keeping in the area. The data collected were mainly qualitative leading to a rich description of the discussions, supplemented by maps, diagrams and some quantitative data from ranking and scoring methods.

Participatory epidemiology was valuable in comparison to more conventional survey methods because it allowed the investigators to explore the social context in which disease occurred, as well as other aspects of the host-agent-environment interaction. For areas that were not well covered by existing surveillance systems, participatory surveillance could rapidly fill gaps in knowledge, and could complement other surveillance methods to provide context and interpretation of other data. The approach also strengthened relationships between livestock keepers and veterinarians, leading to improved engaged with animal health services such as outbreak reporting and participating in disease control programmes.

An early example of the application of PE were during the rinderpest eradication programme in South Sudan in the early 2000s, when participatory surveillance was carried out in high-risk areas in order to contribute evidence of the elimination of rinderpest virus, to complement outbreak reporting and investigation and serological surveys [4]. This approach was later successfully adapted for highly pathogenic avian influenza surveillance in Egypt, and in East and West Africa [5].

PE was used during field studies of peste des petits ruminants (PPR) outbreaks in Ngorongoro District, Northern Tanzania [6], which found that there was a wide variation in the clinical presentation and severity of PPR disease and the different syndromes were associated with a variety of local disease names, which had important implications when communicating with livestock keepers about PPR reporting and vaccination. Similar field studies in pastoralist areas of Ethiopia led to the training of Ethiopian vets based in lowland areas to carry out participatory surveillance for PPR. Participatory surveillance led by these vets detected and confirmed more than one hundred outbreaks and provided information to delineate areas for targeted vaccination of millions of sheep and goats.

PE has also been applied to endemic disease problems in temperate areas, such as a project to improve the management of fasciolosis and triclabendazole resistance on hill sheep in north-west England: sheep farmers came together with veterinarians and researchers to share their experiences of fasciolosis impact and management in regular meetings, and over time learnt and put into practice testing, treatment and management practices that fitted with the hill sheep farming system and reduced the cost and impact of fasciolosis [7].

PE approaches and methods can contribute to field research and surveillance in a variety of contexts to explore complex problems and can complement structured surveys and surveillance methods. The process can be empowering for livestock keepers, depending on the design of the process and the level of participation.

References

[1]. Catley A., Alders R.G., Wood J.L. (2012). Participatory epidemiology: approaches, methods, experiences. Veterinary Journal 191, 151-160.

[2]. Chambers R. (1992). Rural appraisal: rapid, relaxed and participatory. IDS Discussion Paper 311. Institute of Development Studies, UK, 68.

[3]. Mariner J.C., Paskin R. (2000). Manual on Participatory Epidemiology: methods for the collection of action-oriented epidemiological surveillance. FAO Animal Health Manual 10. Food and Agriculture Organization of the United Nations Rome.

[4]. Jones B.A., Ameri A.A., Mogga N.K., Letereuwa S.P., Leyland T.J. (2022). Community-based rinderpest control and surveillance in South Sudan. Chapter 3.9, pages 193-206. In: Taylor W.E., Gibbs E.P.J., Bandyopadhyay S.K., Pastoret P-P., Atang P. (2022). Rinderpest and its eradication. Paris, OIE and FAO, 816 p. (DOI: https://doi.org/10.20506/9789295115606). Licence: CC BY-NC-SA 3.0 IGO.

[5]. Mariner J..C., Jones B.A., Hendrickx S., El Masry I., Jobre Y., Jost C.C. (2014) Experiences in Participatory Surveillance and Community-based Reporting Systems for H5N1 Highly Pathogenic Avian Influenza: A Case Study Approach. EcoHealth doi: 10.1007/s10393-014-0916-0

[6]. Jones B.A., Mahapatra M., Chubwa C., Clarke B., Batten C., Hicks H., Henstock M., Keyyu J., Kock R., Parida S. (2020) Characterisation of Peste Des Petits Ruminants Disease in Pastoralist Flocks in Ngorongoro District of Northern Tanzania and Bluetongue Virus Co-Infection. Viruses, 12, 389. https://doi.org/10.3390/v12040389

[7]. Carson A., Jones B., Grove-White D. (2022), Managing liver fluke on hill farms. Veterinary Record, 191: 115-117. https://doi.org/10.1002/vetr.2105

Emerging and vector borne viral diseases

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In the 1960s-1990s, most vector-borne diseases were not considered a threat to humans or animals. However, since the late 90s, the frequency of epizootics and the geographical distribution of vector-borne diseases (as Chikungunya virus, Dengue virus, West Nile virus, tick-borne encephalitis virus, etc.) have tended to increase, and can pose serious threats to veterinary or public health. Europe is confronted with numerous vector-borne diseases some of them being zoonotic, and with the risk of introduction and emergence of exotic vector-borne diseases.

This paper deals with four specific vector-borne diseases: the epizootic haemorrhagic disease (EHD), African Horse Sickness (AHS), West Nile Fever (WNF) and Tick-borne encephalitis (TBE).

Non-zoonotic emerging infectious diseases

Epizootic haemorrhagic disease

Epizootic haemorrhagic disease (EHD) is a viral disease affecting wild ruminants (especially deer) and domestic ruminants (cattle and, to a lesser extent, small ruminants). Epizootic haemorrhagic disease virus (EHDV) belongs to the Sedoreoviridae family, genus Orbivirus. The virus is transmitted between animals by hematophagous biting insects of the Culicoides genus. It cannot be transmitted to humans. However, in cattle, this disease is potentially fatal. It causes fever, anorexia, lameness and respiratory distress. Small ruminants can also carry the virus but no symptomatic cases have been reported so far. In Europe several suspected EHDV vectors are present, including potential vectors such as: C. imicola and suspected vectors within the Pulicaris and Obsoletus complexes. Because these insect vectors and the virus are killed after the onset of frost, outbreaks are seasonal, typically occurring in late summer or early fall.

EHD was first described in 1955 in New Jersey, USA. A severe outbreak of the disease in white-tailed deer (Odocoileus virgininianus) was reported by the authorities. The virus has since spread to Asia, Australia and Africa, but until last year no cases had been detected in Europe. In 1959, EHDV-serotype 2 was isolated against all expectations in cattle in Ibaraki, Japan in 1959. This virus is able to cross the placental barrier resulting in abortions and malformations. Several studies demonstrated that EHDV serotypes 1, 2, 6, 7 and 8 induce clinical signs in cattle. Clinical signs in cattle are similar to those exhibited by Bluetongue (BT) affected animals. In cattle morbidity varies from 1% to 18%, but mortality is usually low. There is no effective and broadly applicable treatment for EHD.

The EHDV is notifiable in the Member States, under EU Animal Health Law, and has been a listed disease by World Organization for Animal Health (WOAH) since 2008. To date, there are 8 recognised serotypes of EHDV, though it is likely that more exist (Pirbright, 2022). EHDV has been spreading in Europe since November 2022, with the first outbreaks reported in Italy (Sardinia) and Spain. EHDV-8 is the serotype previously reported in Italy, Spain and Portugal. In case of an outbreak of EHD in the EU, key actions should include detection of infected animals, epidemiological investigations, restriction of movements, and eventually, long term surveillance.

At the end of 2022, firsts cases in Europe were reported in Sardinia, Sicily and in Andalusia (Spain).

In 2023, the Spanish Ministry of Agriculture, Fisheries and Food have documented the spread of EHDV across mainland Spain. At the same time, France faced its first outbreak of EHD. Following initial confirmation of EHD in France on 21 September 2023, 3,527 outbreaks have been recorded on farms in southern France, primarily in Pyrénées-Atlantiques, Hautes-Pyrénées and nearby municipalities (MASA 2023). With France and Spain reporting a significant increase in outbreaks on cattle farms, this has caused an expansion of the restriction zone further North to include more Northern departments of France and the whole of Spain being under movement restrictions. This is a consequence of climate change that enables the midge vectors to survive in our regions and to be transmitted by wind from infected surrounding countries.

An extension of EHD geographical distribution is feared in the comining years considering the climatic changes Europe is facing.

African Horse Sickness (AHS)

African horse sickness (AHS) is a major, highly contagious arbovirosis that mainly affects equidae in sub-Saharan Africa. It mainly affects horses; mules, donkeys and zebras are less susceptible. The disease can take four forms: (i) a mild form characterized by fever lasting 5 to 8 days, followed by recovery; (ii) a pulmonary form defined by high fever, cough, frothy nasal discharge and difficulty breathing. The mortality rate is very high (around 95% of infected animals), (iii) a cardiac form characterized by fever, swelling of the head and neck and changes in the mucous membranes. The mortality rate is 50% of cases, and (iv) a cardiopulmonary form in which animals present a mixture of the symptoms described above [2].

The infectious agent is African horse sickness virus (AHSV), a member of the Reoviridae family and the Orbivirus genus, as bluetongue virus. The virus is transmitted by blood-sucking midges of the Culicoides genus during a blood meal. AHSV virus comes in nine antigenic serotypes, between which there is little or no cross-protection. Vaccination is often difficult to implement. In infected or directly threatened countries, vaccination will be carried out using a monovalent vaccine corresponding to the type predominant in these regions. In newly-infected regions, it is necessary to wait for the isolation and characterization of the virus in question before implementing vaccination. As a result of global warming, we are currently witnessing a worldwide expansion in the range of its vectors. Several spectacular epizootics (Iberian Peninsula, 1965-66/1987-90 and Thailand in 2020) have taken the disease out of Africa, alerting veterinary health authorities to the real threat it poses to the world's equine livestock, due to its spectacular presentation and rapid spread. These factors mean that there is every reason to fear that African horse sickness could be introduced into free regions such as France and Europe. Strict control of live equidae when imported, and the establishment of a quarantine system, are currently used to protect free zones. Serological tests may be required, and must be interpreted in the light of any previous vaccination.

Zoonotic emerging infectious diseases

West Nile Fever (WNF) and Tick-borne Encephalitis (TBE)

Within the Flaviviridae family, Orthoflavivirus genus, West Nile virus (WNV) and tick-borne encephalitis virus (TBEV) are circulating in Europe and can cause neurological disorders in humans and equines. The former is transmitted by mosquitoes of the genus Culex, while the latter is transmitted by ticks of the genus Ixodes and Dermacentor.

West Nile virus emerged in Europe in the 1960's in countries located in the Mediterranean border. The virus spred over the 5 continents with the exception of Antarctica. It is maintained in an enzootic transmission cycle between mosquitoes (Culex spp) and birds considered as reservoir and amplifying hosts. Mammalian species can be infected through the bite of an infected mosquito but are considered as dead-end host for the disease. After being bitten by the infected mosquito, and following an incubation period of 5 to 15 days, around 10 to 15% of equids show signs of encephalomyelitis. Other infested animals show no symptoms at all, or frustrated signs associated with a short-lived viremia. No risk factors related to age, sex or breed have been identified.

Initial symptoms are non-specific, and include inconstant fever (up to 40°C), anorexia, lethargy, signs of colic and musculoskeletal disorders (lameness). Neurological disorders occur at a later stage, and are mainly characterized by ataxia (57-100% of cases) and weakness (30-100% of cases), which may affect the forelegs, hindlegs or all 4 limbs, as well as muscular fasciculations, mainly on the head and neck (42-100% of cases). Some horses show brain stem disorders, with drowsiness and/or hyperexcitability (or even aggressiveness), and cranial nerve damage (facial paralysis, bruxism, amaurosis, vestibular syndrome or dysphagia). The severity of clinical signs varies from one individual to the next, and may extend to decubitus and coma. Clinical signs are identical regardless of virus lineage. The mortality rate for animals with neurological disorders is between 25% and 40%; around 20% of animals that survive retain long-term sequelae, such as weight loss, ataxia, weakness or cranial nerve abnormalities. Decubitus animals have a survival prognosis of only 20-40%.

WNV geographical distribution expansion has been confirmed over the last 5 years in Europe affecting Northern and Western countries as Germany, The Netherlands and the Atlantic coast of France. Because of climate change, international exchange, loss of biodiversity, anthropologic factors, etc WNV risk for the 20 coming years is increasing is Europe. This will require a targeted public health response to manage the expansion of WNV with climate change in Europe.

Tick-Borne Encephalitis Virus (TBEV) is the most common arbovirus in Europe. The European-subtype causes meningoencephalitis in humans, with severe long-term sequelae and death in 0.5 to 3% of cases. In Western Europe, the virus circulates naturally between Ixodes ricinus ticks and micro-mammals. Ticks have a long life cycle, and TBEV can survive throughout their developmental stages. Ixodes ticks ingest blood once in a developmental stage, and they have no chance of transmitting TBEV until they feed again. Most European countries have seen an upward trend in the number of human cases since the 2000s. TBEV also infects ruminants and wildlife (deer, wild boar, etc.). The absence of clinical symptoms in these species precludes event-based animal health surveillance. TBEV diagnosis is carried out on symptomatic patients or in direct requests from people who have been bitten by a tick and are developing symptoms. Although this virus is mainly transmitted by the bites of infected Ixodes ticks, the extent to which TBEV is transmitted via the food chain is not known. A total of 1% of TBE cases are thought to have been contracted through consumption of unpasteurized milk or raw dairy by-products from infected farm animals.

Reporting of TBE cases in the EU/EEA is compulsory in 19 countries, voluntary in four (Belgium, France, Luxembourg and the Netherlands) and ‘not specified’ in one country (Croatia), with 2,000 to 4,000 total cases reported yearly. The European Centre for Disease Prevention and Control (ECDC) has reported increases in TBE incidence over the last years and an extension of the distribution of the virus with new foci reported in non-endemic countries, making TBE a growing concern for public health.

TBEV distribution is shaped by the interplay of multiple climatic, environmental and ecological factors that exert a crucial role in the life cycle of ticks and TBEV circulation. As the TBE epidemiological situation in the EU/EEA is changing, close monitoring of such changes is required to timely adapt vaccination recommendations.

Conclusion

During the last decades, we witnessed the emergence or reemergence of vector-borne diseases. These diseases account for more than 17% of all infectious diseases, causing more than 700,000 deaths annually. Many vector-borne pathogens have appeared in new regions in the past two decades, while many endemic diseases have increased in incidence. Most of these emerging and re-emerging infections are of zoonotic origin, which highlights the importance of the human–animal interface. Given the continuous increase of emerging and re-emerging VBDs globally, there is a significant need for intersectoral coordination teams of public health practitioners, researchers, veterinarians, wildlife specialists, clinicians, environmental health specialists, and others to collaborate on emerging VBD research and surveillance in order to propose right counter measures during massive outbreaks.

One health integrated surveillance

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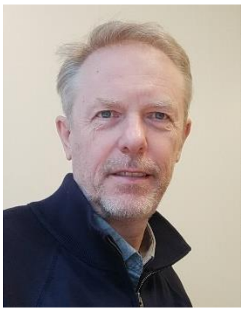

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Pascal Hendrikx is specialized in epidemiological surveillance, with a strong focus on animal health. He has also conducted surveillance activities in plant health and food safety. His work has focused on setting up and evaluating surveillance systems. He has worked in this field in France, notably for the implementation of the French National Plateform for Animal Health Surveillance (www.plateforme-esa.fr). He has also worked internationally, notably in Africa, the Caribbean and the Middle East. He coordinated the development of a surveillance system evaluation method named OASIS (www.oasis-evaluation.com), which has already been used to evaluate over sixty surveillance systems.
After holding positions in international cooperation, then at CIRAD and Anses (Scientific Director for Epidemiology and Surveillance), he is currently a member of the High Council for Food, Agriculture and Rural Areas at the Ministry of Agriculture and Food Sovereignty, where he carries out consultancy, support and evaluation missions for public agricultural policies in France.

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One Health, a concept now well established in the health sector

It is difficult to separate the health of humans, animals and ecosystems. Animal health, particularly through zoonoses, is recognized as a factor in the human environment that impacts on human health. The health of ecosystems, whether through pollution or the risks posed to man by the loss of biodiversity, is also a major factor. Symmetrically, preserving human health by, for example, reducing the presence of chemical compounds harmful to health will preserve ecosystem health and biodiversity by reducing its subsequent chemical contamination.

In 2021, the WHO, OIE, FAO and UNEP set up a One Health High-Level Expert Panel (OHHLEP) competent for all three health areas (human, animal and environmental), which defined the concept [1]: "One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems. It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and interdependent. The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for healthy food, water, energy, and air, taking action on climate change, and contributing to sustainable development".

The emergence of complex epidemiological events challenging One Health surveillance

The risk of infectious diseases requiring a One Health approach has been rising steadily in humans and animals since the end of the Second World War [2], with a trend towards global emergence in the form of pandemics or panzootics.

Several of these emblematic events are linked to changes in the epidemiological form of these diseases, which challenge our capacities for anticipation and surveillance.

This is the case, for example, with highly pathogenic avian influenza (HPAI), which has seen a marked increase in circulation in wildlife over the last few years. This intense circulation also increases the risk of crossing the species barrier with the repeated contamination of wild and domestic mammals. This phenomenon of crossing the species barrier was evident in 2023 in France with the contamination of a domestic cat [3], foxes [4] and bears in captivity [5]. The risk of damage to biodiversity is also apparent, with the impact of the disease on gannet colonies in Brittany in 2022 [6].

If we broaden the geographical scale, we might also mention the Ebola fever virus in West Africa in 2014, which led to an unprecedented epidemic that was completely unexpected in terms of its location and scale, resulting in 17,000 cases of infection in just a few months, including 6,000 deaths in mainly three countries (Liberia, Sierra Leone, Guinea) [7]. Beyond the dramatic health impact and the social disruption that the disease may have caused in the affected countries, the epidemiological enigma remains unanswered in terms of the origin of the infection and therefore the risk of seeing the same event recur [8].

It's hard not to end this list of examples without recalling the surprise effect that followed the onset and spread of Covid-19, which at least had the advantage of popularizing epidemiology and providing the general population with a basic knowledge in infectious diseases.

We could go on and on with a long list of emerging or potentially emerging subjects, or diseases whose evolution has inevitably caught the populations and health authorities concerned off guard. The first consequence of this surprise effect in the face of new health events is the feeling that our surveillance methods and tools are failing. This calls into question our capacity for early detection of the onset of new diseases or the reoccurrence of exotic threats.

From an integrated vision of surveillance to the notion of collaboration

Surveillance as applied to the One Health concept is the subject of numerous definitions. Some simply apply the definition of surveillance by extending the perimeter of the target populations to include humans, animals and the environment [9][10]. A classic surveillance system is organized around a large number of stakeholders distributed from the field (data sources, data collectors) to the intermediate level (for proximity coordination and first-line laboratory analyses) to the central level (coordination, data analysis and interpretation, steering and scientific support). Considering that a One Health surveillance system could potentially integrate several sectors (human, animal, environment), we understand that this system could be extremely complex to design and operate in practice.

This is why some authors include the notion of collaboration in the definition of One Health surveillance [11][12], which Bordier consider to be the central issue when addressing the concept of One Health surveillance [13]. The issue then becomes the collaboration between sectoral surveillance systems dedicated to the same disease but in different sectors. Bordier's work has shown that several models of collaboration (she defines four) can exist between sectoral surveillance systems, which differ in their intensity and level of integration of surveillance systems.

This shows that a One Health surveillance system does not necessarily need to be fully integrated to operate properly. This is an interesting observation, as it allows to envisage the evolution of various systems already in operation towards One Health surveillance, without necessarily calling into question all the existing components. This allows greater respect for existing stakeholders, and avoids the reluctance often expressed when trying to force certain stakeholders to integrate their activities with those of others.

Nevertheless, further work is still needed to enable the systems to communicate, share data and interpretations, and above all to draw up recommendations for action that are consistent across the different sectors they address. The experience of the epidemiological surveillance platforms in animal health, plant health and food chain safety set up in France is interesting in this respect (www.plateforme-esa.fr).

Evaluating One Health surveillance systems

The operation of a One Health surveillance system also raises the question of its evaluation. As with its construction, evaluation can be implemented at several levels. The first level is the sectoral systems constituting the overall One Health system. These systems can be assessed using classic tools such as the Oasis tool [14] (www.oasis-evaluation.com), which has proven its robustness in assessing a wide range of surveillance systems (notably in animal health, plant health, food chain safety and vector surveillance), and which is well suited to assessing each of the sectorial systems of a One Health system.

Collaboration being at the heart of a One Health system, Bordier has developed a collaboration assessment method called Ecosur [15] to assess the degree of “One Healthness” of surveillance and to draw up recommendations for its improvement. Based on the Ecosur principle, a working group on the evolution of the Oasis evaluation tool is in the process of integrating criteria for assessing the collaboration of a sectoral surveillance system.

In practice, an evaluation of a One Health surveillance system could begin with an individual assessment of each of its sectorial surveillance systems, using the Oasis method, and end with an overall assessment of collaboration between systems, using the Ecosur method. This is what was done, for example, for the evaluation of the One Health Salmonella surveillance system in France [16].

References

[1]. Mettenleiter T.C. et al., (2023). The One Health High-Level Expert Panel (OHHLEP), One Health Outlook, 5(1), 18, doi: 10.1186/s42522-023-00085-2.

[2]. Morand S., Walther B.A., (2020). The accelerated infectious disease risk in the Anthropocene: more outbreaks and wider global spread, bioRxiv, p. 2020.04.20.049866, doi: 10.1101/2020.04.20.049866.

[3]. Anses 2023. Anses - Un chat infecté par le virus de l’influenza aviaire. 2023, Anses, 24/01/2023, https://www.anses.fr/fr/chat-infecte-virus-influenza-aviaire

[4]. OMSA 2023. OMSA - France - Influenza A de haute pathogénicité – Notification immédiate. WAHIS, 06/03/2023, https://wahis.woah.org/#/in-review/4941

[5]. Durand V. (2023). Grippe aviaire : un ours de la Réserve africaine de Sigean contaminé décède lors d'une anesthésie générale. L’indépendant, 2023, 28/02/2023, https://www.lindependant.fr/2023/02/28/grippe-aviaire-un-ours-de-la-reserve-africaine-de-sigean-est-mort-en-octobre-dernier-11028287.php

[6]. Tour du Valat. (2022). Influenza aviaire- Mortalités massives observées chez les fous de Bassan de la réserve des Sept-îles - Questions à Pascal Provost. Tour du Valat [En ligne], 24/11/2022, https://tourduvalat.org/dossier-newsletter/ influenza-aviaire-mortalites-massives-observees-chez-les-fous-de-bassan-de-la-reserve-des-sept-iles-questions-a-pascal-provost/

[7]. Loungou S. (2015). L’épidémie d’Ebola en Afrique de l’Ouest. L’Espace Politique [En ligne], 26(2). doi:10.4000/espacepolitique.3467

[8]. Calvignac-Spencer S., De Nys H.M., Peeters M., Leendertz F. H. (2015). Maladie à virus Ebola : une zoonose orpheline ? Bull. Acad. Vét. France, 168(3). doi:10.4267/2042/57933. 233-238

[9]. Stärk K.D.C. et al. (2015). One Health surveillance – More than a buzz word?, Prev. Vet. Med., 120(1), 124-130, doi: https://doi.org/10.1016/j.prevetmed.2015.01.019.

[10]. Berezowski J., Akkina J., Vilas V.D., DeVore K., Dórea F.C., Céline Dupuy C.D., Streichert L. (2016). Is There a Need for One Health Surveillance (OHS)? Online Journal of Public Health Informatics, 8(1). https://doi.org/10.5210/ojphi.v8i1.6411

[11]. Hattendorf J., Bardosh K.L., et Zinsstag J., (2017). One Health and its practical implications for surveillance of endemic zoonotic diseases in resource limited settings, Fate Neglected Zoonotic Dis., 165, 268-273, doi: 10.1016/j.actatropica.2016.10.009.

[12]. Karimuribo E.D. et al., (2012). Towards one health disease surveillance: the Southern African Centre for Infectious Disease Surveillance approach: proceeding, Onderstepoort J. Vet. Res., 79(2), 1-7.

[13]. Bordier M., Uea-Anuwong T., Binot A., Hendrikx P., Goutard F.L., (2020). Characteristics of One Health surveillance systems: A systematic literature review., Prev. Vet. Med., 181, 104560, doi: 10.1016/j.prevetmed.2018.10.005.

[14]. Hendrikx P. et al., (2011). OASIS: an assessment tool of epidemiological surveillance systems in animal health and food safety, Epidemiol. Infect., 139(10), 1486-1496, doi: 10.1017/S0950268811000161.

[15]. Bordier M., Delavenne C., Dung N, Thi T., Goutard F.L., Hendrikx P., (2019). One Health Surveillance: A Matrix to Evaluate Multisectoral Collaboration, Front. Vet. Sci., 6, 109, doi: 10.3389/fvets.2019.00109.

[16]. Bordier M., Benhmidene G., Delavenne C., (2020). Assessment of collaboration between the networks contributing to the salmonella surveillance system in France., 77, 85-102.

The added value of molecular biology and bio-informatics in epidemiology

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Steven Van Borm obtained his PhD in Biology (Molecular Ecology) from the University of Leuven, Belgium. He joined the Virology Department of the former Veterinary and Agrochemical Research Center, now part of Sciensano, in 2003, successively working as project scientist and senior scientist, and leading the Molecular Platform group (a centralized molecular virology expert pool). He is currently working in the Avian virology and immunology unit, Belgium's national reference laboratory for avian influenza and Newcastle disease virus.

His main activities are in the field of the development and validation of molecular diagnostic assays for livestock priority virus detection, and in the genetic characterization of animal viruses. Over the last 12 years, he has been involved in the application of Next Generation Sequencing (NGS) data to veterinary virology and the use of viral genomic data in molecular epidemiology.

He coordinated two European research projects on molecular epidemiology and sequencing technologies and was partner in several international and national research projects, resulting in 83 peer-reviewed publications.

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Massive parallel sequencing technologies have revolutionized many areas of biological sciences and medicine. Benefits include unprecedented sequencing capacity, cost per information unit (nucleotide), flexibility for targeted vs. unbiased sequencing, scalability, and the capacity to sequence virus populations in individual samples in depth.

Veterinary virology is no exception, with published research applications including quasispecies analysis, unbiased characterization of mixed infections, virome analysis in diseased animals or reservoir species, host-pathogen interaction, and viral evolution under immune or treatment pressure.

The technology is on the verge of bridging the gap between the research and diagnostic laboratory, with potential applications in full genome or targeted genetic characterization (genotyping, phenotyping, molecular markers), metagenomic identification of unknown or unexpected pathogens, and high resolution molecular epidemiology and outbreak tracing.

This talk will illustrate the current and future diagnostic added value of NGS data, some obvious pitfalls in its application in veterinary virology, using the highly pathogenic avian influenza H5 outbreaks.

Biological weapons and epidemiology

Prof. Dr. Maria J. Espona

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Maria J. Espona, Biologist (1994), Master in Terrorism Studies (2013) and Doctor in Criminology (2019). She is an expert in the WMD field, especially in the CBW arena and export control. She has several publications on those topics. She teaches in universities in Argentina, Georgia and Peru, on Information Quality, CBRN export control and dual-use and responsible use of data.
Currently she is the leader of the following project: TI CBRN Export Control on Dual-Use Materials and Intangible Technologies in Central Asia (ISTC). She also participates as SME in several Health Security Partners and Coalescion projects on biorisk management and export control, among other topics, in Latin America and other regions. She is South America's EU P2P Regional Coordinator and works with SCK-CEN on an export control-related project.
In the past, she participated in EU-funded projects on CBRN and export control of dual-use goods and technologies.
She is a member of the WHO's Technical Advisory Group on the Responsible Use of the Life Sciences and Dual-Use Research (TAG-RULS DUR).
She holds several awards for her work on Information Quality and leadership. Since 2021, she has been the CDO Ambassador to Argentina from CDOIQ, isCDO, and CDO Magazine.
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According to the WHO, biological and toxin weapons are either microorganisms like viruses, bacteria, or fungi or toxic substances produced by living organisms that are deliberately produced and released to cause disease and death in humans, animals, or plants.

The categories of biological risks caused by infectious diseases considered here range from a naturally occurring outbreak or the accidental release of a pathogen (for example, a lab accident) to the intentional use of biological agents, including biocrime, bioterrorism, and biological warfare.

Since infectious diseases occur, generally with a consistent pattern, it is possible to consider that any anomalies are events that require further investigation. But infectious diseases don’t occur in a vacuum; they happen to humans, animals, and plants that live on our planet, which undoubtedly is experiencing an accelerated climate change process affecting all living beings (causing their extinction or adaptation) and the environment and other man-made phenomena such as wars. Consequently, epidemiological studies of infectious diseases have gone up in complexity over the past few years and require an even broader range of experts and data to understand a disease outbreak and its origin.

When an outbreak is detected, the first impression is the same for any of the categories mentioned above: humans, animals, or plants are getting sick. However, the values of the disease parameters will tell more about its origin, for example, location, affected living being, time, mortality, transmissibility, etc. So, to understand what is going on, the surveillance mechanisms in place should be able to answer the what, where and when questions.

In 2020, we had the SARS-CoV-2 pandemic, whose origin was controversial, and many scientists considered it the result of a lab leak in China. Others supported its natural origin, and this hypothesis is most accepted today. In the last few months, zoonotic disease experts have been challenged by the spread of avian influenza across the regions and new and unexpected hosts such as sea mammals and, later, cows. Is it the transmissibility ability of the virus changing in such a way that it will become the next pandemic? What will happen with the agribusiness and the economies that depend on their cattle and other farm animals if the animals start to die massively or must be killed to avoid further transmission? These questions are difficult to answer, and the probable scenarios are scary.

For many years, biological weapons experts have considered the possibility of agroterrorism as an intentional event most dangerous because of the spillover effect over the economy and society at the country, region and world level.

But there is not all bad news. Technological advances are helping to detect diseases accurately and, in many cases, early, reducing their impact or allowing real-time tracking of their progress, helping to contain outbreaks.

Also, living in the information age has the benefit of having almost all the activities that take place worldwide leave a digital footprint, which generates data that leads to information that could be later analyzed. This is happening in some countries, but unfortunately, it is not to the extent that it would have a meaningful contribution to early detection and reducing the impact of an infectious disease outbreak worldwide.

Some information is usually collected and accurately traced, like the geographical distribution or identification of the specific strain involved. But other sources can even be traced and it is not that complicated, such as:

- Outbreak alerts: from official or non-governmental sources such as PROMED;
- Identification of the strains present in the sick/dead organism: amount, features and genetic information (including bioinformatics analysis of the available data);
- Change in the patterns of emergency calls or requests for nurse assistance (and the equivalent for animal and plant health);
- Changes in over-the-shelf medicament sales (and the equivalent for animal and plant health);
- Out of usual use of vaccines or other available treatment;
- Reports of abnormal situations from slaughterhouses and silos and grain collectors;
- School and work absence record;
- Other changes in usual social patterns (decrease in the use of cars or public transport, attendance to restaurants or other public places, etc)

The constant tracking of the above-mentioned indicators could be used as an early warning alert that will identify any anomaly, consequently, trigger a timely response, and help determine the outbreak's origin.

But these indicators must also be considered in the broader picture of the geographical location in which the anomaly is detected. That includes considering whether there is a conflict (involving both states or terrorist organizations), whether the actors have or are suspected of having a biological weapons arsenal, massive migrations (of people but also animals), the presence of high-containment labs, environmental changes, etc.

Made by experts and/or with the help of artificial intelligence, a better understanding and response to outbreaks is closer than ever, despite their origin, by collecting and analyzing the available data. This is an improvement that will contribute to enforcing the much-needed One Health approach.

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Selected Oral Presentations

Selected oral presentations

Modeling High Pathogenicity Avian Influenza: Integration of Sociological and Environmental Factors

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Since 2015, the recurring outbreaks of High Pathogenicity Avian Influenza (HPAI) have posed significant challenges for the French poultry industry, leading to substantial economic and social consequences. Despite improvements in biosecurity protocols and regulatory revisions, ongoing epizootics highlight the need for a deeper understanding of the virus transmission mechanisms. Our project aims to understand the introduction and the spread mechanisms of HPAI in poultry farms in France and to analyze feasible control measures considering their efficacy and their acceptability for stakeholders in the poultry sector. A critical aspect of our approach is the integration of social and economic components into epidemiological modeling, a crucial tool for understanding the mechanisms of pathogen spread. Remarkably, literature in the field of animal diseases rarely incorporates these important components, a gap our study intends to fill by specifically addressing the HPAI issue in France.

To achieve our objectives, we are developing an agent-based spatio-temporal epidemiological model using the Gama platform, which has already demonstrated its effectiveness in addressing similar issues in human populations. This model is designed to incorporate various parameters, including both socio-economic factors and environmental variables. Our approach adopts a multidisciplinary framework that draws on diverse research techniques. The socio-economic component of the study employs a participatory approach involving interviews and focus groups with various stakeholders, including farmers, veterinarians and decision makers. Tailored interview guides are designed to ensure detailed data collection. The resultant insights are pivotal for addressing questions such as, 'What are the sociological and economic determinants of infection dynamics and their interplay with epidemiological processes?' These insights are instrumental in informing the multi-agent-based epidemiological model, ensuring a dynamic integration of socio-economic reasoning with epidemiological processes.

Regarding environmental variables, we analyzed the 2022-2023 HPAI outbreaks in poultry farming to examine the common environmental variables associated with the outbreaks. The k-medoids clustering with Gower distances was applied to detect clusters of outbreaks based on similar environmental characteristics. Random forests were employed to assess the importance of environmental and intrinsic variables of poultry farms in the building of these clusters. This approach was conducted twice: first considering all variables, then focusing on environmental variables (e.g., neighboring farm number, high-risk areas, roads,), to measure their role in the cluster building. This identified two clusters with similar characteristics in both scenarios. Farm characteristics, such as type and species of poultry farming, were crucial. Additionally, environmental factors like proximity to highrisk areas, number of neighboring farms, and distance to the coast were relevant, allowing for equivalent classification of outbreaks irrespective of the intrinsic farm characteristics.

This ongoing work is, to our knowledge, the first attempt to integrate environmental, social, and economic components into an HPAI-focused agent-based model within the French context whereas such approach was used in numerous models for human populations. Therefore, our study aims to enhance our understanding of the mechanisms of HPAI introduction and spread while identifying and assessing effective and feasible control strategies. This comprehensive approach promises to offer valuable insights for managing HPAI outbreaks more effectively in the future.

A highly efficient ELISA to specifically detect CCHFV antibodies in animals and humans

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Introduction:

Crimean-Congo hemorrhagic fever (CCHF) is a tick-borne illness caused by the Crimean-Congo hemorrhagic fever virus (CCHFV). It sporadically affects humans in Africa, South Asia, and Southern Europe, causing a potentially fatal hemorrhagic illness. While infected animals are asymptomatic, viraemia and anti-CCHFV antibodies can be detected. This study validates a new CCHF double antigen ELISA for anti-CCHFV nucleoprotein antibodies detection on serum/plasma and filter paper (FPS)/dried blood spot (DBS) samples. This recombinant protein-based ELISA can be run under standard biosafety conditions.

Materials and Methods:

Sensitivity was assessed on 95 cattle and 176 small ruminants' sera with confirmed antibody status with 3 serological assays. Specificity was evaluated on 402 cattle and 804 small ruminants' sera from CCHFV-free areas (France, Germany). Monkeys, camels, rats, ferrets, raccoon dogs, raccoons, foxes, hares, pigs, and humans' negative sera were tested to ensure the ELISA's efficacy across multiple species. FPS/DBS application was validated by testing 8 CCHF-negative samples and serial dilution of 4 CCHFpositive samples.

Results:

All negative sera (n=2136) were confirmed by this new ELISA, indicating a specificity of 100% [99.8-100]. Measured diagnostic sensitivity was 98.9% [96.8-99.8]. Analytical sensitivity obtained with DBS is slightly inferior compared to serum application, which does not affect diagnostic sensitivity of the FPS/DBS application. All samples tested in parallel with serum and filter paper protocols gave the same results. Conclusion: This novel ELISA demonstrates excellent specificity and sensitivity, adapted to the accurate detection of anti-CCHFV antibodies in animals and humans, on serum/plasma or filter paper/dried blood spot samples.

Forest dynamics and acari-borne diseases: lessons from a scoping review

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Forest cover has been under considerable change that has accelerated for the past decades. Acari vectors like ticks and chigger mites are closely related to forest ecosystems because of the hosts and suitable microclimate they provide. We don't know how forest cover change and forest dynamics will impact acari vectors and the pathogens they carry in the future. What are the impacts of forest dynamics on the risk of acari-borne disease worldwide in the literature?

The objective of this work is to estimate the global effects of forest dynamics on acari-borne diseases worldwide. We performed a scoping review to answer this question.

From this work, it appears that the influence of forest dynamics on acari-borne diseases remains a primarily Western centric concern (Ixodes and Lyme disease). We didn't find a proper consensus in the literature: a fair number of articles recorded either a protective or a risk effect, a nonlinear relationship, and the presence of dependent or a non-significant effect both for the pathogen or the vector regardless of forest dynamic and location studied.

It remains difficult to speak about reforestation, conversion, and impacts in a tropical context as there is a tiny sample. We show a difference in result tendency when we compare the whole article sample and when we select only the empirical studies. The dilution effect is overestimated in literature reviews compared to how it is observed in empirical studies. We identified an absence of scrub typhus disease in the context of forest dynamics.

Such a synthesis had never been done. So this scoping review gives a comprehensive view on the literature worldwide on the impacts of forest dynamics and enables us to identify research gaps to target in the future.

Uncovering New Pathogens in Bovine Diseases through Comparative 16S rRNA sequencing

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Traditionally, the characterization of bacterial pathogens relied on in vitro culture, a method limited by the fastidious nature or slow growth of clinically significant organisms, often leading to diagnostic challenges in complex samples. To address this diagnostic gap, modern techniques such as DNA sequencing have emerged.

Here, we present our investigation aimed at identifying new causal pathogens associated with common diseases in cattle by comparing the bacterial populations present in swabs from healthy and sick animals. Focusing on two prevalent conditions, bovine respiratory syndrome (BRD) and endometritis, we sampled both sick and healthy control animals for 16S ribosomal RNA (rRNA) gene sequencing.

Analysis revealed notable findings for BRD, including the significantly elevated presence of *Helcococcus ovis*, *Ureaplasma diversum*, and *Mycoplasma dispar* in post-mortem lung samples with macroscopic lesions compared to healthy counterparts.

In endometritis cases, we observed lower bacterial diversity with an increased abundance of Firmicutes and Fusobacterium phyla. Notably, *Helcococcus ovis* emerged as the fourth most prevalent bacterium in endometritis samples, significantly more abundant than in healthy cows.

Our findings underscore the potential role of these newly suspected causal pathogens in BRD and endometritis. By implementing routine PCR targeting these organisms in diagnostic workflows, we aim to validate our observations and address the diagnostic challenges encountered in unresolved cases of endometritis and BRD.

This approach promises to enhance our understanding of disease etiology and improve diagnostic accuracy in cattle health management.

Challenges on data collection on antibiotic use in companion animals and horses

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Reporting antibiotic (AB) use in the data collection system (DCS) Sanitel-Med has been legally mandatory for veterinarians since 27 February 2017 for pigs, broilers, laying hens and veal calves, and since 10 August 2023 for all other cattle and poultry. AB-use notifications collected in Sanitel-Med are processed by the data analysis unit of AMCRA, according to a specific methodology, to benchmarking reports for farmers and veterinarians on the one hand and summary reports for the animal sectors and the Government on the other hand. From 2026 onwards, data collection on AB-use will be obliged in all EU-member states for horses (food and non-food producing) and from 2029 onwards for companion animals (dogs, cats and fur animals), following the implementation of the European Regulation 2019/6.

The need to and preferred methodology for analyzing and reporting AB-use at the level of these sectors and the responsible veterinarians (or practices) is currently a topic of discussion in Belgium. In collaboration with the federal agency for medicines and health products, and veterinarians from the companion animal and horse sectors, AMCRA is exploring the challenges specifically coming along with these two sectors. Benchmarking reports for veterinarians and/or practices should not only provide feedback on their application of AB, but also have an awareness-raising effect. Benchmarking has already proven successful in reducing AB-use in food-producing animals.

Crucial in a fair benchmarking system are reliable denominator data, consisting of the population ‘at risk’ (number of animals at risk x weight/animal), which requires a different approach than for food-producing species, where all animals present in a farm are considered ‘at risk’ for AB-treatment and standard weights are linked to age or production categories. Existing Belgian databases for companion animals and horses lack easy access and are difficult to get up-to-date. Information on the number of animals ‘at risk’ as well as on the animal weight should therefore be gathered at the practice level, however in a standardized manner. Since animals in both sectors are more diverse, actual hence more accurate animal weights, which require careful recording by the veterinarian, need to be considered against easier implementable yet more crude standard weights. As for the numerator data, being the amount of AB administered, provided or prescribed by the veterinarian or the pharmacist, a dose-based numerator is preferable to negate dose differences between AB of different potency.

Collecting additional information concerning the AB-use, such as (e.g.) vet specializations, and age of animals treated needs to be carefully considered according to its (administrative) costs/benefits. In AMCRA’s experience, aiming for a more simple, yet efficient collection system, quickly launchable yet gradually expandable or refinable over time, is to be preferred over aiming directly for an ‘all-in’, (time-)costly system.

Synergistic approaches to gastrointestinal nematode control in sheep and goat flocks

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This study presents a comprehensive follow-up of gastrointestinal nematode infestations in a total population of 60 sheep and goat flocks distributed in the Walloon region of Belgium. The flocks, with a median size of 54 animals (min 8 - max 1230), were closely monitored throughout the grazing season for two consecutive years. Regular coprological analyses were carried out to assess the degree of nematode egg excretion in the faeces of randomly sampled individuals. The aim was to assess the prevalence and intensity of gastrointestinal parasitic infestations in the herds studied, and to identify potential risk factors (herd management and external factors). In addition to coprological examinations, farmers were actively involved in evaluating potential signs of parasitic infestation through a scoring system. This included assessment of body condition, cleanliness of the hindquarters and coloration of the eye mucosa. In addition, breeders were asked to observe and record the presence of clinical signs such as submandibular edema and alterations in coat condition.

While the study revealed expected variations in nematode egg excretion between different herds, it appears that herd management factors as well as environmental conditions have a direct effect on the degree of infestation. Furthermore, the use of the scoring system clearly highlighted the fact that the signs judged by breeders as "associated" with a parasitic infestation are not strictly correlated with a high degree of parasitic excretion.

These elements illustrate the need to combine observation of animals and carrying out coprological analyzes in order to achieve reasoned management of gastrointestinal nematode infestations in sheep and goats.

A first One Health integrated analysis of antibiotic resistance surveillance data in France

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Background:

National and international organizations are calling for integrated approaches to surveillance of antimicrobial resistance (AMR) in humans, animals and the environment. In France, a recent mapping of the surveillance system for AMR, antimicrobial use (AMU) and antimicrobial residues showed that France has a highly complex and fragmented surveillance system made of 48 programmes, each having their own protocols, data management and data analysis procedures, as well as annual communication of the results. Part of these programmes contributes to the EU joint inter-agency antimicrobial consumption and resistance analysis (JIACRA) reports. However, no similar attempt to jointly analyze surveillance data available at national level had been performed so far.

Building on the meta-network PROMISE (amrpromise.fr) initiated in 2021 to facilitate cross-sectoral collaborations to tackle AMR in France, the objective of this study was to explore the feasibility of a joint analysis of AMU and AMR data in humans and animals in France.

Methods:

Ten surveillance programmes on AMU and AMR in humans and animals contributed with available data over a 10-year period (2012-2021). Data were collected in a harmonized format using a common template targeting 15 combinations of bacteria-antibiotic of interest (for AMR data), and 12 antibiotic classes or substances (for AMU data). A pan-susceptible E. coli summary indicator (i.e. E. coli susceptible to a predefined panel of antibiotic classes common to human and animals) was also calculated. Data were aggregated at a regional and/or national level prior to submission. Data visualisation was performed to identify those bacteria-antibiotic combinations with sufficient coverage and data quality in both humans and animals. Geographical and temporal trends were displayed, and associations between AMU and AMR were explored both within and between sectors, using univariate and multivariate regression analyses. Results and discussion: The large dataset allowed characterisation of E. coli resistance trends at a regional level in all populations (at hospital, in the community and nursing homes and by separate animal species) over the last years. Trends differed between regions and/or populations, particularly for cephalosporins. Statistical analysis of pansusceptible *E. coli* in humans and animals showed significant associations between AMU and AMR within each sector, demonstrating that this summary indicator is relevant to confront AMU and AMR trends in humans and animals. However, no significant association between the occurrence of pan-susceptible *E. coli* in humans and animals was observed.

This work paved the way for an increased collaboration across sectors to improve our understanding of AMR, feeding on-going activities to develop a joint data warehouse and a One Health interactive report of AMU/AMR surveillance in humans and animals in France. Further steps include the addition of environmental data once these become available on a regular basis at national level.

Exposure risk of the Belgian population to antimicrobial-resistant bacteria originating from pets

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Pet cats and dogs can become infected by antimicrobial-resistant bacteria from various sources, including their environment, food, other animals, or even humans. Furthermore, their direct or indirect consumption of antimicrobials can promote the selection of resistance in both commensal and pathogenic bacteria. Therefore, pet cats and dogs can potentially act as reservoirs for antimicrobial-resistant bacteria. This may pose a serious threat to public health given the importance of antimicrobials in modern medicine, the growing population of pets in Belgium, and the lack of both data gathering and sensitization of pet owners and veterinarians regarding antimicrobials usage. The goal of this study is to assess the risk for a human to be exposed to resistant bacteria originating from pets.

To achieve this, we are developing a quantitative risk assessment model. This model integrates data coming from laboratory analysis, public surveys, previous studies and expert opinions through a Monte-Carlo algorithm to compute an estimate of the risk. Then, different scenarios can be tested by modifying the parameters of the model and observing the variations of this estimate. The model is divided into three modules, each representing transmission between pets and close-contact humans, pets and the general population, and pets and the general population.

The risk pathways identified include meal preparation, feces/urine, blood, surfaces, hair/dead skin, physical interactions, biting/scratching, living carriers, airborne transmission and vertical transmission. The populations and the pathways linking them together are represented by estimations, formulas and probability distributions.

At present, we do not yet have results from the risk analysis. The results of this model will provide insight on the magnitude of the risk of spread of AMR from pet animals to the human population. Moreover the results could help decision-makers in identifying effective ways to mitigate this risk of transmission and could be used as a basis for implementing a surveillance system in pets.

Evaluation of the performances of a M. avium subsp. paratuberculosis Ab ELISA in young cattle

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The objective of this study, was to assess sensitivity and specificity of an ELISA test for detection of paratuberculosis in cows younger than 5 years-old through a longitudinal approach.

The study is based on individual results (ELISA and PCR) of 3660 cattle coming from 82 herds registered in a voluntary program for the control of paratuberculosis which were at least tested once with ELISA between 2 and 4 years old and on which at least one PCR test was performed after 5 years old. Based on results obtained after the age of 5 years, cows with at least 1 positive ELISA and 1 positive PCR test results was classified as “infected” (n= 150) and cows with at least 3 negative ELISA and 3 negative PCR, as “free” (n=119). The results obtained with the ELISA test (ID Screen® Paratuberculosis Indirect, IDVet®, Montpellier, France) between year 2 and year 4 of age on “infected” and “free” animals were used to assess respectively the sensitivity and the specificity of the test.

On « infected » animals, 251 ELISA were performed before the age of 5 years whose 24 with a positive result which corresponds to a sensitivity of 9.6% (IC 95% : 5.9-13.2). Within the « free » animals, all of the 204 ELISA tests performed before the age of 5 years were negative indicating a specificity of 100%.

Our study confirms the poor sensitivity of serology approach for detecting paratuberculosis in cows younger than 5 years-old.

Bovine besnoitiosis: A serious threat to animal health in Belgium

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Background:

Bovine besnoitiosis is a bovine disease caused by a protozoan parasite *Besnoitia besnoiti* resulting in serious economic concern to cattle industry and also compromising animal welfare. At the beginning of the twentieth century, the disease was only identified in southwest Europe where it is considered as endemic for decades. The disease is not known to be enzootic in Belgium although sporadic cases have been described in imported animals, but is considered to be at high risk of emergence through imports of animals from endemic regions. A first outbreak was detected in a herd with clinically affected animals in May 2019. 4 other herds were later confirmed infected through grazing contact or sales of infected animals. Besnoitiosis is not a notifiable disease in Belgium where no legal measures exist to prevent its introduction nor to manage infected animals.

This study describes the results of a collective vigilance campaign carried out in the southern part of Belgium during 3 years after this first outbreak.

Materials and methods:

The serum submitted to the laboratory of the Regional Association for Animal Registration and Health (ARSIA) for IBR control at introduction were used to perform a systematic serological control of besnoitiosis on animals originated from countries considered to be at risk (France, Spain, Portugal, Italy and Switzerland). The detection of antibodies against *B. besnoiti* on these sera was performed using an indirect bi-well ELISA according to the manufacturer's instructions (The ID Screen® Besnoitia Indirect 2.0, Montpellier, France).

A Western Blot confirmation test was systematically performed on the serum of seropositive animals by the Laboratoire of ANSES (Maisons-Alfort/Niort, France).

Results:

From January 2018 to December 2022, 11.864 imported animals were screened for besnoitiosis. These animals were imported from France (99%), Spain and Switzerland. From 2018 to 2020, 0.10% of tested animals (n= 6099) were detected seropositive versus 0.40% (n=5765) in 2021-2022. The odds ratio to obtain a positive result for B. besnoiti over the years 2021-2022 versus the previous period was 4,07 (95% IC: 1,66-10,00). All positive animals came from France and from twelve different departments. Infected animals were diagnosed in 22 herds, 14 following French imports, 4 from grazing contact and 4 following purchase of animals from Belgian herds infected by imported cattle.

Conclusions:

The risk of introduction of the disease in historically free regions, through import of infected animals from endemic ones is growing each year, mainly due to the intensification of animal trade and to the lack of measures in infected countries. A legal framework is being prepared by the Belgian authorities in order to make the screening of animals originating from endemic region compulsory and to impose a quick culling of animals confirmed as infected. Given the economic impact of this disease and in order to protect European countries that are still "free", it should probably be appropriate to add besnoitiosis in the list of diseases regulated in the Animal Health Law.

In vitro and in vivo characterization of four bacteriophages targeting Aeromonas Salmonicida

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The Gram-negative bacteria *Aeromonas (A.) salmonicida* is a primary fish pathogen that causes furunculosis in salmonids as well as septicemia in a variety of fish. In one hand because this disease is responsible for significant losses in salmonid production worldwide and in the other hand because of the frightening tendency of this bacteria to exhibit antimicrobial (multi)resistances, phage therapy could represent a leading alternative to treat this infection in aquaculture. The aims of this study were to create a collection of *A. salmonicida* strains, isolate phages targeting these strains, phenotypically and genomically characterize these newly isolated phages and finally assess their potential for phage therapy in the preliminary in vivo model of *Galleria (G.) mellonella* larvae.

Four new phages active against *A. salmonicida* were isolated from water samples collected in fish farms and natural aquatic environments in southern Belgium. Genomic analysis showed that 3 of these phages, named vB_AsaM_ULASA2 (170,823bp), vB_AsaM_ULASA3 (164,381bp) and vB_AsaM_ULASA4 (171,205bp), belong to the Straboviridae family while vB_AsaM_ULASA1 (47,813bp) stays in the unclassified part of the Caudoviricetes class. All 4 presented a myovirus morphotype.

Four days efficacy experiments in the preliminary in vivo model of *G. mellonella* larvae showed that 3 of these 4 phages were responsible for a significant extension in the larval survival time at the 2 treatment doses tested (MOI 10 and 100).

In light of these results, these phages targeting *A. salmonicida* could represent potential new candidates for the development of anti furunculosis phage treatments in aquaculture.

Antimicrobial resistance characterization of MRSA and MRSP isolated in dogs and cats in Belgium

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Introduction

Methicillin-resistant *Staphylococcus aureus* (MRSA) and methicillinresistant *Staphylococcus pseudintermedius* (MRSP) have been observed in healthy and diseased dogs and cats. The interaction between humans and pets is increasing over the years and this could imply a potential risk of contamination of humans with these bacteria from infected or colonized animals. In addition, there is a possibility of transfer of resistance genes/bacteria such as *mecA* or *mecC* which code for the production of a modified penicillin binding protein, leading to resistance to β-lactam antibiotics. One of the aims of the PET-AMR project, in a One Health approach, is to assess this risk and characterize the resistance of MRSA and MRSP isolated from clinical cases in dogs and cats.

Materials and methods

Samples were collected by veterinarians and sent to different laboratories for clinical diagnosis. Once confirmed as MRSA or MRSP, the isolates were sent to Sciensano for further investigation. In this study, the isolated strains were confirmed using a triplex real-time PCR method detecting the *Staphylococcus aureus* specific gene, *nuc*, the presence of the *mecA* gene responsible for methicillin resistance and the *mecC* gene variant.

The PCR used for the detection of *mec* genes in MRSA was also used to detect *mec* genes in MRSP. The broth micro-dilution method was used to perform MIC determinations for a panel of molecules selected either for their relevance in human medicine and/or their frequent use in veterinary medicine (Sensititre EUST2 panel).

Results and conclusion

Of the 63 MRSA samples tested, 28 were from cats and 35 from dogs. All strains were positive for the *nuc* gene, 49 for *mecA* (22 cats and 27 dogs), 2 for *mecC* (1 dog and 1 cat) and 12 had neither the *mecA* nor the *mecC* gene (5 cats and 7 dogs).

For the 108 MRSP analyzed with the same PCR method as for MRSA, none of them had the *nuc* gene, as expected. Of these 108 strains, 106 were positive for *mecA* (5 cats and 101 dogs), none carried the *mecC* gene, leaving 2 strains (1 cat and 1 dog) without either resistance gene.

For the 12 MRSA strains and the 2 MRSP strains lacking typical methicillin resistance genes, further investigation would be needed to assess their resistance mechanism. Susceptibility testing of the collected MRSA and MRSP is ongoing and will give more information on their antibiotic resistance patterns.

In the context of a "One Health" approach, it is important to continue research on these zoonotic bacteria in order to safeguard human and animal health.

Stability and lytic activity assessment in milk of bacteriophages targeting E. coli causing mastitis

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Bovine mastitis is a major production disease in dairy cattle and complementary treatments to antimicrobials are urgently needed. Intramammary phage therapy is a promising approach but characterizing isolated phages in milk is a crucial initial step. This study aimed to compare the stability and lytic activity of 10 phages targeting *E. coli* in milk and assessing their stability at different temperatures and pH.

Ten bacteriophages isolated from wastewater were spotted on 53 *E. coli* strains isolated from bovine mastitis to evaluate their host range. The stability of the phages was evaluated across different pH (2-12) and T°C (25-60°C). Stability in milk was assessed after 6h of incubation at 37°C. The optimal multiplicity of infection (MOI) was determined for each phages and used in subsequent lytic activity assays. These assays involved inoculating milk with *E. coli* and phages at the determined MOI and tracking bacterial titers at different timepoints in raw, heat-treated and UHT milk.

A narrow host spectrum was observed for the phages and stability was maintained at pH ranging from 4 to 10 and temperatures ranging from 25 to 45°C. At 60°C, only 5/10 phages persisted but with a significant degradation. Stability analysis in milk showed that all phages remained stable in raw and heat-treated milk. Lytic activity assays demonstrated a bacterial decrease with all phages, but for 5/10 phages, bacterial regrowth occurred after 5h of incubation.

In conclusion, milk components are not an obstacle for phage therapy to control bovine mastitis. However, bacterial regrowth suggests the presence of resistances that could be bypassed with the use of phage cocktails. DNA sequencing of the phages will be performed to ensure their safety and sequencing of the bacterial collection will allow us to determine their serotypes, which are linked to the phages host range.

Acknowledgements:

This program benefited from a financial support of Wallonia in the frame of a BioWin's Health Cluster and Wagralim's Agri-food Innovation Cluster program (Vetphage). The authors acknowledge the "Agence Régionale de Santé et d'Identification Animale" (ARSIA, Ciney, Belgium), the Care-FEPEX (ULiège, Liège, Belgium) and the "Association intercommunale pour le démergement et l'épuration des communes de la province de Liège" (AIDE, Liège, Belgium).

The genetic diversity of Ehrlichia ruminantium strains in West African amblyomma variegatum tick populations: A contribution to the development of an effective vaccine against heartwater

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Introduction:

Ehrlichia ruminantium (ER) is a rickettsia transmitted by the trixene tick *Amblyomma variegatum* in West Africa, causing heartwater. The disease has a mortality rate of up to 90% in herds of exotic breeds and small tropical ruminants, posing a significant challenge to the economy and development of tropical livestock farming. However, an effective vaccine has not yet been developed due to cross-protection limitations caused by the high genetic diversity of rickettsia strains.

Material and Methods:

To address this issue, we conducted a Multilocus Sequence Typing analysis based on the *sucA, lepA, sodB, lipB,* and *groEL* loci to separately infer the diversity and structuration of the population from two types of samples. The field sample consists of 18 strains from Benin, Burkina Faso, and Niger, while the monitoring sample comprises 75 strains isolated in Banakélédaga during a natural cattle infestation experiment.

For the analyses, 23 reference sequences of isolates from South, East, and West Africa were added to each of these two samples. The study assessed phylogenetic relationships using various methods, including the clonal tree, phylogenetic trees constructed under the maximum likelihood model, a heat map, and a phylogenetic network. The latter was supported by pairwise homoplasy index (PHI) and recombination tests to evaluate the impact of recombination on the evolutionary process of ER.

Results:

The two samples each showed a grouping of ER strains into two distinct groups. West African and Pan-African. The circulating strains originate from the recombination of five ancestral genotypes that emerged in West Africa. The dissemination of these divergent groups is thought to have been ensured by the movement of cattle during the domestication of *Bos taurus* and their sustainability through clonal processes. Additionally, the two samples exhibited a robust genetic diversity, resulting in the emergence of new standard sequences (ST). The BK 242 strain remains the most common in Benin and Burkina Faso, while it has not been identified in Niger. Furthermore, a new ST specific to Burkina Faso was identified and found to be highly prevalent.

Conclusion and perspective:

This finding highlights the genetic diversity of ER in West Africa and raises concerns about the efficacy of generic vaccines in the field. In addition, the joint role of panmixis and clonality in evolution of ER strains was evidenced. For future challenge and cross-protection experiments a new ST should be taken into consideration in addition to the BK242 strain.

However, further research is required to establish this vaccine, including a more representative sampling and studying the correlation between the MLST genotype and immunological properties. Additionally, a genomewide association study should be conducted to identify candidate loci for a detailed analysis of the antigenic diversity of ER strains.

A new pen-side test to confirm RVF clinical suspicions in the field

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Introduction:

Rift Valley fever (RVF) is a zoonotic disease causing an acute infection in domestic ruminants, with a high mortality rate among young animals. IDvet developed a multispecies cELISA for the detection of RVFV specific antibodies, and ruminant RVFV specific IgM antibodies. Fast and reliable tools are needed to rapidly diagnose suspected clinical cases. Diagnostic performances of a new pen-side test to detect RVFV in less than 15 minutes: the ID Rapid® Rift Valley fever are presented here.

Materials and methods:

The test is based on biological materials raised at CIRAD [1]. Anti-RVFV nucleocapsid-specific antibodies are bound to colloid gold particles or immobilized onto the membrane test line. A control line validates the migration. The kit contains a migration buffer dropper and micropipettes for sample transfer (15 µl serum, 30 µl blood). Diagnostic specificity was assessed by testing 580 negative sera (292 cattle, 96 small ruminants and 192 camelids) and 184 heparinized whole blood (cattle) from RVF free areas. Analytical sensitivity was evaluated using a titrated RVFV strain (Smithburn) spiked in negative whole blood or serum (bovine and caprine).

Results:

Measured specificity on serum was 99.7% (98.1 – 99.9%) for cattle, 99.0% (94.3 – 99.1%) for small ruminants and 100% (98.0 – 100%) for camelids ; on bovine whole blood was 98.9% (96.1% – 99.7%). For this Mab pair, inclusivity had been previously assessed using different RVFV viral strains, all successfully detected, indicating 100% inclusivity. Exclusivity with flaviviruses and alphaviruses were also documented, excluding possible cross-reactivity with other viral genera with same clinical features. The limit of detection (LOD) was 3.5x103 pfu for serum, and 7.5 x104 pfu for whole blood. Diagnostic sensitivity on serum of a previous similar test having the same LOD was previously assessed by testing 25 isolated strains of from different geographical origins mimicking clinical specimens and 10 clinical samples from the 2019 Mayotte outbreak, which were positive by RTqPCR [2]. Diagnostic sensitivity was 100% (CI95%: 90,1 – 100 n = 35).

Conclusion:

The ID Rapid® Rift Valley fever antigen demonstrates very high levels of specificity and inclusivity, and a sensitivity level adapted to a specific, accurate and rapid detection of RVFV in serum or whole blood. It is a reliable tool able to confirm a RVF clinical suspicion and enhance virus detection during an outbreak in less than 15 minutes directly on the field, without any specific lab equipment.

Reference

[1]. Cêtre-Sossah, C., Pédarrieu, A., Juremalm, M., Jansen Van Vuren, P., Brun, A., Ould El Mamy, A. B., ... & Cardinale, E. (2019). Development and validation of a pen side test for Rift Valley fever. PLoS neglected tropical diseases, 13(9), e0007700.

[2]. Bird, B. H., Bawiec, D. A., Ksiazek, T. G., Shoemaker, T. R., & Nichol, S. T. (2007). Highly sensitive and broadly reactive quantitative reverse transcription-PCR assay for high-throughput detection of Rift Valley fever virus. Journal of clinical microbiology, 45(11), 3506-3513.

Usutu virus circulation in wild birds, Wallonia 2023

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In a context of early detection of high impact mosquito-borne-flavivirus in Wallonia, over 600 wild birds originating from seven wildlife rehabilitation centers were subjected to analysis in 2023. Autopsies were conducted in the Faculty of Veterinary Medicine (ULiege) and organ samples were analyzed performing RT-qPCR assays targeting mosquito-borne flavivirus belonging to the Japanese encephalitis serocomplex. Results revealed that over 10% of the analyzed samples tested positive for the Usutu virus. Spatio-temporal epidemiological date for the for the Usutu virus could aid in determining its potential endemicity in the study zone.

Comparison of herd mortality rates in Wallonia

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Introduction:

Mortality control is of vital importance to livestock farmers, not only because it improves animal welfare, but also because death means financial and investment losses. To monitor the mortality rate and set achievable individual improvement targets, the livestock stakeholders need standardized methods and target-related thresholds in farming conditions of our region. In the literature, the data (age categories, whether or not stillbirths are taken into account, etc.) vary from one study to another and do not reflect the specific characteristics of Wallonia (breeds, management).

The aim of this work is therefore

(1) to develop age categories for which the mortality risks are different, and which correspond to our conditions,
(2) to adapt the calculation of the mortality rate taking into account animal movements, which can lead to a bias in the interpretation of the results, and
(3) to compare the herds with others.

These adaptations have been made to ensure the data easier to understand for the breeder and his veterinary.

Material and Methods:

Using data from Sanitel, the rendering plant and ARSIA from 2015 to 2023, the mortality rates for each day of life for Wallonia were calculated by considering exported animals and slaughtered animals for consumption. This represents a total of 1.844 different breeding herds, 5.379.898 cattle including 3.982.968 births and 625.472 deaths for the rendering plant.

Age categories were created on the basis of age-related mortality risks. The categories used are

- Days 0 to 7 (D0-7),
- Days 8 to 30 (D8-30),
- Months 1 to 3 (M1-3),
- Months 3 to 8 (M3-8),
- Months 8 to 12 (M8-12),
- Months 12 to 24 (M12-24),
- More than 24 months (M24+).

A mortality rate is calculated for each age category of each herd according to a formula that considers the number of days present on the farm and takes into account sales, introductions of animals and changes in age category during the studied period, which can bias the calculation methodology.

Herds are grouped by category according to the number of annual births and type of farming (Dairy/Beef/Mixed) in order to allow a comparison of these herds which, by their nature, present differences in management.

Then, the 25, 50 (median) and 75 percentiles are calculated for each type of herd and each category.

Results:

In particular, in herds with 100 to 199 births per year, a lower mortality rate is observed in dairy herds between 1 month and 24 months (M1-3: 1.98%; M3-8: 1.27%; M8-12: 0.00%; M12-24: 0.00%) compared with beef herds (M1-3: 2.20%; M3-8: 2.42%; M8-12: 0.85%; M12-24: 1.16%), while the mortality rate is higher in adults older than 24 months in dairy herds (M24+: 4.44% versus 2.03%).

An hypothesis to explain these differences is the greater susceptibility of beef cattle to respiratory diseases and the higher rate of metabolic disorders in dairy cows. This study makes it possible to calculate the Walloon distribution of mortality rates and to set targets, such as the median of similar herds, for farms interested in improving their performance.

Optimizing surveillance strategies of highly pathogenic avian influenza in live bird markets across southeast Asia

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Interpretative summary:

Surveillance for avian influenza in live-bird markets is invasive, poorly tolerated by vendors, and requires trained technical staff. Environmental sampling provides a promising alternative to live-bird sampling. By estimating the efficacy of environmental sampling to live-bird sampling in multiple southeast Asian nations, we provide actionable intelligence for local veterinary public health authorities to inform their surveillance strategies.

Abstract:

Highly pathogenic avian influenza viruses (HPAIVs) pose a severe on-going threat to domestic poultry and wild birds. They are also a public health threat due to their ability to reassort with other influenza viruses. Early detection of infected premises and monitoring of circulating strains are essential to optimizing public health strategies in areas of endemicity. Live bird markets, prevalent throughout southeast Asia where HPAIVs are endemic, have been identified as ideal locations for conducting such surveillance. Previous research in Vietnam had revealed that surveillance strategy effectiveness varied by AIV strain, with environmental samples just as effective as live bird samples for H5N1 and duck samples better than environmental samples at detecting H5N6. However, it is uncertain if these conclusions can be extended across seasons and to other endemic countries.

Using multiple years of surveillance data from Vietnam, Cambodia, Lao PDR, and Myanmar, Bayesian latent class analysis was used to determine the effectiveness of chicken, duck, and environmental samples in detecting various AIV subtypes in LBMs. In Vietnam, estimated market-level prevalence of influenza A was 0.46 (95% credible interval 0.43–0.48), whereas in Lao PDR estimated prevalence was 0.2 (0.17–0.23). For H5N1, H5N6 and H5N8 subtypes in Vietnam, oropharyngeal duck samples outperformed environmental samples which outperformed chicken samples. In Lao PDR, similar though less pronounced trends emerged. In Myanmar, H5N1 was best detected by environmental samples, whereas H5 subtypes outside of H5N1, H5N6 and H5N8 saw environmental samples as less sensitive than both duck and chicken samples. In Cambodia, duck samples outperformed chicken samples for the H5 subtypes.

Observed differences in prevalence and sensitivity reflect the varied dynamics between countries and between years, highlighting the necessity of situation-specific surveillance. Environmental samples, though promising, have not been determined to be as efficacious as live bird samples, and so live bird sampling will continue to be the recommended surveillance strategy in spite of the perceptions of market vendors and the general public.

Veterinary students' perception of zoonotic diseases and their prevention through an online survey in three Belgian universities

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Introduction:

To assess the perception of vet students on zoonotic diseases and their prevention, the ULiège Faculty of Veterinary Medicine, through its Biosecurity Unit, launched an online survey aimed at vet students of the French-speaking part of Belgium, i.e. University of Liège (ULiège), University of Namur (UNamur) and Catholic university of Louvain (UCLouvain).

Materials and methods:

The survey consisted in an online questionnaire including several categories of items:

i) general information,
ii) personal profile on daily habits,
iii) risk perception and severity of zoonoses,
iv) efficacy of several prevention and control measures,
v) possible constraints and
vi) intention of implementing several targeted measures in the future practice.

The targeted measures were the following:

(i) Hand disinfection (or washing with bactericide soap) before and after any medical act;
(ii) Ask for the country of origin of the patient;
(iii) Wearing adapted gloves (examination / surgical);
(iv) Wearing a mask during procedures with a splashing risk (e.g. necropsy, descaling);
(v) Wearing safety goggles during at risk procedures (e.g. splashing risk);
(vi) No re-capping of needles;
(vii) Washing working clothes / personal protective equipment (PPEs) separately, with a cycle ensuring disinfection;
(viii) Rabies vaccination;
(ix) Correct contention to avoid injury;
(x) In case of injury (scratches, bites), immediate washing with soap (antiseptic);
(xi) Continuing education and staying informed of evolutions and news in terms of zoonoses and their prevention;
(xii) Wearing single-use overalls and gowns; and
(xiii) (xiii) Strict washing of boots upon leaving a farm.

Two surveys were launched, i.e. one aimed at students of bachelor and one at students of master, but the content was similar (questions adapted to the academic status). The survey will be closed by March 31.

Expected outcome:

A comparison will be performed at different levels, i.e. level of academic cursus (bachelor vs. master) and between universities. The results will give an overview of the students' perception of zoonoses and prevention measures. It will help assessing the need for making students more aware of the importance and risk of zoonoses for veterinarians, from the beginning of their cursus. The implementation of targeted measures must be done through an evidence-based approach, that rely on clear, logical and coherent justification, at each step of the cursus. The need to adapt and/or re-orient the teaching of biosecurity will be assessed as well, with a special emphasis on zoonoses and the way to prevent them.

Horizon scanning for plant pests at EFSA: tools and methods

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The activity of horizon scanning of emerging threats in plant health started at EFSA with a mandate from the European Commission in December 2016. Since then, thanks to the collaboration with the Europe Media Monitor (EMM) team of the Joint Research Centre (JRC) and the cooperation of the French Agency for Food, Environmental and Occupational Health & Safety (ANSES), numerous activities and methods have been developed and maintained on this field in order to enhance preparedness of EU decision makers.

We monitor more than 23,000 sources (including scientific journals) that provide every day 200-300 items with signals concerning known and new pests. After an expert-based content selection, a monthly newsletter is published, retaining not more than 30-40 articles. During this screening we can identify new (meaning unknown and/or unregulated) pests: in this case weapply the so-called "PeMo" methodology. PeMo consists in a fast assessment based on a scoring matrix, that compares the pest under evaluation with already well-known ones:

based on the results of this screening, EFSA is able to a) raise the attention of EU decision makers about the potential threat that a given pest represents, or b) keep monitoring it and waiting for more evidence. This activity has been recentlytransferred to online platforms, conceived to allow also external users to test differentpests for their specific needs. In addition, a free-access dashboard has been published and is updated in line with the monthly newsletter, and a series of webinars and workshops on the topic are in agenda for the next three years.

We are aware that what we are achieving and developing in our specific field is easily transferrable to other types of biological hazards. The continuous evolution of this project supports thetimely reaction of EU decision makers in a quickly changing environment.

The consumption of veterinary antibacterial products in Belgium in 2022 and its evolution since 2011

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The annual consumption of veterinary antibacterial products in Belgium and its evolution since 2011 are reported in the BelVet-SAC report under the authority of the Belgian Federal Agency for Medicines and Health products (FAHMP). The report includes sales data since 2011, covering all animal species and collected from distributors and compound feed manufacturers, and also use data since 2018, collected at farm level via the data collection system Sanitel-Med. Until recently, use data only covered the use in pigs, broilers, laying hens and veal calves, but mandatory data-collection has expanded to all other cattle and all other poultry of the species chicken and turkey since August 10th, 2023.

Overall, the results achieved in 2022 were very good: a total of 122,4 tonnes of active substance were sold, almost 50 tonnes below the 2021 total (171,6 tonnes) and 177 tonnes below the total of the reference year 2011. Taking into account the biomass, the standardised consumption of 61,3 mg antibacterials/kg biomass showed a record decrease of -24,5% compared to 2021 and an overall reduction of -58,2% since 2011. This represents a major leap towards the -65% reduction target included in the AMCRA vision for the end of 2024, and set to evolve towards the median use in Europe (approx. 50 mg/kg biomass). Furthermore, the reduction targets for use of critically important antibiotics, colistin and medicated premixes were all maintained or achieved in 2022.

These positive results are confirmed in the Sanitel-Med use data of pigs and veal calves, where the number of treatment days (BD100) at species level in 2022 as compared to 2021 decreased with -28,2% and -9,8%, respectively. For poultry, an increase of +11% was reported, mainly due to an increased use in broilers. Although this setback should raise awareness in that sector, it does not necessarily mean a cause for alarm yet, as the obtained reduction in previous years still resulted in very few broiler farms with a red benchmark colour score (< 1%) or an alert user status (0,1%).

Further progress is also required in pigs in order to meet the sector-specific reduction pathways and to reduce the number of alarm users (4,5% in 2022) to the aim of maximum 1% by 2024. The most challenging perspectives remain for the veal calf sector, which is still furthest away from these reduction targets with 21% of farms having a red benchmark colour score and almost 14% being defined as an alarm user.

Conclusion:

Many challenges are still ahead, but the 2022 results are encouraging for all stakeholders to continue and strengthen their combined efforts in the future.

Predicting mosquito biodiversity and abundance using land use and climate changes

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One known consequences of climate change is the geographic expansion of mosquito distribution, particularly well demonstrated for the tiger mosquito (*Aedes albopictus*), which has been quietly and systematically moving north into Europe and North America in the past four decades. Beyond the tiger mosquito, there are more than 80 species in Canada on which the impact of climate change is unknown. Apart from ambient air warming and precipitation regime, there are many other factors that will change in the future and have a role on mosquito distribution and abundance, notably, land use type (a known proxy for mosquito habitat, reproduction locations and life cycles characteristics (including egg-laying period and feeding habits).

To illustrate the importance of taking into account land use changes in addition to climate changes in the study of future distribution of mosquitoes, we relied on data collected in the East of the province of Ontario (Canada) by the provincial surveillance program for the West Nile virus from 2002 to 2020. Based on this data, we developed two generalized additive statistical models to predict the daily abundance of Culex pipiens-restuans (CPR), main vector for West Nile virus in Eastern Canada, and the annual Shannon biodiversity index, calculated using all mosquitoes species sampled (including CPR). The predicting variables were meteorological (cumulative degree days, cumulative precipitation, mean temperature), and land use (forest, agricultural and urban territory) variables.

At a spatial resolution of 25 ⍰ 25 km, we use these two models to predict the daily abundance of CPR and the annual Shannon biodiversity index within our study region using an average of five Regional Climate Models (RCMs) (CanRCM4, CRCM5-UQAM, CRCM5-OUR, RegCM4 and WRF_v3.5.1) estimated for RCP 4.5 and 8.5, and three land use change scenarios developed in previous work[1], representing on-going urban development, protection of natural capital, and increased urban development.

Our results show the importance of forest and agricultural cover as well as cumulative precipitation over 1 month, cumulative temperature over 9, 30 and 90 days on the abundance of CPR. Also, whatever the climatic and land use scenario considered, we predicted a decrease in the average CPR abundance across our sampling region for 2030, 2050 and 2070. There is considerable spatial heterogeneity in the results and areas of abundance hotspots seem to move from the north to the south of the study region. These spatial hotspots are particularly noticeable for middle-warming scenarios (4.5) than for the high warming scenarios (8.5). Results for possible changes in biodiversity are not yet available at the time of this summary writing.

However, these preliminary results show us the importance of taking into account land use heterogeneity when predicting the changes in mosquito distribution in the future, and not only climate warming. Although the approach we used is more complex than traditional methods, we showed it is more precise and allows to better qualify the increased risk of transmission of mosquito-borne diseases transmitted to humans and animals. Literature Future landuse change predictions using Dyna-Clue to support mosquito-borne disease risk assessment.

Reference

[1]. M. R. Rakotoarinia, O. Seidou, D. R. Lapen, P. A. Leighton, N. H. Ogden, A. Ludwig, Environmental Monitoring and Assessment 2023 Vol. 195 Issue 7.

RAG-CA and RAG-V-EZ - two initiatives from the FASFC to sustain authorities facing emerging zoonoses

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In the beginning of the year 2020, Belgium was facing one of the first cases of animal infection by SARS-CoV-2, a human-borne virus. Constituting exemplary and unexpected cases of "reverse zoonosis", SARS-CoV-2 infections in animals required quick responses from authorities regarding to logical questions coming from the society. It also required risk management policy based on scientifically-based opinions, very often on poor or limited knowledge bases. In this context and on a mandate from the Belgian Risk Assessment Group (RAG), the Federal Agency for the Safety of the Food Chain (FASFC) and the Scientific Committee of the FASFC established a working group, called RAG-CA (Risk Assessment Group Covid Animals), aiming at delivering scientific opinions on various subjects closely related to the risk of SARS-CoV-2 infections in animals in the field.

During approximately 2 years of activities, 17 scientific opinions, recommendations, communications and position paper were published to sustain animal and public health authorities. Under coordination of the SciCom and of the Staff direction for Risk Assessment of the FASFC, the RAG-CA was composed of members from authorities, universities, scientific institutions and the reference laboratory as well as experts from the Regions (first president prof. E. Thiry then prof. J. Dewulf).

As the work of the RAG-CA during 'war-time' was highly appreciated by authorities, a new expert group was founded early 2023 to continue the work of the RAG-CA during 'peace-time' and to extend its roles: the RAG-V-EZ (Risk Assessment Group-Veterinary-Emerging Zoonoses). The role of the RAG-V-EZ is to follow the epidemiological situation of zoonoses and regularly assess all zoonotic risks that are pertinent for the epidemiological situation in Belgium. As such, they are participating to the preparedness and response of the Belgian authorities to any emergence of zoonosis in animals, providing veterinary expertise to public health authorities which are also represented in the group, notably via the RAG, and with which it works closely, according to the One Health concept.

Under the coordination of the FASFC and its Staff direction for Risk Assessment, the RAG-V-EZ gathers once again experts from federal and regional authorities (including the Chief Veterinary officer and the delegate to the WOAH) as well as from Belgian scientific institutions. The RAG-V-EZ is currently presided by prof. J. Dewulf, UGent (vice-president prof. C. Saegerman, ULiège). Invited experts can temporarily join depending on the required expertise. Since the beginning of its activities, the RAG-VEZ has already published a FAQ on the current pandemic of Highly Pathogenic Influenza virus A (H5N1), a scientific opinion on the need of reinforced monitoring of influenza virus infections in swine and a risk assessment specifically relying on HPAIV A (H5N1) infection in mammals is in preparation. Further information on the activities of the RAG-CV-EZ can be found here: https://favv-afsca.be/fr/rag-v-ez-informationsconcernant-le-risk-assessment-group-veterinary-emerging-zoonoses-rag-v-ez..

Sweet stingless beekeeping from the middle of the world

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Background:

Stingless bees are effective pollinators of native flora in the Tropics. They provide the environmental service of pollination through pollen flow, increasing reproductive success in crops, and genetic variability in native plants. The management of stingless bees, Meliponiculture, is used in sustainable agricultural systems, part of the 9.5% of global agricultural production for human consumption. The present study aims to describe stingless beekeeping systems in two different climatic zones in Ecuador, to characterize the biosecurity, and health risks aspects of meliponiculture practices, and to determine pot-pollen resources as a key to the conservation of stingless bees.

Methods:

To assess the state of management practices we applied an online survey, opened for nine months in two languages with a target group of stingless beekeepers with experience in managing at least one nest. To visualize the data state, we developed two quantitative tools: a spider and a barometer. To identify the origin of pollen we developed and compared two methodologies, scanning electron microscopy and meta barcoding using ITS2 and rbcL as molecular markers.

Results:

The Stingless Bees Hospital HASA, in the Amazon region, is a great example of a conservation approach, it manages 3 – 36 genetics by species, using good feeding and management practices, as a tool for the recovery of damaged nests. Regarding biosecurity measures, hand washing (79%), material sterilization (75%), and personal protective equipment use (48%) were the main aspects accomplished for Ecuadorian stingless beekeepers. Among the possible causes of losses (15% Nest Dead Rate) were: nest invasion (>11 invaders), nearby sources of pollution mainly from agrochemical use on crops, and unusual behaviors in stingless bees (>10 signs). The main pollen resources determined were from the families Melastomataceae, Asteraceae, and Myrtaceae, including 12/64 introduced species of the total Amplicon Sequence Variants (ASVs).

Conclusions:

Meliponiculture in Latin America, especially in Ecuador is a growing industry, and support from academia is required to establish correct guidelines for the management. The overall status of this practice was acceptable (~ 40% according to the barometer tool), however, some points need to be addressed from a One Health perspective, to ensure aspects such as food safety, bee conservation, and environment preservation.

Surveying tick control practices on dairy farms in subtropical areas of continental Ecuador

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Background:

Tick control strategies for tropical dairy cattle depend heavily on farmers' knowledge, perceptions, and acceptance of control measures. The purpose of this study is to identify common and uncommon tick control practices used by dairy farmers in subtropical areas of Ecuador and link them to the presence of infestation and acaricide resistance.

Materials and methods:

The data was collected by a cross-sectional survey and participatory meetings. Multiple correspondence analysis was performed to explore the association between management variables and the level of tick infestation and resistance.

Results:

It was found that the primary method of acaricide control is still chemical, mainly through spray baths. Usually, when this form of application is used, acaricides are overdosed, whereas, with the pour-on method, underdosing is common. When chemical treatment fails, farmers use overdoses of products, mix different acaricides, and use focused treatments (wipe cloth) with irritant substances. The absence of a high level of infestation was related to acaricide dips every 3 to 4 weeks and the use of intensive grazing.

On the other hand, the high infestation was related to the use of organophosphates, wipe cloth application, and the report of tick-borne diseases (TBDs).

A small group of farmers have good knowledge and seek alternatives to chemical control, experimenting with biological controls, herbal extracts, manual tick removal, and paddock control.

Conclusion:

The present information is critical to improving tick control management in Ecuador, particularly through implementing practices that mitigate resistance to acaricides and ensure long-term solutions that help maintain the efficacy of tick control treatments.

Assessing acaricide treatment expenses on dairy farms in subtropical areas of Ecuador

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Background:

Due to Ecuador's location on the equatorial line, most of the country experiences a tropical and sub-tropical climate providing environmental conditions conducive to the development of ticks. Livestock in these areas suffer from tick infestations almost all year round, causing direct and indirect economic losses, which have not been quantified in Ecuador. The objective of this study is to quantify indirect losses by quantifying the cost of acaricide treatment at the farm and animal levels using a farm systems approach.

Materials and methods:

Between November 2020 and March 2021, 105 dairy cattle farms were visited in two sub-tropical areas of Ecuador located in the occidental and oriental foothills in the Ecuadorian Andes. Due to the absence of a sampling frame, the farms were selected using the snowball sampling technique. Regression and classification trees were used to study the relationship between tick control, acaricide resistance, and the presence of a high level of tick infestation in the farm system.

Results:

Out of 105 farms tested, 48 (46%) had a high tick infestation. The percentage of resistance to alpha-cypermethrin was 53%, amitraz 49%, and ivermectin 37%, regardless of the tick infestation. The amount of the production budget spent on tick control, both at the farm and animal level, varies according to the degree of technification and farm size. Technified farms have a lower expenditure on acaricide treatment (1.3% of total production cost) compared to semi-technified (3.4%) and non-technified farms (6.2%). In large and technified farms the cost of treatment per animal is 8.5 USD. Medium farms were grouped into 2 terminal nodes where the cost of animal treatment is 13.0 USD and 19.5 USD and varied according to the acaricide control practices used. The cost of treatment on small farms was 23.9 USD and 28.4 USD due to the difference in farms with high levels of infestation present at each node. Although alpha-cypermethrin resistance plays a role in the formation of the decision tree, it does not affect the cost of acaricide treatment if the farm has resistance. At these nodes, the cost of treatment was affected by acaricidal practices and the level of infestation.

Conclusion:

These results can motivate the development of control programmers targeted to the reality of small and medium farms that are the most affected in terms of the money they invest in controlling ticks.

First Expert Elicitation of Knowledge on Drivers of Emergence of Bovine Besnoitiosis in Europe

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Bovine besnoitiosis (BB) is a chronic and debilitating parasitic disease in cattle caused by the protozoan parasite *Besnoitia besnoiti*. South European countries are affected and have reported clinical cases of BB. However, BB is considered as emerging in other countries/regions of central, eastern and northern Europe. Yet, data on drivers of emergence of BB in Europe are scarce.

In this study, fifty possible drivers of emergence of BB in cattle were identified. A scoring system was developed per driver. Then, the scoring was elicited from eleven recognized European experts to: (i) allocate a score to each driver, (ii) weight the score of drivers within each domain and (iii) weight the different domains among themselves.

An overall weighted score was calculated per driver, and drivers were ranked in decreasing order of importance. Regression tree analysis was used to group drivers with comparable likelihoods to play a role in the emergence of BB in cattle in Europe. Finally, robustness testing of expert elicitation was performed for the seven drivers having the highest probability to play a key role in the emergence of BB: i.e., (i) legal/illegal movements of live animals from neighbouring/European Union member states or (ii) from third countries, (iii) risk of showing no clinical sign and silent spread during infection and post infection, (iv) as a consequence, difficulty to detect the emergence, (v) existence of vectors and their potential spread, (vi) European geographical proximity of the pathogen/disease to the country, and (vii) animal density of farms.

Provided the limited scientific knowledge on the topic, expert elicitation of knowledge, multi-criteria decision analysis, cluster and sensitivity analyses are very important to prioritize future studies, e.g., the need for quantitative import risk assessment and estimation of the burden of BB to evidence and influence policymaking towards changing (or not) its status as a reportable disease, with prevention and control activities targeting, firstly, the top seven drivers. The present methodology could be applied to other emerging animal diseases.

Bee Tox Wax: real time tool for calculation of the toxicity risk of waxes that have been subjected to a pesticide analysis

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Bees are pollinators of crops and plants. Their health is essential and depends on many factors (beekeeping practices, introduction and spread of pathogens, habitat degradation, availability or quality of nutrient resources, climate change, poor quality queens, as well as exposure to agricultural and beekeeping pesticides). This presentation describes a real-time tool (Bee Tox Wax - https://www.beetools.uliege.be/beetoxwax/) that roughly estimated the risk posed by the use of beeswax regarding pesticides.

An online tool was developed to enable beekeepers and wax traders to calculate wax toxicity to honey bees based on the residues concentrations reported in a laboratory analysis report and the pesticide residue acute median lethal dose (DL50). The tool gives an automated real-time advice on the (re)use or the discard of the tested wax based on threshold defined by the current scientific literature: contact HQ value over 250 are considered to have significant toxicity and elevated toxicity over 5,000 [2]. The tool is a web-based calculator of wax toxicity; its use could be an important strategy to sanitize beeswax sector. A classification based on a colour code expressing the toxicity to bees of contact LD50 has been used throughout the tool. Meaning of the LD50 has been exposed to avoid confusion. An user guide is available in the appendix 2 of the paper from El Agrebi et al. (2021).

References

[1]. El Agrebi N, Traynor K, Wilmart O, Tosi S, Leinartz L, Danneels E, de Graaf DC, Saegerman C. (2020). Pesticide and veterinary drug residues in Belgian beeswax: Occurrence, toxicity, and risk to honey bees. Sci Total Environ., 745:141036. doi: 10.1016/j.scitotenv.2020.141036.

[2]. Traynor, K.S., Pettis, J.S., Tarpy, D.R., Mullin, C.A., Frazier, J.L., Frazier, M., vanEngelsdorp, D. (2016). In-hive pesticide exposome: assessing risks to migratory honey bees from in-hive pesticide contamination in the Eastern United States. Sci. Rep. 6, 33207.doi:10.1038/srep33207.

New real time biosecurity tool in your hands

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Livestock biosecurity gained increasing attention during the last decades. According to a recent survey that include 316 participants from the 5 continents, the most popular definition of the biosecurity is related to the rules of 5 Bs [3]. The biosecurity are all measures:

(i) to limit the risk of introduction (**bio-exclusion**);
(ii) to limit the spread of the pathogen within the same facility, e.g., by isolating excreting animals (**bio-compartmentation**);
(iii) to limit the spread of the disease agent outside the facility (inter-herd transmission) (**bio-containment**);
(iv) to prevent the risk of human contamination (**bio-prevention**); and
(v) to prevent any environmental bio-contamination and persistence of the pathogen (**bio-preservation**) [3].

This definition fit well with the new definition of the One Health concept [2]. In addition, promoting compliance with biosecurity in livestock is a key issue [4]. Indeed, we developed a new real time biosecurity tool directly in your hands based on the rules of the 5 Bs and the SAF model to select a strategy. The SAF model integrated: the suitability (does the strategy overcome the difficulties that were identified in the analysis of biosecurity ≈ efficacy?), the acceptability (apart from any practical considerations of possible implementation, is the measure acceptable to you, i.e. is it appropriate, fair and reasonable? A measure could be acceptable but not necessarily feasible on your farm) and the feasibility (would the measure be feasible on your farm?).

It is a farm specific biosecurity measures tool (choice your species, the disease of interest, known associated risk factors and choice the appropriated biosecurity measures to mitigate the introduction and the spread of the disease). The tool offers a real time assessment (with a dashboard), a real time visualization of improvements, and give a final report in your hands. Each tool is primarily tested with students in field conditions (refining) before its free delivery.
The first BSMTOOLS was developed as part of the EFSA project entitled: "Developing an integrated approach to assess the emergence threat associated with influenza D viruses' circulating in Europe"[1].

References

[1]. Alvarez et al., Developing an integrated approach to assess the emergence threat associated with influenza D viruses circulating in Europe. External scientific Report, approved at 1st February 2024. doi:10.2903/sp.efsa.2024.EN-8641.
[2]. One Health High-Level Expert Panel (OHHLEP), Adisasmito WB, Almuhairi S, Behravesh CB, Bilivogui P, Bukachi SA, et al. (2022). One Health: A new definition for a sustainable and healthy future. PLoS Pathog 18(6): e1010537. doi: 10.1371/journal.ppat.1010537.
[3]. Saegerman C, Parisi G, Niemi J, Humblet MF, Ron-Román J, Souley Kouato B, Allepuz A, Porphyre V, Rodrigues da Costa M, Renault V. (2023). Evaluation Survey on Agreement with Existing Definitions of Biosecurity with a Focus on Livestock. Animals (Basel), 13(9), 1518. doi: 10.3390/ani13091518.
[4]. Smith J.M., Saegerman C., Vaillancourt J.P. (2023). Promoting compliance with biosecurity in animal production. Front Vet Sci. 10:1215433. doi: 10.3389/fvets.2023.1215433.

An R-Shiny application to assess the risks of introduction of infectious animal diseases in Belgium

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Emerging and re-emerging animal diseases have clear adverse effects on animal health and on the general economy through loss of income and social costs resulting from outbreaks. An accurate forecast of the risk of emergence would make it possible to put in place measures to avoid the introduction of the disease or at least to be better prepared for it, for faster detection and a more effective response. This would have direct and indirect favorable effects on animal health and related industries.

Potentially useful information to estimate these risks of emergence is already recorded in national and international databases. Consequently, our project aims to develop a web application which allows the monitoring of several risk indicators and to combine these indicators to assess the risk of entry of the pathogen into Belgium. This risk analysis focuses on the risks of entry into Belgium of pathogens linked to animal diseases, hence the acronym MORISKIN for "Modeling the Risk of Introduction". The risks of the Belgian host population becoming infected, the risks of spread and the economic consequences of the diseases are not studied in this project. Two diseases are currently monitored in MORISKIN: African swine fever (ASF) and lumpy skin disease (LSD). The case of ASF is particularly interesting given the combinations of risks associated with domestic pigs and wild boars.

The R-Shiny MORISKIN application is intended to be "user-friendly" and allows the visualization on dynamic maps as well as on time series of information on (1) diseases: the number of cases of ASF and LSD declared in each European country (ADIS database), (2) movements such as the number of imports of live animals and germinal products (TRACES) as well as the number of people entering Belgium by plane (Eurostat) and (3) the risks via an estimation of the probability of introduction of pathogens from countries at risk. Being updated monthly, this tool is intended to be a support for risk assessors for the early detection of risks of introduction of infectious animal diseases in Belgium.

Cross-sectional serosurvey of HEV in Belgian pig farms and identification of risk factors

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Background:

Hepatitis E virus (HEV) is the causative agent of hepatitis E disease in humans. In industrialized countries, sporadic cases of hepatitis E are usually asymptomatic and self-limiting. However, immunocompromised individuals may develop a chronic form of hepatitis E, leading to liver cirrhosis. These cases are typically due to HEV genotypes 3 or 4, for which pigs are now considered as a major animal reservoir of human infection. However, the burden that the porcine HEV reservoir imposes on public health is still unclear.

Materials and methods:

To provide an overview of the current dissemination of HEV in Belgian pig herds (2020-2021), this study was designed as a randomized, robust, large-scale, cross-sectional, serological survey. HEV genotypes and subtypes recently circulating in Belgium (2020–2021) were investigated. Finally, to evaluate the relationship between the serological data and various exploratory variables, the serological survey of HEV herd-infection status was paired with a recently made mandatory questionnaire on general biosecurity measures undertaken in the farms.

Results:

The wide circulation of HEV in the Belgian pig population was shown and a change in the circulating HEV strains may have occurred in the last decade. The multivariate analysis showed a 67% reduction in odds for mixed farrow-to-finish farms, an 86% reduction for slaughter farms and a 90% reduction for other farms, as compared to closed farrow-to-finish farms. For every ten-fold increase of herd size, the odds of being a HEV positive herd increased by a factor of 2.6.

The combination of the serological survey with the questionnaire showed the purchase of piglets, the absence of a free-range system and the presence of either a footbath, a boot-washer or the changing of boots between compartments as protective factors for increased HEV-herd serological prevalence. Finally, based on those identified risk factors, an index was applied to predict the HEV-serological statuses of all Belgian pig farms.

Conclusion:

The identification of HEV-infected farms and possible risk factors for herd HEV-seropositivity is a first crucial step in the control of HEV spread amongst domestic pigs and thus the development of measures mitigating its zoonotic transmission to humans.

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