EWDA 2026 Conference

Novi Sad, Serbia
29.IX – 03.X 2026

The Wild Future:
Challenges of Integrating
Health
Welfare
Biodiversity

Book of Abstracts

Hosted by:

SCIENTIFIC VETERINARY INSTITUTE NOVI SAD
+1950+

EWDA
Wildlife Disease Association

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Welcome letter

Dear colleagues and friends,

It is our great pleasure to welcome you to ***16th European Wildlife Disease Association Conference - EWDA 2026***, hosted by the Scientific Veterinary Institute "Novi Sad". We are truly delighted to open our doors — and our hearts — to researchers and friends from across Europe and beyond, here in the vibrant city of Novi Sad.

This year's theme, ***"The Wild Future: Challenges of Integrating Health, Welfare and Biodiversity"*,** reminds us that the well-being of wildlife is inseparable from the well-being of our shared planet. As researchers, we all know how fascinating and complex this field can be — yet, beyond the data and analysis, there is also a shared passion that connects us: the drive to understand, protect, and respect the natural world and its many living systems.

Over the few conference days, we will exchange knowledge, ideas, and experiences, but also — hopefully — form new collaborations and friendships that will continue to grow after the conference ends. The health of wildlife is a challenge that unites us all, crossing borders, species, and disciplines. Together, we can work on the bridge between wildlife, environment, domestic animals, and humans.

On behalf of the organizer, the Scientific Veterinary Institute "Novi Sad," warmly welcomes you to EWDA 2026 Conference, to our city, and our country. Novi Sad is known for its hospitality, history, and heart — and we invite you to experience all of it during your stay.

Welcome to Serbia, welcome to Novi Sad and welcome to 16th European Wildlife Disease Association Conference - EWDA 2026 — where science meets friendship and shared purpose.

With warm regards,

In front of the Organizing Committee of 16th EWDA Conference "EWDA 2026"

Sara Savić, DVM, MSc, PhD, Principal Research Fellow &
Tamaš Petrović, DVM, MSc, PhD, Principal Research Fellow

Director of the Scientific Veterinary Institute "Novi Sad"

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EWDA 2026

29.09 – 03.10.2026

Hosted by: Scientific Veterinary Institute "Novi Sad"

The Wild Future: Challenges of Integrating Health, Welfare, Biodiversity

Entrance of the Confe - rence rooms coridor		HALL 1	THE MAIN CONFERENCE HALL				HALL 2	Saturday
		Monday 28.09.2026	Tuesday 29.09.2026	Wednesday 30.09.2026	Thursday 01.10.2026	Friday 02.10.2026	Poster Hall & coridor	03.10.2026
REGISTRATION AND INFO DESK WORKING HOURS from Monday to Friday (08.00 –-19.00)	8.30 - 9.00	Student workshop 08.30 - 10.30						Infront the Fair main entrance at 09.45
	9.00 - 10.00			SESSION 3 Vectors & vector-borne diseases in wildlife 09.00 - 11.30	SESSION 5 Avian influenza, African swine fever & potential pandemics in wildlife 09.00 - 11.00	SESSION 8 Emerging and re-emerging zoonotic pathogens & diseases in wildlife 09.00 - 11.00	POSTER PRESENTATION & VIEWING from TUESDAY 29.09.2026 to FRIDAY 02.10.2026	
	10.00 - 10.30		Official opening & Keynote speaches 10.00 - 11.30					
	10.30 - 11.00	Coffee break			Coffee break	Coffee break		
	11.00 - 11.30	Student workshop 11.00 - 13.00						
	11.30 - 12.00		Coffee break	Coffee break	SESSION 6 Food safety of game meet, AMR and ecotoxicology 11.30 – 13.30	SESSION 9 Endemic, neglected and non-communicable diseases 11.30 - 13.00		10 - 16 h Excursion day Additional Fee Not included in registration
	12.00 - 12.30		SESSION 1 Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control 12.00 - 14.00	SESSION 4 Challenges in wildlife health, conservation, climate change and biodiversity 12.00 - 14.00				
	12.30 - 13.00				Lunch break	Lunch break		
	13.00 - 13.30	Students Lunch break						
	13.30 - 14.00		Lunch break	Lunch break				
	14.00 - 14.30	Student workshop 14.00 - 15.00			SESSION 7 One Health Initiatives: integrated surveillance of zoonotic pathogens in wildlife & future pandemic preparedness 14.30 - 17.00	SESSION 10 Treats to ectoterms, urban wildlife, wild pets, fish and exotic animals 14.00 - 15.45		
	14.30 - 15.00							
	15.00 - 15.30		SESSION 1a Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control 15.00 - 17.00	SESSION 4a Challenges in wildlife health, conservation, climate change and biodiversity 15.00 - 16.40		CONFERENCE CLOSING REMARKS		
	15.30 - 16.00	EWDA Network meeting 15.30 - 17.00						
	16.00 - 16.30			Regional Workshop & Panel discuss on wildlife dis.				
	16.30 - 17.00				Turistic City Walk with guide 16.45 - 18.30			
	17.00 - 17.30	Coffee break	Coffee break	Coffee break	Coffee break with POSTER presentation & viewing SESSION 17.00 - 18.30	Free time		
	17.30 - 18.00	EWDA Network meeting 17.30 - 19.00	SESSION 2 Health and diseases of bats & rats 17.30 - 18.30	16.45 - 18.30				
	18.00 - 18.30							
	18.30 - 19.00		Annual meeting (AGM) 18.30 - 20.00		Free time			
	19.00 - 19.30	Icebreaker coctail & welcome 19.00 - 21.00h (Congress venue)						
	19.30 - 20.00				Traditional Serbian buffee dinner with Auction 19 - 22h „Zlatna dvorana" (at the Congress venue)	Gala Dinner at the Danube River bank with music and dancing Restaurant „RIBARAC" 19.00 – 24.00h		
	20.00 – 20.30		Student mentor Mixer with snacks and drinks 20.00 - 23.00h („MAGACIN" – 100 m away from the Conference rooms)	Free evening time				
	20.30 – 21.00							
	21.00 – 22.00							
	22.00 – 22.30							
	22.30 – 23.00							
	23.00 – 24.00							

Keynote lecture

Budimir Plavšić DVM, MSc, PhD, Research Associate

WOAH, Regional Representative for Europe - b.plavsic@woah.org

Dr. Budimir Plavsic is a veterinary professional with extensive experience in animal healt international standards and policy. He holds a Doctor of Veterinary Science (PhD), Master of Sc strong educational background including a Bachelor of International Business Administration (BIBA) and diploma in diplomacy.
Dr. Plavsic has held significant positions, including his current role as the World Animal Health Organization (WOAH) Regional Representative for Europe since November 2018. Prior to this, he served as the Head of the Animal Health and Welfare Department at the Ministry of Agriculture of Serbia's Veterinary Directorate and was the Permanent Delegate of Serbia in OIE/WOAH. His expertise spans a wide range of areas, including:

- Promoting and implementing WOAH international standards.
- Leading and managing animal disease and zoonoses prevention and control programs.
- Developing and utilizing the PVS evaluation methodology.
- Coordinating One Health activities in Europe and fostering collaboration between Quadripartite partners (FAO, UNEP, WHO, and WOAH).
- Coordinating GF-TAD's activities in Europe.
- Organizing and conducting numerous training programs.
- Transposing EU legislation and international standards into national legal frameworks.
- Managing and implementing capacity-building programs and national/international projects.

Dr Plavsic also has experience in finance and budgeting, communication and research, and has published numerous scientific articles. He is a member of several professional organisations and has contributed to various international events and training programmes. He is a permanent member of the Veterinary Academy of Serbia and a guest lecturer on One Health.

Epidemiological Situation in Europe: Wildlife-Associated Emerging and Re-emerging Diseases – Regional Priorities, Integrated Surveillance and Strategic Preparedness

Wildlife is an integral component of the epidemiological landscape of emerging, re-emerging and transboundary animal diseases (TADs) in Europe. The dynamics of multi-host pathogens at the wildlife–domestic animal–human–environment interface are influenced by animal movements, migratory pathways, vectors, environmental persistence, legal and illegal wildlife trade and associated value chains, land-use and climate change, as well as by human behaviour and production practices. Their consequences extend beyond livestock health and agricultural production to public health, animal welfare, biodiversity conservation and ecosystem resilience.
Within the GF-TADs framework for Europe, WOAH, FAO, the European Commission, Member Countries and technical partners have jointly identified priority TADs requiring sustained regional coordination, including African swine fever, highly pathogenic avian influenza, rabies, Lumpy skin disease, Foot-and-mouth disease and Peste des petits ruminants, with sheep pox and goat pox increasingly addressed within the regional agenda for small-ruminant diseases.
The role of wildlife differs among these diseases, ranging from maintenance and transboundary dissemination of infection to spillover, spillback, sentinel value and direct impacts on vulnerable wildlife populations. African swine fever, highly pathogenic avian influenza and rabies particularly demonstrate the importance of passive surveillance, investigation of morbidity and mortality events, wildlife population monitoring, cross-border coordination and timely information sharing. However, wildlife health surveillance remains constrained by incomplete knowledge of population denominators, limited access to sick or dead animals, opportunistic sampling, logistical and diagnostic challenges, fragmented institutional responsibilities and uneven reporting capacity.
The report will review the principal wildlife-associated disease threats in Europe and place them within the strategic framework of the WOAH Wildlife Health Strategy 2026–2030. Particular attention will be given to integrated and institutionalised multisectoral surveillance, systematic and iterative risk analysis, including hazard identification, risk assessment, risk management and risk communication, early detection, transparent reporting through WAHIS and complementary wildlife health intelligence systems, stronger diagnostic and genomic capacities, and continuous engagement among Veterinary Services, public health authorities, environmental agencies, conservation actors, laboratories, hunters, researchers and local communities.
Moving from reactive outbreak management towards upstream prevention will require science-based standards, sustainable partnerships, proportionate, context-specific and evidence-informed risk-management measures, and operational delivery adapted to national and regional contexts. Protecting wildlife health is therefore essential not only for disease prevention and preparedness, but also for healthier animals, more resilient ecosystems and a safer planet.

Keywords: wildlife health, transboundary animal diseases, integrated surveillance, risk analysis, WOAH

Keynote lecture

Richard Kock President of Wildlife Disease Association

Royal Veterinary College, University of London, UK -
President@wildlifedisease.org

Vet scientist (conservation, wildlife health and disease Africa and Asia). 1980-1983 General Veterinary Practice.1983-2010 Zoological Society of London (ZSL) including 1991-2006 secondment to the Kenya Wildlife Service (parastatal wildlife authority), and epidemiology unit, the African Union IBAR Nairobi, Kenya. 2011 – 2022 Professor Wildlife Health and Emerging Diseases Royal Veterinary College, London. Chair IUCN Wildlife Health Specialist Group SSC 2001-2022. Retired independent scholar and consultant, lectures internationally. President of the Wildlife Disease Association. Chief Editor: Elsevier Zoonosis Major Reference Work. FAO Bronze Medal (2010) and African Union IBAR certificates of appreciation (2022) for contributions to eradication of rinderpest; Tom and Beth Williams Award – Wildlife Disease Association (WDA) for exceptional contributions to wildlife health science and policy. Member of Academia Europaea,

Zoonoses and Zoonotic Diseases – What is the difference?

The invitation for abstracts' title of the session of the conference, "*Emerging and re-emerging zoonotic microbial and parasitic pathogens & diseases in wildlife - Avian influenza, African swine fever & other potential pandemic diseases in wildlife*", encouraged me to speak for more clarity on what we talk about in this field. Why is this? For example, here, I am assuming the subject of the session is zoonoses and zoonotic origin diseases, yet the diseases highlighted are neither significant endemic zoonoses nor pandemic human pathogens, whilst avian influenza is a zoonotic part of the origins of human influenza. Perhaps pandemic was used only in the context of animal disease rather than spill over risk from animals i.e. zoonotic risk, but this is not clear?

Whatever the intention, this paper accepts that there is confusion around terminologies in this field, leading to sometimes false and distorted narratives around disease at the non-human animal – human animal interface. The paper will offer a review of the challenges related to the terminology, offering a historical overview of the words and concepts used to describe infection at the interface and provide evidence for the realities of wildlife zoonoses and their role in emerging infectious disease of humans.

Key pathways to zoonosis and the emergence of human pathogens with zoonotic origins are outlined, with reference to exemplary papers that provide the best available evidence. The role of wildlife (which also needs careful definition) is not what it seems, and the very limited evidence for direct zoonosis from wildlife is presented. The need for prioritization of endemic zoonoses, and how this should be done are highlighted as critical for health investment, particularly since zoonosis is often considered a disease of poverty. Pandemic risk and emergence are a complex and misunderstood aspect of zoonosis (with some relevance to wildlife), whilst some helpful emerging frameworks exist to guide definitions on emerging infectious diseases (of humans). Attention is given to disease burden to inform policy and prioritization, supported by current knowledge and methods for assessment.

The paper recommends the evolution of terminology for greater clarity, which can aid in more precise narratives and targeted focus within the field. Finally, it is suggested that a structural One Health approach to address zoonosis and the risks posed by emerging pathogens is adopted in a proportionate manner to risk and burden.

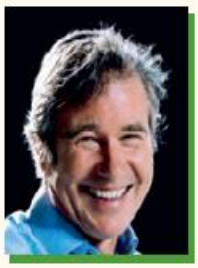
Keywords: Zoonoses, Zoonotic, Pandemic, Emerging Infectious Disease

Acknowledgement: to the co-editors and authors of a pending comprehensive reference work titled Zoonosis and Zoonotic Disease commissioned by Elsevier for providing me as chief editor, the contemporary background for this presentation.

Invited Speakers

Dr. Relja Beck
Croatian Veterinary Institute, Zagreb, Croatia
Session: Emerging and re-emerging zoonotic microbial and parasitic pathogens & diseases in wildlife
Title: Hidden in plain sight: Are "new" zoonotic cestodes truly emerging in the Western Balkans?

Prof. Dolores Gavier-Widen
Swedish Veterinary Agency, Uppsala, Sweden
Session: One Health Initiatives: integrated surveillance of zoonotic pathogens in wildlife, risk assessment and early warning systems & future pandemic preparedness
Title: One Health initiatives-perceptions and facts on the linkage wildlife-human health



Prof. Thijs Kuiken
Erasmus University Medical Centre, The Netherlands
Session: Challenges in wildlife population health, conservation, dimate change and biodiversity
Title: Between hope and terror: visions for a just and sustainable society in the face of global warming and biodiversity loss

Prof. Andrei D. Mihalca
University of Agricultural Sciences and Veterinary Medicine Cluj-Napoca, Romania
Session: Host-pathogen interacations & disease dynamics in wildlife, diagnostic methods and wildlife disease control
Title: The wildlife-livestock strongyle nemabiome: a hidden dimension of European bison conservation

Dr. José Francisco Ruiz Fons
Institute for Game and Wildlife Research, Ciudad Real, Spain
Session: Vectors & vector-borne diseases in wildlife
Title: The role of wildlife and the consequences for wildlife health of vector-borne diseases

16th European Wildlife Disease Association Conference

EWDA 2026

September 28th – October 3rd, 2026
Novi Sad Fair "Master Congress Center" – Novi Sad, Serbia

P R O G R A M M E

Monday, September 28th, *2026*

08:00 – 18:00	**Registration/ Speakers check-in/ information desk – Corridor**
08:30 – 10:30	**Student Workshop** (Hall 1)
10:30 – 11:00	**Coffee break**
11:00 – 13:00	**Student Workshop** (Hall 1)
13:00 – 14:00	Student Lunch break (Restaurant)
14:00 – 15:00	**Student workshop** (Hall 1)
15:00 – 15:30	Working pause
15:30 – 19:00	**EWDA NETWORTKING MEETING** (Hall 1)
15:30 – 16:00	National monitoring of wildlife mortality during the HPAI H5 panzootic- the Dutch perspective Valentina Caliendo
16:00 – 16:30	The value of citizen science reporting of wildlife mortality to appraise disease impact in the UK Rob Robinson
16:30 – 17:00	Improving the estimates of wild boar mortality due to African Swine Fever: the experience of the Lombardy region, Italy, during the epidemic outbreak 2023-2025 Mario Chiari (Marco Sordilli)
17:00 – 17:30	**Coffee break**
17:30 – 18:00	Harnessing wildlife mortality reporting data in Sweden – challenges and opportunities Aleksija Neimanis
18:00 – 18:30	Panel discussion
18:30 – 19:00	EWDA Network general discussion & future plans
19:00 – 21:00	**Icebreaker cocktail & welcome** (Congress venue)

Tuesday, September 29th, *2026*

08:00 – 18:00	**Registration/ Speakers check-in/ information desk – Corridor**
The main Conference Hall - Auditorium	
10:00 – 11:30	**Opening Ceremony**
	Welcome addresses: **- Sara Savič & Tamas Petrović** (Local Organizing Committee) **- Marko Pajić** (Director of Scientific Veterinary Institute Novi Sad) **- Erik Ågren** (EWDA Chair) - **Milan Maletić** (President of the Expert Committee of the Veterinary Chamber of Serbia) - **Slađan Nešić** (President of the Serbian Veterinary Association) **- Representatives of Local Administration and Ministries** - **Representative of Veterinary Directorate** (Chief Veterinary Officer)
10:30 – 11:00	**Keynote lecture 1**: **Budimir Plavšić** (WOAH, Regional representative for Europe) "Epidemiological Situation in Europe: Wildlife-Associated Emerging and Re-emerging Diseases – Regional Priorities, Integrated Surveillance and Strategic Preparedness"
11:00 – 11:30	**Keynote lecture 2**: **Richard Kock** (President Wildlife Disease Association) "Zoonoses and Zoonotic Diseases – What is the difference?"
11:30 – 12:00	**Coffee break & poster viewing**
12:00 – 14:00	**Plenary Session 1** **Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control** **Chairs: Miriam Mass, Eric Agren, Milan Miljević**
12:00 – 12:20	**Invited lecture**: The wildlife-livestock strongyle nemabiome: a hidden dimension of European bison conservation Andrei-Daniel Mihalca et al. (University of Agricultural Sciences and Veterinary Medicine of Cluj-Napoca, Cluj-Napoca, Romania)

12:20 – 12:35	A long-term eco-epidemiological study of a wild mammal host-pathogen system – what have we learnt in 50 years? Richard (Dez) Delahay et al.
12:35 – 12:50	Real-time genomic pathogen, resistance, and host range characterization from passive water sampling of wetland ecosystems Albert Perlas et al.
12:50 – 13:05	A comprehensive evaluation of alternative source materials in wildlife serology Dedeke Rockx-Brouwer et al.
13:05 – 13:20	The presence of non-lethal parasites equalizes biomass distribution across host stages in a biomass model E. Rosa Jolma et al.
13:20 – 13:35	Investigating *Trichomonas gallinae* transmission risks associated with supplementary feeding of garden birds Susie Gold (Becki Lawson) et al.
13:35 – 13:50	Avian cholera as a cause of mass mortality at penguin mega-colonies in Antarctica Matteo Iervolino (Lineke Begeman) et al.
13:50 – 14:00	General discussion
14:00– 14:45	**Lunch break (restaurant)**
14:45– 15:00	Alice Mistrou: **The Ceva Wildlife Research Fund**
15:00 – 17:00	**Session 1a** **Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control** **Chairs: Ruiz Fons, Sara Savić**
15:00 – 15:15	How wild birds have shaped the viral dynamics of HPAI H5N1 in France, 2021–2023 Manon Couty et al.
15:15 – 15:30	What makes bats such important reservoirs for zoonotic viruses? An explainable machine learning approach Marianne Houle et al.
15:30 – 15:45	Multi-Host Dynamics of Animal Tuberculosis: Estimating R_0 across the Iberian Peninsula Beatriz Cardoso et al.
15:45 – 15:55	Elimination of bovine tuberculosis in wildlife as an exotic disease outbreak Graham Smith & Zara Gerard
15:55 – 16:10	25 years of wild boar disease surveillance in Sweden following the exponential growth of the population Karin M. Olofsson et al.

16:10 – 16:25	Non-invasive genetic sampling to estimate epidemiological parameters in cryptic carnivore species: Sarcoptic mange in the Iberian Wolf Joana Ferreira-e-Silva et al.
16:25 – 16:35	A ten-year European CWD anniversary – is the antler pointing down or up? Jørn Våge
16:35 – 16:45	Hedgehog arterivirus-1 in European hedgehogs in England and Wales Hannah Davies et al.
16:45 – 16:55	Opportunistic transmission and selective establishment structure *Leucocytozoon* parasite diversity in passerine birds Claudio Navarrete et al.
16:55 – 17:00	General discussion
17:00 – 17:30	**Coffee break & poster viewing**
The main Conference Hall - Auditorium	
17:30 – 18:30	**Session 2** **Health and diseases of bats and rats** **Chairs: Ivana Budinski, Valentina Ćirković**
17:30 – 17:45	Insights into Bat Health, Mortality, and Pathogen Surveillance: Findings from the Interdisciplinary Project 'Bat Health in Central Germany – From Pathology to Protection' Amelie Lisa Arnecke et al.
17:45 – 18:00	Molecular Characterization and Haplotype Analysis of *Neoehrlichia mikurensis* in Bat-Associated Ticks in Serbia Valentina Ćirković et al.
18:00 – 18:15	The Calm City? Landscape Drivers of Cortisol in Urban Pipistrelles Javier Millán et al.
18:15 – 18:25	Wild rats as carriers of disease Ellinor Spörndly-Nees et al.
18:25 – 18:30	General discussion
18:30 – 20:00	**EWDA Annual meeting (AGM)**
20:00 – 23:00	**Student mentor Mixer with snacks and drinks** (restaurant/bar Magacin)

Wednesday, September 30th, 2026

08:00 – 18:00	**Registration/ Speakers check-in/ information desk – Corridor**
The main Conference Hall - Auditorium	
09:00 – 11:30	**Session 3** **Vectors and vector-borne diseases in wildlife** **Chairs: Andrei Mihalca, Snežana Tomanović, Marko Pajić**
09:00 – 09:20	**Invited lecture:** The role of wildlife and the consequences for wildlife health of vector-borne diseases Francisco Ruiz-Fons (CSIC-UCLM-JCCM & Instituto de Salud Carlos III, Spain)
09:20 – 09:35	Open-access training videos for arthropod vector identification and wildlife sampling to support wildlife disease surveillance Ivancho Naletoski (Andrei Mihalca) et al.
09:35 – 09:50	Molecular screening of wild carnivores in Israel uncovers widespread *Babesia negevi* and *Hepatozoon canis* prevalence Gad Baneth et al.
09:50 – 10:05	Detection of zoonotic *Bartonella* species in wild canids from Israel Shimon Harrus et al.
10:05 – 10:15	*Babesia banethi* in red foxes: description of a novel species with epidemiological and clinical data Mariaelisa Carbonara et al.
10:15 – 10:25	Ectoparasite Specialization Shapes *Bartonella* Circulation in Armenian Bats: Evidence from High-Throughput Pathogen Screening Gohar G. Grigoryan (Sargis A. Aghayan) et al.
10:25 – 10:35	Vector-Borne RADAR project: investigating *Orthoflavivirus* infections of wild birds in the United Kingdom Arran J. Folly (Mariana Santos) et al.
10:35 – 10:45	West-Nile virus in Red-footed falcons (*Falco vespertinus*) and Common kestrels (*Falco tinnunculus*) at the start of breeding season and pre-migratory Autumn roosting Károly Erdélyi et al.

10:45 – 10:55	An overlooked ectoparasite at the urban human-avian interface: pathogens in the Common House Martin Bug Péter Takács et al.
10:55 – 11:05	Mosquito vectors of *Setaria tundra*: an emerging threat to wildlife health in Serbia Mihaela Kavran et al.
11:05 – 11:15	Vector tick species and mammal reservoirs for emerging tick-borne Yezo virus Mebuki Ito et al.
11:15 – 11:25	Integrated biodiversity monitoring in a Crimean-Congo hemorrhagic fever virus circulation zone in the South of France Mélanie Gippet et al.
11:25 – 11:30	General discussion
11:30 – 12:00	**Coffee break & poster viewing**
The main Conference Hall - Auditorium	
12:00 – 14:00	**Session 4** **Challenges in wildlife health, conservation, climate change and biodiversity** **Chairs: Thijs Kuiken, Sara Savić, Jovan Mirčeta**
12:00 – 12:20	**Invited lecture:** Between hope and terror: visions for a just and sustainable society in the face of global warming and biodiversity loss Thijs Kuiken (Erasmus University Medical Centre, The Netherlands)
12:20 – 12:35	Development of National Wildlife Health Surveillance James Paul Duff et al.
12:35 – 12:50	WildEpi: A New Path for Global Information Sharing on Wildlife Health Claire Cayol (Valeria Colombo) et al.
12:50 – 13:05	WOAH's Global Wildlife Health Strategy: A Strategic Framework to Strengthen Wildlife Health Systems Worldwide Sophie Muset (Valeria Colombo) et al.
13:05 – 13:20	Threats to Biodiversity from Disease Outbreaks Associated with Non-Native Parasites in Europe Anthony W Sainsbury et al.
13:20 – 13:30	Systematic mammal abundance estimates across Europe Graham Smith et al.

13:30 – 13:40	Mitigating disease risks in conservation translocations through a proportionate approach to disease risk analysis (DRA) Helen Donald
13:40 – 13:50	Badger vaccination as a complementary tool for controlling bovine tuberculosis in France: eco-epidemiological analyses of a 4-year trial. Stéphanie Desvaux et al.
13:50 – 14:00	General discussion
14:00– 15:00	**Lunch break (restaurant)**
The main Conference Hall - Auditorium	
15:00 – 16:30	**Session 4a** **Challenges in wildlife health, conservation, climate change and biodiversity** **Chairs: Antonio Lavazza, Debbie Myers, Branislav Kureljušić**
15:00 – 15:15	Capture-related mortality: disentangling individual vulnerability, capture conditions and prior experience in roe deer Thelma Sitter (Emmanuelle Gilot-Fromont) et al.
15:15 – 15:30	Complex Causes behind Poor Growth and High Mortality among Moose Calves Bjørnar Ytrehus et al.
15:30 – 15:45	Anthropogenic Drought Leads to Gut Inflammation in Wild and Domestic African Herbivores Alice M. Burton et al.
15:45 – 16:00	Monitoring of *Protoparvovirus carnivoran1* in Eurasian lynx (*Lynx lynx*): implications for disease surveillance and conservation Ivona Ćorić et al.
16:00 – 16:10	Surveillance of high-stakes viruses for Eurasian lynx population in France Julien Hirschinger et al
16:10 – 16:20	A citizen-science serological survey of myxoma and rabbit haemorrhagic disease viruses in Iberian rabbit populations Nuno Santos et al.
16:20 – 16:30	The rise of amphibian herpesviruses: All that we do not know Francisco C. Orrigi et al
16:20 – 16:40	General discussion
16:45 – 18:30	**Touristic City Walk with guide** (starts in front of the Conference venue)
18:30 -	***Free evening time***

The main Conference Hall - Auditorium	
16:45 – 18:30	**Workshop** **Regional Workshop & Panel discussion on wildlife diseases** **Chairs: Boban Đurić, Jovan Mirčeta**
16:45 – 17:15	**Invited lecture:** Sampling, diagnostic material (sample) packaging and transportation of samples to the diagnostic laboratory Jovan Mirčeta (Directorate for Food Safety, Veterinary & Phytosanitary Affairs, Podgorica, Montenegro)
17:15 – 17:45	**Coffee break & poster viewing**
17:45 – 18:30	**Panel discussion**
18:30 –	***Free evening time***

Thursday, October 1st, *2026*

08:00 – 18:00	**Registration/ Speakers check-in/ information desk – Coridor**
The main Conference Hall - Auditorium	
09:00 – 11:00	**Session 5** **Avian influenza, African swine fever and potential pandemics in wildlife** **Chairs: Jasna Prodanov Radulović, Dejan Vidanović**
09:00 – 09:15	Environmental Risk Mapping of African Swine Fever in Wild Boar Using MCDA with Exploratory Fly-Based Surveillance Helen Jäkel et al.
09:15 – 09:30	Integrating Hunting with Strategies for African Swine Fever Control in Wild Boar: Lessons from Europe Alessandro Cristalli (Carmen Iscaro) et al.
09:30 – 09:45	Genetic evolution of a panzootic pathogen – African swine fever virus complete genome sequencing in Germany Sten Calvelage et al.

09:45 – 09:55	Re-emergence of African Swine Fever in Spain: early spread dynamics and control in wild boar Xavier F. Aguilar et al.
09:55 – 10:05	African swine fever in Lombardy: strategies for the management of the disease in wild boars Francesca Meriggi et al.
10:05 – 10:20	Relevance of wildlife rescue centres in the epidemiological surveillance of high pathogenicity avian influenza in France Lorette Hivert et al.
10:15 – 10:35	Identifying undersurveilled wild bird species associated with highly pathogenic avian influenza outbreaks using large-scale citizen science data Gauthier Vercher et al.
10:35 – 10:50	Exposure to diverse avian influenza viruses in sympatric UK seabirds Hannah M. Ravenswater (Fiona Greco) et al.
10:50 – 11:00	General discussion
11:00 – 11:30	**Coffee break & poster viewing**
The main Conference Hall - Auditorium	
11:30 – 13:30	**Session 6** **Food safety of game meet, AMR and ecotoxicology** **Chairs: Jelena Petrović, Branko Velebit, Radomir Ratajac**
11:30 – 11:45	Antimicrobial resistance at the wildlife–environment interface: a planetary health perspective Zorana Kovačević et al.
11:45 – 12:00	White-tailed eagles (*Haliaeetus albicilla*) as a reservoir of resistant and virulent *Escherichia coli* strains in the protected "Gornje Podunavlje" biosphere reserve Dalibor Todorović et al.
12:00 – 12:15	Genomic characterization and clonal relationship of Multidrug-Resistant *Staphylococcus pseudintermedius* isolated from surgical wounds in rescued wild carnivores Virginia Filipello et al.
12:15 – 12:30	Commercial brown bear (*Ursus arctos*) meat products are highly contaminated with lead (Pb) from hunting ammunition Helle B. Hydeskov et al.
12:30 – 12:45	GPS tracking reveals emerging NSAID-induced mortality in a critically endangered Griffon vulture (*Gyps fulvus*) population Nili Anglister et al.

12:45 – 13:00	Persistent Risk of Lead Exposure in Captive Scavengers: Evidence from Two Andean Condors Dajana Davitkov et al.
13:00 – 13:15	GreenBait – Progress Toward Environmentally Safer Rodenticides Hans Kristian Mjelde et al.
13:15 – 13:30	General discussion
13:30– 14:30	**Lunch break (restaurant)**
The main Conference Hall - Auditorium	
14:30 – 17:00	**Session 7** **One Health Initiatives: integrated surveillance of zoonotic pathogens in wildlife & future pandemic preparedness** **Chairs: Gudrun Wibbelt, Tamaš Petrović, Ljubo Barbić**
14:30 – 14:50	**Invited lecture:** One Health initiatives: perceptions and facts on the linkage between wildlife and human health Dolores Gavier-Widén (Swedish Veterinary Agency, Uppsala, Sweden)
14:50 – 15:05	Contrasting effects of anthropogenic environmental changes on zoonotic disease risk from small mammals Miriam Maas et al.
15:05 – 15:20	Advancing wildlife-borne pathogen surveillance by determining mammal species' vulnerability to land use change Sara S. Schneemann et al.
15:20 – 15:30	High-risk activities for the zoonotic spillover of pathogens in the legal wildlife trade Tirion Cobby & Irene Bueno
15:30 – 15:45	When Science Sings: International One Health Collaboration Communicating Wildlife-Associated Disease Risks Through Music Anja Globig et al.
15:45 – 16:00	The OneBAT project: One Health approach to understand, predict and prevent viral emergencies from bats Stefania Leopardi et al.
16:00 – 16:10	Integrating Ecological–Diagnostic Surveillance in Bats: A Comparative One Health Case Study in Italy and Spain Tiziana Trogu et al.
16:10 – 16:20	Surveillance of emerging viral pathogens in insectivorous bats in Ukraine Denys Muzyka et al.

16:20 – 16:30	Tracking Avian Influenza Virus in the environment: A longitudinal study across Scotland Lina González Gordon et al.
16:30 – 16:40	Beyond dogs: multilocus microsatellite typing (MLMT) reveals wildlife as putative reservoirs of *Leishmania infantum* in northeaster Italy Elena Carra et al.
16:40 – 16:50	Wild Boars as Sentinels and Victims of Viral Diseases in Croatia Lorena Jemeršić et al.
16:50 – 17:00	General discussion
17:00 – 18:30	**Poster Session** **Coffee break with POSTER presentation & viewing**
18:30 – 19:00	***Free time***
19:00 – 22:00	**Traditional Serbian dinner with Auction** (Restaurant „Zlatna dvorana" at the Conference venue)

Friday, October 2nd, *2026*

08:00 – 18:00	**Registration/ Speakers check-in/ information desk – Corridor**
The main Conference Hall - Auditorium	
09:00 – 11:30	**Session 8** **Emerging and re-emerging zoonotic pathogens and diseases in wildlife** **Chairs: Vesna Milićević, Dejan Bugarski**
09:00 – 09:20	**Invited lecture:** Hidden in plain sight: Are "new" zoonotic cestodes truly emerging in the Western Balkans? Relja Beck (Croatian Veterinary Institute, Zagreb, Croatia)
09:20 – 09:35	Environmental risk mapping of *Echinococcus multilocularis* infections in wild carnivores on Rügen Island Hannes Bergmann et al.
09:35 – 09:50	*Echinococcus multilocularis* in red foxes in the Netherlands: current situation and comparison of detection methods for surveillance Laura Derks et al.

09:50 – 10:05	Shared transmission pathways of zoonotic helminths at the wildlife–domestic interface: evidence from Serbia Milan Miljević et al.
10:05 – 10:20	First confirmed case of Aujeszky's disease in a grey wolf (*Canis lupus*) in Central Europe Wojciech Wójcik et al.
10:20 – 10:35	Serosurvey of shrew-associated parahenipaviruses in white-toothed shrews and potential contact animals Viola C. Haring et al.
10:35 – 10:50	Prion Protein Gene (*PRNP*) Diversity in European Cervid Populations – A Review Sonja Ernst et al.
10:50 – 11:00	General discussion
11:00 – 11:30	**Coffee break & poster viewing**
The main Conference Hall - Auditorium	
11:30 – 13:00	**Session 9** **Endemic, neglected and non-communicable diseases** **Chairs: Karoly Erdelyi, Jakov Nišavić**
11:30 – 11:45	Unexpectedly prolonged half-life of neutralising antibodies against Crimean-Congo haemorrhagic fever virus infection in red deer Francisco Ruiz-Fons et al.
11:45 –12:00	Implication of *Clostridium botulinum/baratii* in paretic syndrome of antic islands National Park in Spain: a field study Ursula Höfle et al.
12:00 –12:15	Long-term seroepidemiology of European Brown Hare Syndrome in European and Italian hares in Tuscany (Italy), 2003 to 2019 Maria Chiara Fabbri (Antonio Lavazza) et al.
12:15 –12:30	Do clusters of tumour-like disease in wild red squirrels suggest a common cause? Paul Duff et al.
12:30 – 13:00	General discussion
13:00– 14:00	**Lunch break (restaurant)**

The main Conference Hall - Auditorium	
14:00 – 16:00	**Session 10** **Treats to ectotherms, urban wildlife, wild pets, fish and exotic animals** **Chairs: Becky Lawson, Miloš Vučićević, Nikolina Milošević**
14:00 – 14:15	Betanodavirus Infections in Mediterranean and Atlantic Groupers: Epidemiology, Host Interactions, and Conservation Implications Francesc Padrós & Anna Toffan
14:15 – 14:30	Amphibian scanning disease surveillance for threat detection: Bufonid herpesvirus 1 infection in common toads (*Bufo bufo*) in Great Britain Sarah Haddow (Katharina Seilern-Macpherson) et al.
14:30 – 14:45	Parasitic spillover in endangered fresh water turtles in France Guillaume Le Loc'h et al.
14:45 – 15:00	Deepening the spatial ecology of human leishmaniasis in Spain Alfonso Peralbo-Moreno et al.
15:00 – 15:15	Is urbanization a driver of differences in bacterial communities among native and invasive rodents in Northern Senegal? Julia Emerit et al.
15:15 – 15:30	Respiratory disease in rehabilitating European hedgehogs (*Erinaceus europaeus*): Pathological and microbiological findings Yannick Van de Weyer et al.
15:30 – 15:45	General discussion
15:45 – 16:30	**CONFERENCE CLOSING REMARKS**
16:30 – 19:00	***Free time***
19:00 – 24:00	**Gala Dinner with music and dancing** (Restaurant „RIBARAC" at the Danube Riverbank)

Saturday, October 3rd, *2026*

09:45 –	**Gathering on the parking place oposit to the Fair main entrance**
10:00 – 16:00	**Post meeting excursion day** ***Excursion to the „Zasavica" Nature Reserve***
16:00 -	***Doviđenja, goodbye, verabschiedung, au revoir, arrivederci, adiós***

LIST OF POSTERS

Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control

P001 Erik Ågren & Karin Olofsson-Sannö
Remote digital necropsy of wildlife.

P002 Alberto Perelló et al.
Advancing non-invasive wildlife monitoring: environmental drivers and applications of eDNA in eco-epidemiology.

P003 Sofia M. Soares et al.
Altitudinal patterns of tick–host–pathogen interactions in a mountain ecosystem: insights from the PyrTick project.

P004 Patrick Scherrer et al.
When Parasites Shape Predators: Investigating *Toxoplasma gondii* infections in free-ranging Wolves.

P005 Branislav Kureljušić et al.
Retrospective analysis of possible associations between *Pneumocystis spp*. and five viral pathogens in three wild carnivore species.

P006 Pierre Bessiere et al.
Using dogs as a model to identify alternative matrices for canine distemper serology in wildlife surveillance.

P007 Charlotte Parker et al.
Detection of a canine coronavirus in British red foxes (*Vulpes vulpes*).

P008 Roberta Moriano et al.
Selected emerging parasitic diseases in expanding Serbian populations of golden jackal *Canis aureus* and grey wolf *Canis lupus*.

P009 David Kiss et al.
Detection and genotyping of tapeworm eggs in faecal samples of grey wolf (*Canis lupus*) in the Czech Republic.

P010 Sara Mrabet (Alice Ranucci) et al.
Whole genome sequencing of recent parvovirus from domestic and wild animals in central Italy.

P011 Marta Cresci et al.
Dynamics of canine distemper virus circulation in wildlife in Central Italy.

P012 Javier Millán et al.
Results from the first years of the Carnivore Diseases Monitoring Program in Navarre (Northern Spain).

P013 Martina Macejková (Nahliková) et al.
Surveillance of parvoviruses and canine circovirus in fecal samples of free-ranging carnivores.

P014 Elina Thorsson et al.
Breaking the cycle: Eliminating urban *Echinococcus multilocularis* in Uppsala, Sweden.

P015 Ioana Bianca Mitrea et al.
Ancylostomatidae in carnivores from Romania: new host associations, haplotype diversity and presence of *Ancylostoma caninum*.

P016 Debby Bonnaire et al.
An ELISpot-based methodology for characterizing IFN-γ responses to *Mycobacterium bovis* in European badgers (*Meles meles*).

P017 James Stranks et al.
Culling-induced changes to individual movement behaviour in an intensively studied badger (*Meles meles*) population.

P018 Alžbeta Königová et al.
Fenbendazole treatment for gastrointestinal nematodes in captive bison (*Bison bonasus*) in Slovakia.

P019 Sara Mrabet (Alice Ranucci) et al.
First detection of Small Ruminant Lentivirus in a roe deer (*Capreolus capreolus)* in Italy.

P020 Nele Lechleiter et al.
A metagenomic study of the European bison microbiome.

P021 Francesca Dall'Acqua (Valentina Zenobio) et al
Evidence of Bluetongue virus circulation in wild ruminants and its relationship with livestock outbreaks in Central Italy.

P022 Johan Espunyes et al.
Sixteen years of endemic circulation of Border Disease Virus after a severe outbreak in a Pyrenean chamois population from Andorra.

P023 Krešimir Severin (Dean Konjević) et al.
Impact of short-term freezing on morphology and hatchability of *Fascioloides magna* eggs.

P024 Camilla Sangiovanni et al.
Across Italian ecosystems: what shapes parasite dynamics in wild boar?

P025 Milan Miljević et al.
Molecular survey of *Calodium hepaticum* in small mammals in Serbia.

P026 Anton Alina Johanna et al.
Prevalence, Genetic Diversity, and Landscape Associations of *Orthohantavirus puumalaense* in Bank Voles (*Clethrionomys glareolus*) from Northern Sweden.

P027 Claudia Maistrelli et al.
Preliminary findings on ha-MYXV infections in European Brown Hares (*Lepus europaeus*) in Lower Saxony, Germany.

P028 Mihaela Teneva et al.
Pathological Features of Fulminant Leptospirosis in a Zoo-Housed Red-Necked Wallaby (*Notamacropus rufogriseus*): A Case Report.

P029 Ljubica Andrić et al.
Antimicrobial Resistance of Indicator Commensal *Escherichia Coli* in Wild Animals and Birds in the Territory of the Republic of Serbia.

P030 Ane López-Morales et al.
Shifts in the Microbial Core: Does Avian Influenza Alter the Faecal Bacteriome of Mallards?

P031 Ni Made Ayudita A.L. Wedayanti (Judith M.A. van den Brand) et al.
Presence and Tissue Tropism of Avian Coronaviruses in Wild Birds in the Netherlands.

Health and diseases of bats & rats

P032 Alex Barlow & Geoff Billington
Active Railway Tunnels as a little investigated cause of mortality in bats.

P033 Valeriia Bohodist et al
EBLV-1 confirmation and clinical behavioral patterns in *Cnephaeus serotinus* from Ukraine.

Vectors & vector-borne diseases in wildlife

P034 Víctor Luque-Castro et al.
Does biodiversity buffer tick-borne pathogens? A systematic review of empirical evidence.

P035 Alessia Franzoso et al.
Circulation of Tick-Borne Pathogens in wildlife-derived ticks form North-Eastern Italy.

P036 Neus Abella et al.
Composition and geographical distribution of wild ungulate-associated tick species in Catalonia, northeastern Spain.

P037 Marina Žekić et al.
An overlooked hotspot of *Babesia/Theileria* circulation in deer from the Western Balkans.

P038 Jasmin Kinnunen et al.
Co-circulation of epizootic haemorrhagic disease virus and bluetongue virus in wild ruminants in Catalonia (NE Spain).

P039 Helena Costa et al.
Using amplicon-based next-generation sequencing for detection of vector-borne bacteria and parasites in Danish roe deer (*Capreolus capreolus*).

P040 Tamas Petrovic et al.
Seroprevalence of West Nile infection in wild mammals: wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*) populations just before the emergence of the first WNV epidemic in Serbia.

P041 Vladimir Gajdov et al.
Serological survey of West Nile virus antibodies in domestic donkeys in Vojvodina, Serbia.

P042 Péter Takács (Károly Erdélyi) et al.
West-Nile virus circulation and impact monitoring of hosts and vectors at Northern Goshawk (*Astur gentilis*) breeding habitats.

P043 Catarina Fontoura-Gonçalves et al.
Longitudinal serological dynamics of Bagaza virus in red-legged partridges from southern Portugal: insights from integrated analyses at population and individual level.

P044 Maria Puig Ribas et al.
Haemosporidian infections in alpine bird communities of the Cantabrian Mountains, Spain.

P045 Gaia Porporato et al.
Genomic content in avian haemosporidian parasites suggests co-regulation of apicoplast and mitochondrial nucleoids.

P046 Manan Asikyan et al.
Low Prevalence of Haemosporidian Parasites in *Phylloscopus* Warblers in Armenia.

P047 Andrea S. Ingebretsen (Helena Costa) et al.
Molecular detection of avian hesperidia's in Norwegian tawny owls (*Strix aluco*).

P048 Gohar Zhamakochyan et al.
Diversity and Distribution of Psychodidae in Armenia.

P049 Anna Didkowska et al.
Molecular detection of vector-borne pathogens in wild felids from Poland.

P050 Patricia Parreira Perin et al.
Assessment of the exposure to *Phlebotomus perniciosus* in red foxes and wolves using lung extract as a sample matrix.

Challenges in wildlife health, conservation, climate change and biodiversity

P051 Ladislav Molnar et al.
Aspects of brown bears management in Slovakia and effect of health conditions on behavior changes.

P052 Ladislav Molnar et al.
Veterinary aspects of field capture of European bison.

P053 Magda Sindičić et al.
Systematic health monitoring in reintroduction and population reinforcement projects – the case of *Chlamydia felis* in Eurasian lynx.

P054 Lorette Hivert et al.
From individual care to disease surveillance: how French wildlife rescue centres feel towards this paradigm shift.

P055 Marlene Hirdes et al.
Reliability of arterial oxygen content calculations made by the AVOXimeter-4000 co-oximeter and Enterprise Point-of-Care blood gas analyser in immobilised White rhinoceroses (*Ceratotherium simum*).

P056 Nia Weinzweig et al.
Water vole reintroduction in the UK: is it a success without indices of health, welfare, or genetic diversity?

P057 Ilze Brila et al.
Prevalence of tick-borne and rodent-associated pathogens in restored Scottish wetlands.

P058 Stamatios Alan Tahas et al.
Comparison of physiologic and acid-base variables in anaesthetised wild muskoxen (*Ovibos moschatus*) herded above the arctic circle by helicopter or by land.

P059 Marine Montblanc et al.
Hematology and biochemistry reference values for white-bellied *(Phataginus tricuspis)* and black-bellied *(Phataginus tetradactyla)* pangolins from a rescue center in Cameroon.

P060 Alex Barlow & Daniel Hargreaves
Heat related mortality in Brown long-eared bat (*Plecotus auritus*) pups in England.

P061 Yael Langenegger et al.
Increasing Prevalence of Heart Murmurs in Swiss Eurasian Lynx (*Lynx lynx*): Risk Factors and Echocardiographic Insights.

P062 Janna Niehaus et al.
Inbreeding depression in a reintroduced lynx population: a genetic defect causing fatal disease.

P063 Tetiana A. Kuzmina et al.
Taenia arctos in European brown bears (*Ursus arctos*): Is moose (*Alces alces*) the sole intermediate host in Slovakia?

P064 Gábor Árpád Czirják et al.
Estimating *Toxoplasma gondii* exposure in Swedish wolverines (*Gulo gulo*) – a retrospective study.

P065 Thomas Branchereau (Emmanuelle Gilot-Fromont) et al.
Visual Syndromic Surveillance of Alpine Chamois (Rupicapra rupicapra) in Écrins National Park, France: A 21-Year Cost-Benefit Analysis and Protocol Optimization.

P066 Jelena Apić (Siniša Grubač) et al.
Reproductive status of red deer hinds (*Cervus elaphus*) in two hunting grounds in Vojvodina (Serbia) during the 2024/2025 hunting season: a pathomorphological study.

P067 Božana Tošić et al.
Modeling future distributions of zoonotic helminths in *Apodemus* mice.

P068 Alba Palomo et al.
Species specific disparity in incidental pulmonary silicates depositions in mammals at Barcelona Zoo.

P069 Daniela Losada-Medina et al.
Antimicrobial resistance in wild animals in captivity (*ex situ*): a scoping review.

P070 Kim van de Wiel et al.
The great 'trait-off': Host traits and infection patterns at the wildlife–livestock interface.

P071 Ján Pavelka et al.
Influence of geographical location on embryotoxic potential of *Vipera ammodytes* snake venom originating from different regions of the Balkan peninsula

P072 George Lewis et al.
An open-source thermal camera platform to monitor wildlife: a pilot study in thermoregulatory behaviour of European adders (*Vipera berus*).

P073 Dejan Bugarski et al.
Copper deficiency in wild ruminants in Vojvodina (Republic of Serbia).

P074 Dejan Bugarski et al.
Welfare of game animals in fenced hunting grounds and breeding facilities.

P075 Anna Bergfeldt et al.
The emergence and spread of fibropapillomatosis in red deer (*Cervus elaphus*) in Norway.

P076 Ivana Lojkić et al.
Circulation of Domestic Dog Viruses in Wild Carnivores: Evidence from a Large-Scale Croatian Monitoring Program.

P077 Omar Jimenez-Lopez ez al.
Is captivity associated with different microbiomes in two species of raptors?

P078 Stevan Rodić et al.
Advanced Methods for the Analysis of Pheasant Semen Quality.

P079 Philippe DeSoye (Yael Langenegger) et al.
Novel Description of Cartilage and Bone at the Aortic Base of Free-Ranging Eurasian Lynx (*Lynx lynx*) from Switzerland.

P080 Marti Iris Andrea et al.
Analgesia and Wildlife Immobilisations – a promising start in the Eurasian lynx.

P081 Katie M. Beckmann et al.
Smarter disease risk analysis for better conservation translocation decisions.

P082 Anlore Steele et al.
Radiographic Prevalence of Metabolic Bone Disease in a Population of South-West England European Hedgehogs (Erinaceus europaeus) and Associated Risk Factors.

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Session 1

Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control

Oral Presentations

Invited lecture

The wildlife-livestock strongyle nemabiome: a hidden dimension of European bison conservation

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The recovery of the European bison is usually framed through genetics, habitat, and demography, yet parasitism adds a less visible dimension with direct relevance to reintroduction success. In human-shaped landscapes, the strongyle nemabiome offers a particularly informative view because it reflects not only parasite diversity, but also connectivity between wildlife, livestock, and shared grazing environments. Recent data from Romania show that European bison harbor a diverse gastrointestinal strongyle community, with 32 taxa across 16 genera identified by ITS2 metabarcoding, including dominant species such as *Haemonchus contortus*, *Ostertagia ostertagi*, *Cooperia oncophora*, *Trichostrongylus colubriformis*, and *T. axei*. This pattern is highly suggestive of a strong livestock-related transmission risk, especially as broad overlap is evident with cattle and sheep, while parasite community structure appears to be shaped more by host association than by geography. Rather than reflecting a closed and conserved parasite fauna, the bison nemabiome appears connected to a wider multi-host transmission network at the wildlife-livestock interface. The same interface is also reflected by other recent findings from Romanian bison populations: fatal dictyocaulosis caused by *Dictyocaulus viviparus*, ocular infection with *Thelazia rhodesi* and *T. skrjabini*, and the detection of *Anaplasma phagocytophilum* and *Babesia divergens* in reintroduced animals. These observations point in the same direction, that livestock-associated parasites and pathogens are part of the ecological reality into which European bison are being restored. This has important conservation implications for a post-bottleneck species with low genetic variability and potentially reduced resilience to infection. Monitoring the strongyle nemabiome but also other parasites and pathogens in re-introduced species could provide an early-warning tool for spillover risk and a practical framework for integrating wildlife health into conservation and highlighting the need for parasite surveillance and control in sympatric livestock.

Keywords: European bison; nemabiome; strongyles; livestock interface; conservation

A long-term eco-epidemiological study of a wild mammal host-pathogen system – what have we learnt in 50 years?

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Long-term studies of mammal populations are uncommon, and the inclusion of host-pathogen interactions is even rarer. The bacterium *Mycobacterium bovis* (the cause of bovine tuberculosis) circulates between European badgers (*Meles meles*) and cattle in parts of the UK and elsewhere in Europe, posing a significant challenge for disease control. The long-term intensive study of a badger population at Woodchester Park in southern England, from 1976 to date, has generated an unrivalled database of the life histories and infection status of over 3200 individual badgers from more than 16,200 capture events. During its lifetime the study has identified important drivers of transmission in this host-pathogen system. Badger population density in the study area increased to a peak in the 1990s, declining thereafter, but bears no simple relationship with the prevalence of disease. The organisation of the host population into territorial social groups and movements amongst these groups are important determinants of the distribution of infection in badgers. A subset of infected animals exhibits persistent and/or multi-site shedding of bacteria and enhanced mortality rates. The potential for certain infected individuals to play a pivotal role in transmission and pathogen persistence is borne out by social network analysis and epidemiological modelling. Recent genotyping work has highlighted the influence of sociality and kinship on transmission dynamics amongst badgers. Furthermore, comparison of *M. bovis* genotypes obtained from infected badgers and local cattle supported the existence of clades circulating exclusively in each host population and transmission in both directions between the two host populations. This project demonstrates the value of long-term studies in revealing key epidemiological and ecological trends and informing disease management strategies.

Keywords: TB, *Mycobacterium bovis*, badger, cattle.

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Real-time genomic pathogen, resistance, and host range characterization from passive water sampling of wetland ecosystems

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Wetland ecosystems provide interfaces for the transmission of microbial pathogens and antimicrobial resistances (AMR) between migratory birds, wild and domestic animals, and human populations. The efficient surveillance of wetlands is, however, challenging, since the typically low concentration of pathogens typically requires the sampling of large volumes of water and subsequent targeted detection, which is inherently limited to a few pathogens or AMR genes of interest. Here, we present a holistic, accessible, and cost-efficient framework to characterize the pathogen and resistance load of water sources together with their potential associated hosts by combining passive water sampling through torpedo-shaped devices with nanopore sequencing technology. We used this framework to characterize anthropogenically influenced and natural wetland ecosystems along the East Atlantic Flyway, where we obtained robust assessments of the microbial communities from long-read metagenomic and RNA virome data, and showed that anthropogenically impacted wetland ecosystems consistently exhibited higher relative abundances of pathogens and AMR genes. By focusing on avian influenza viruses (AIV), we finally highlight the additional need for targeted screening and whole-genome sequencing of pathogens of interest; we detected and characterized AIV at a third of the monitored sites and used environmental DNA (eDNA) to explore potential animal hosts to better understand the role of wetland ecosystems as One Health interfaces.

Keywords: Environmental surveillance, Metagenomics, Avian Influenza, eDNA

A comprehensive evaluation of alternative source materials in wildlife serology

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Serological techniques are commonly used in wildlife disease studies to determine the presence of pathogen specific antibodies. They have the advantage that, even for pathogens that only have a short time frame for molecular detection, antibodies remain present long after infection. For serological assays, ideally serum from whole blood is used, but researching wildlife often involves opportunistic sampling of animals that are hunted or found dead. This severely limits the collection of whole blood and leads to large variations in type and quality of the sample. The aim of this study is to provide an overview of alternative source materials to serum collection for use in serological assays with a focus on wildlife animals.
A scoping review was performed comparing available alternative methods and identifying knowledge gaps. Studies were selected that performed serological assays using serum and alternative materials in terrestrial (often wild) mammals.
Our results show that only a third of the papers describing alternative source materials make a direct comparison between serum and these alternatives using paired samples (samples taken from the same animal). These papers mainly focused on muscle juice/extract and dried blood spot papers, and in general sampled large mammals. Based on the scoping review, we are currently performing a comprehensive comparison of serum and various alternative source materials in small mammals. In this comparison, we also consider the ease of use for collection, processing procedure and transportation requirements.
The anticipated final overview can be used as a guideline to determine what source material is best to collect for serology-based assays, taking into account the size and state of the animal.

Keywords: wildlife, serology, surveillance, alternative materials

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The presence of non-lethal parasites equalizes biomass distribution across host stages in a biomass model

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Most parasites do not kill or castrate their hosts but rather limit host energy available for other processes like growth and reproduction. While virulent parasites are known to be capable to regulate host populations, the impact of benign energy-tapping parasites on host populations and their structure is less well known. Often parasites infect only certain stages of a host's life history so potentially affecting intraspecific competition and the resulting host population structure. We set out to investigate if parasites that merely tap some of host's energy can affect host population structure and total host biomass.
We built a stage-structured biomass model that was parameterized to fit a model system consisting of blue mussel (*Mytilus edulis*) hosts and intestinal copepod parasites which have simple life cycles. The model included three host stages, two of which were susceptible, and three parasite stages. All energy fluxes were accounted for including feeding, maintenance, growth, reproduction, mortality, immune response and parasite feeding.
Without parasites the host population was dominated by the small adult stage for most of the ranges of the intraspecific competition factor and host mortality rate parameters, while with parasites host population biomass was relatively evenly distributed across juveniles, small adults and large adults at a wider range of parameter values.
This implies that the presence of typical benign (energy-tapping) parasites can prevent host population stunting which, in turn, can affect 1) food availability for predators that consume only certain host stages and 2) host availability for other parasites that rely on certain host stages for the completion of their life cycles.

Keywords: ectothermic species, energy budget model, host population effect, non-lethal parasites, stage-structured model

Investigating *Trichomonas gallinae* transmission risks associated with supplementary feeding of garden birds

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Supplementary feeding of wild birds in garden habitats is a common practice in Great Britain. However, concerns have been raised regarding elevated risks of pathogen transmission amongst birds which utilise these shared food and water resources. Trichomonosis emerged in finches in Great Britain and has caused significant national declines of breeding Greenfinch *Chloris chloris* (~75% for 2006-2023) and Chaffinch *Fringilla coelebs* (~39% for 2013-2023) sufficient to prompt conservation concern. Our objective was to investigate direct and indirect transmission opportunities for *Trichomonas gallinae* to inform evidence-based guidance for disease mitigation.

Householders from 15 gardens with active finch trichomonosis outbreaks and 5 control gardens were recruited to participate in a field study, 2024-2025. A survey detailing supplementary food and water provision was conducted, combined with measurements of bird behaviour (using video cameras) and testing for viable *T. gallinae* (using culture, microscopy and PCR) contaminating food and water sources over a series of 3 visits.

Sick finches spent significantly longer at feeders and water sources, had a lower peck rate, and dropped food and water more frequently than apparently healthy finches.

Detections of viable *T. gallinae* occurred at 23% (6/26) of water-baths, 25% of pond edge samples (1/4) and 5% (4/79) of feeders (e.g. base trays) within disease gardens, indicating that both water source and feeders pose a risk of indirect transmission. Sick birds showed more aggressive interactions than healthy birds, with few observations of bill-to-bill contact that might risk direct transmission. Sick birds of a variety of finch species were observed, illustrating potential for intra and interspecific transmission.

Our study illustrates the value of targeted research that complements scanning surveillance efforts, to identify higher risk activities that can be used to focus development of disease management policy with greatest likelihood of positive impact to wildlife health. Findings will be used to improve best practice guidance for supplementary feeding (e.g. feeder type and design) and methods for water provision to garden birds.

Keywords: Trichomonosis, supplementary feeding, Chaffinch, Greenfinch

Avian cholera as a cause of mass mortality at penguin mega-colonies in Antarctica

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Knowledge on causes of wildlife mortality are essential to aid surveillance and wildlife conservation efforts. Antarctica's relative paucity of people and high wildlife densities cause wildlife mortality to be easily missed, and therefore there is lack of knowledge of such events. Avian cholera, caused by systemic infection by *Pasteurella multocida,* has been described as a cause of mass mortality in a variety of bird species and regions, including penguins in Antarctica. *P. multocida* can also be detected in oral and fecal swabs of healthy birds, suggesting birds can be carriers. The aim of our study is to describe an unusual mortality event caused by avian cholera in Antarctica.

In March 2024, a multidisciplinary expedition set out aiming to investigate the spread and impact of High Pathogenicity Avian Influenza H5N1 in Antarctica. The Danger Islands were selected as one of the sites visited, because of its exceptional abundance and diversity of seabirds, including two mega-colonies of Adélie penguins (*Pygoscelis adeliae*). We detected unusual mortality of seabirds, including thousands of Adélie penguins. Carcasses were mainly adults in good body condition, and moderately autolysed. Samples were collected for molecular detection of infectious agents (33 penguins, 11 skuas, 3 sheathbills, 1 giant petrel, 1 fur seal), in addition to tissues for histology from a subset of carcasses.

Pathological findings revealed that although influenza virus was present at low levels in some carcasses, the most likely cause of the mortality for the adult Adélie penguins was avian cholera. The diagnosis was based on the combination of *P. multocida* DNA by PCR in all samples investigated, the detection of micro-abscesses by histology in liver, and co-localization of the *P. multocida* bacteria with micro-abscesses as demonstrated via a newly developed *in situ* hybridization assay. Phylogenetic analyses of *P. multocida* sequences showed a close relation with strains previously reported in Antarctica and at Subantarctic Islands, suggesting regional dispersal and long-term persistence of this pathogen.

This study confirms avian cholera as a relevant cause of mortality in the Antarctic region and highlights the importance of considering avian cholera in setting up of surveillance schemes for mortality of wild birds and mammals in Antarctica.

Keywords: Antarctica, avian cholera, mass mortality, pasteurellosis, seabird

Funding source or Acknowledgement: The HPAI Australis Expedition was funded by the International Association of Antarctica Tour Operators (IAATO) and Ocean Expeditions. MI, AG, TMB, BBM, LL, MB, TK, LB were funded by the European Union under grant agreement 101084171 (Kappa-Flu). Views and opinions expressed are, however, those of the authors only and do not necessarily reflect those of the European Union or REA. Neither the European Union nor the granting authority can be held responsible for them.

Session 1a

Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control

Oral Presentations

How wild birds have shaped the viral dynamics of HPAI H5N1 in France, 2021–2023

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Highly Pathogenic Avian Influenza (HPAI) H5N1 clade 2.3.4.4b viruses have caused large-scale and recurrent outbreaks across the world in recent years. In France, severe epizootics highlighted that HPAI remains a major threat to both wild birds and poultry. A large range of wild bird species have been affected but their precise role in the underlying mechanisms of viral dynamics remain poorly understood, as they result from a complex interplay of viral, epidemiological, ecological and environmental factors.
To address these gaps, we conducted Bayesian phylodynamic analyses of a comprehensive dataset of HPAI H5N1 clade 2.3.4.4b sequences collected from wild birds and poultry in France between 2021 and 2023, representing the three major circulating genotypes (EA-2020-C, EA-2021-AB, and EA-2022-BB). We first used compartmental phylodynamic models to investigate viral introductions into France, and test their association with wild bird migration movements, using EURING ringing data. We then examined within-France transmission dynamics among and between wild bird groups by inferring key epidemiological parameters. We further explored viral dynamics in France by implementing phylogeographic analysis to evaluate potential environmental and ecological drivers of viral spread, including landscape and climate variables as well as species abundances.
Our results show that, across genotypes, viral introductions into France were most frequent from Central, North and Northwest Europe. Most introductions events happened during post-breeding migration and non-breeding periods, and were positively associated with migration movements of several species moving from these regions. Within France, the inferred effective reproduction numbers (Re) were higher within wild bird groups than between groups, and varied across genotypes and time periods, with *Anatidae*, *Laridae*, other waterbirds, seabirds and raptors contributing differently. Phylogeographic analysis further indicated that viral lineages preferentially circulated in wetlands areas and regions with higher occurrence of *Anatidae*, *Ardeidae* and *Laridae*.
These findings improve our understanding of HPAI H5N1 spread by linking viral dynamics to environmental and ecological factors. They provide new insights into the mechanisms shaping viral dissemination in France and in Europe and highlight key elements to refine surveillance strategies, including targeting high-risk areas and key species regarding the risk of introduction. Such measures are essential for mitigating future HPAI epizootics.

Keywords: HPAI, wild birds, France, phylodynamics

What makes bats such important reservoirs for zoonotic viruses? An explainable machine learning approach

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As zoonotic viruses emerge and spillover to human populations, monitoring biodiversity and wildlife disease is essential but extremely limited by financial, time and human resources. Machine learning approaches can mitigate some of these limitations to guide zoonotic risk assessment by predicting which species can serve as reservoirs of zoonotic viruses. Predictions returned by these models can be difficult to trust and to translate into action because they have low epistemic transparency: we know what the model predicts, but we cannot convey why. In this context, explainable machine learning (xML) is emerging as a series of methodological practices that generate more interpretable models and model outcomes, with demonstrated potential to improve adoption of these models among policymakers. Our main objectives are to interpret individual predictions given by a machine learning model to make these results more trustworthy for zoonotic risk assessment, and to contribute to a better understanding of underlying biological processes that govern host-virus interactions.

We are using ecological traits and phylogenetic relationships for 1,335 bat species to train a machine learning model to predict the zoonotic status (host or non-host) of each species for beta-coronaviruses. We then apply four well-established post-hoc xML methods to understand the model's predictions and improve its transparency: Shapley values, conformal predictions, counterfactual explanations and hybrid learning.

Our results showed that certain traits contribute similarly across all families to predicting the zoonotic status of bat species, while other traits contribute very strongly within specific families. For example, body mass is an important trait determining the status of hosts from the *Pteropodidae* family, known for containing the largest bat species. Based on conformal predictions, we classified species as sure hosts, sure non-hosts and unsure hosts which we consider as high-priority targets for empirical evaluation. We are conducting the counterfactual explanations analyses for these unsure hosts which will identity what trait would need to change for these species to be listed as sure hosts or sure non-hosts. The results are currently being analysed.

Our study highlights how traits are key factors to predict the zoonotic status of bats, and how the determining traits vary from one host to another. This suggests that different bat reservoirs are hosting viruses for very different reasons. We were also able to assess the uncertainty of our model, which is not common in machine learning practices, to list priority targets for empirical evaluation.

Keywords: Host-virus interactions, zoonoses, bat reservoirs, beta-coronaviruses, explainable machine learning

Multi-Host Dynamics of Animal Tuberculosis: Estimating R_0 across the Iberian Peninsula

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Animal tuberculosis (TB) is a multi-host disease caused by the Mycobacterium tuberculosis complex (MTBC). TB impacts public and animal health and causes revenue losses in the cattle trade, making it a priority for eradication programs in Europe. However, eradication programs have recently seen their initial success stall. Difficulties in diagnostics and the presence of diverse wild host communities are some of the obstacles faced.

In complex epidemiological scenarios, the basic reproduction number (R_0) helps quantify the role of each host in the transmission and persistence of pathogens like MTBC, thereby informing effective TB control strategies.

Here, we collected data from 17 sites located across the Iberian Peninsula to calculate the R_0 for three of the most relevant TB hosts, the wild boar, red deer and cattle. Using a Bayesian framework, we estimated several epidemiological parameters included in the R_0 equation. True prevalence (adjusted for diagnostic performance) was calculated for each site and host, using gross pathology, bacteriological culture or ELISA using P22 protein complex for wild hosts, and the single intradermal tuberculin test for cattle. Abundance was estimated for each site and host using space-to-event models of camera-trapping data. Shedding was estimated for each host by quantitative real-time PCR for MTCB in oral, nasal, and rectal swabs collected from animals with evidence of TB exposure and extrapolated across sites. Finally, uninformative distributions were used as an approximation for intra and interspecific transmission rates.

Our results showed that epidemiological dynamics vary widely across sites. In 12 of 17 sites, the wild boar was the most relevant host in terms of R_0. Additionally, it had a similar R_0 to red deer in three sites. Red deer and cattle only had the highest R_0 in one location each. In most localities (n=13), the R_0 was higher than one for at least one host species, suggesting that TB is usually not an obligatory multi-host disease in these systems. In most sites (n=10), spillovers from wild boars to other species seemed to be the most common source of inter-species transmission, which might contribute to the persistence of the pathogen in the study areas and to infections in cattle.

The epidemiology of TB is diverse, and therefore, eradication efforts should adapt to the specific conditions of the area. Overall, the wild boar is a key species for the epidemiology of TB in the Iberian Peninsula and thus should be central in control efforts.

Keywords: basic reproduction number; disease ecology; wild ungulates; livestock

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Elimination of bovine tuberculosis in wildlife as an exotic disease outbreak

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Bovine tuberculosis (bTB) is a disease that costs over £150m per annum due to infection in cattle and it is endemic in badgers in many parts of the south and west of England. Its occurrence elsewhere can be treated as an exotic disease outbreak. Here, we report on the successful control of such an outbreak in both cattle and wildlife.

Following a cluster of cases of bTB in cattle in Cumbria, northern England, Whole Genome Sequencing (WGS) indicated that the disease was originally imported from Ireland. When three badgers were submitted in 2017 that had identical bTB an adaptive management response was initiated. A systematic survey for badger setts was performed, and a Minimum Infected Area was defined that encompassed all three positive badgers' territories plus the grazing land where infected cattle were, from those cases where infection was probably due to wildlife. A buffer was defined around this area to account for uncertainty, and a cull was performed by a local company set up by the farmers. Each year the management area was redefined based on subsequent herd breakdowns and positive badgers. After two years, badger vaccination was initiated in part of the buffer, and this adaptive approach continued until 2025. No positive badgers have been found since a single PCR positive in 2021 and no confirmed cattle cases of this bTB clade since 2018, although subsequent infection in cattle due to recent importation cannot be ruled out. WGS showed that most transmission was within species, but cross-species transmission was probable in both directions.

This is the first time that responsive action has eliminated bTB in badgers in Europe. The ability to perform adaptive management and utilise various tools as required, as well as the support of local farmers has shown that bTB control in a two-species system is possible.

Keywords: badgers, cattle, disease control, TB

Funding source: This work was funded by DEFRA.
Acknowledgement: We would like to thank all the field vets, ecologists and advisors, as well as the local community for supporting the work.

25 years of wild boar disease surveillance in Sweden following the exponential growth of the population

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After being accepted as wild fauna in Sweden again in 1986 the wild boar population has grown remarkedly. Several disease introductions have occurred, highlighting the importance of wildlife disease surveillance. The Swedish surveillance program is based on voluntary reporting, subsequent necropsy and ancillary testing of submissions. Digital records of findings are stored in searchable databases. The study aim was to compile the findings in wild boars submitted through the programme to increase the understanding of disease occurrence and causes of death within freerange wild boar.
Reports for all submitted material from wild boar 2000 to 2024 were analysed. Material submitted in research projects, captive wild boar and samples from active surveillance programs were excluded. In the evaluation, cause of death and additional findings were categorised according to the registered diagnosis and through reading the necropsy reports.
998 submissions were included from the databases, including 424 samples diagnosed through targeted testing without a full necropsy. 31 animals lacked a cause of death, i.e. the material was too decayed or submission included unsuitable material. In the remaining 543 cases, gunshot/euthanasia was the most frequent cause of death, followed by cachexia, sepsis (several pathogens), and road killed. The remaining causes of death categories occurred in six or less animals. Remarkable findings with long-term effects were *Salmonella enterica* serovar Choleraesuis first diagnosed in 2020 and African swine fever in 2023. Other infections with potential transmission to domestic pigs and/or humans included *Streptococcus suis*, *Listeria monocytogenes, Yersinia enterocolitica, Actinobacillus pleuropneumoniae*, *Glaesserella parasuis, Pasteurella multocida,* porcine parvovirus and circovirus. Furthermore, old shotgun wounds were occasionally seen in peripheral tissues, commonly with secondary emaciation. Malformations were rarely seen and were considered incidental findings. Lung worm was a common finding, occasionally suggested as predisposing for suppurative pneumonia. Neurological signs rarely had a diagnosed cause if not bacterial. Interestingly, wild boar with nutritional deficiencies were noted throughout the period, possibly induced by unbalanced feeding by hunters.
The submissions to the wildlife disease surveillance program are biased towards severe disease occurrence. However, the comprehensive review of wild boar submissions highlights the risk of transmission of disease to and from domestic pigs and the zoonotic potential of wild boar as a game. Possible pathogen occurrence calls for awareness in both pig producers and hunters, as well as consumers of wild boar meat.

Keywords: wild boar, disease surveillance, endemic disease, zoonoses, wildlife livestock interface

Non-invasive genetic sampling to estimate epidemiological parameters in cryptic carnivore species: Sarcoptic mange in the Iberian Wolf

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Sarcoptic mange is a highly contagious disease caused by the burrowing mite *Sarcoptes scabiei*. It has been linked to mortality in wild canid species, with the potential to cause demographic impacts. *S. scabiei*'s DNA can be detected in the faeces of canids, presumably from overgrooming by infected animals. Some wild species pose sampling challenges due to their cryptic behaviour and/or low densities, as is the case with the Iberian wolf. Here, we apply non-invasive genetic tools to estimate epidemiological parameters of sarcoptic mange infection in two demographically contrasting Iberian wolf populations of Portugal: Alto Minho (AM), characterised by higher and more stable densities, and South of Douro (SD), a declining and fragmented population.

Molecular detection of *S. scabiei* was performed on over 1,300 faecal samples, collected between 2006 and 2025, all of which had been previously submitted to individual genetic identification. Multievent capture-recapture models, implemented within a Bayesian framework, were used to estimate epidemiological parameters, including incidence and survival of infected and non-infected individuals. Our model shows that for both wolf populations, the survival probability of non-infected individuals – 0.845 (CI_{95} 0.704-0.968) in AM and 0.855 (CI_{95} 0.648-0.980) in SD – was significantly higher than that of infected ones – 0.428 (CI_{95} 0.325-0.526) in AM and 0.559 (CI_{95} 0.433-0.676) in SD. Mean incidence was 0.387 (CI_{95} 0.139-0.667) for AM and 0.507 (CI_{95} 0.218-0.831) for SD. The estimated diagnostic test sensitivity was low – 0.175 (CI_{95} 0.130-0.240) – , which was expected, given the methodology used to detect a dermatological parasite in faecal samples.

Our findings suggest that sarcoptic mange may have a relevant effect on survival of the endangered wolf populations of Portugal. This study highlights the applications of non-invasive sampling in epidemiology, establishing it as a particularly valuable resource for disease surveillance of cryptic wildlife.

Keywords: *Canis lupus*, *Sarcoptes scabiei*, faecal samples, multievent capture-recapture model, survival.

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A ten-year European CWD anniversary – is the antler pointing down or up?

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As the USA is about to round the 60-year mark of known Chronic Wasting Disease (CWD) occurrence, Norway, and thus Europe, just ticked off 10 years after the emergence of what could be called a game changer. CWD most probably is the biggest potential threat to cervid populations in Norway in modern times. Prion diseases are not possible to prevent; they are incurable and invariably fatal. The fact that prions in the environment harbour infectivity over years complicate disease management of strains that possesses the ability to spread between live animals.

Past 2016 and the famous dying female reindeer of Nordfjella in Southern Norway, the national surveillance program have tested more than 200 000 cervids of the species reindeer (*Rangifer tarandus*), roe deer (*Capreolus capreolus*), moose (*Alces alces*) and red deer (*Cervus elaphus*). Different strains of CWD prions have been identified, and an eight-year fallowing period is about to end, with an upcoming reintroduction of reindeer to the mountain range. The fallowing being a result of the biggest culling effort, about 2500 animals, to control disease in Nordic cervids.

The talk will discuss disease understanding and management in light of the last decade of battling emergent CWD and what knowledge has been gained of the discovered European prion strains.

Keywords: CWD, prion, cervid, management, emergent

Hedgehog arterivirus-1 in European hedgehogs in England and Wales

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A novel member of the family *Arteriviridae*, hedgehog arterivirus-1 (HhAV-1) was recently identified in cases of fatal encephalitis in hedgehogs. Furthermore, the virus was shown to be the causative agent of the encephalitis by co-localisation of viral antigen with brain lesions. The present study aimed to expand our understanding of HhAV-1 in hedgehogs by assessing positivity to the virus, investigating potential transmission routes, and further characterising its genetic diversity.

Between August 2024 and October 2025, a total of 449 deceased hedgehogs were submitted to the APHA from rescue and rehabilitation centres. The recorded causes of death varied and included trauma, respiratory, gastrointestinal and neurological diseases, and unknown. We used next-generation sequencing (NGS) to characterise the genetics of HhAV-1 in positive hedgehogs and to identify potential co-infections.

Initial screening of lung tissues revealed a HhAV-1 positivity of 80%. HhAV-1 was also detected in urine, faeces and nasal swabs, but inconsistently, demonstrating potential virus transmission via urine, faeces and nasal secretions. Limited investigation of *in utero* transmission was possible through a single pregnant case in which HhAV-1 was detected in the embryos. A DEmARC-based pairwise distance analysis of 18 HhAV-1 genomes indicated that these HhAV-1 strains may represent a new species, "Xiarterivirus erinaceid," within a new genus of the subfamily *Heroarterivirinae*. Phylogenetic analysis based on HhAV-1 ORF5 sequences revealed distinct geographical clustering of viral sequences, with an overall nucleotide identity ranging from 69% to 100%. Analysis of the lung virome data identified five additional viruses: papillomavirus, paramyxovirus, parvovirus, coronavirus, and circovirus. Retrospective screening using specific qPCR assays identified co-infection with two or more viruses in most cases.

This study revealed a high positivity of HhAV-1 in hedgehogs tested across England and Wales. Analysis of more clinical specimens will be required to gain further insights into the genetic evolution of HhAV-1 and to understand its biological effects, epidemiology, and transmission dynamics. The exact clinical implications of these newly identified viruses in lung tissues remain unclear.

Keywords: Hedgehog, arterivirus, encephalitis, phylogeny, genetic diversity

Funding source or Acknowledgement Scanning Surveillance for Wildlife Diseases in England and Wales (ED1600) project. Our sincere thank you also goes to all hedgehog rescue centres and hospitals which contributed to this study.

Opportunistic transmission and selective establishment structure *Leucocytozoon* parasite diversity in passerine birds

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Host shifts have shaped the diversification of *Leucocytozoon* parasites in birds, likely driven by the generalist feeding preferences of their dipteran simuliid vectors. Yet emerging evidence suggests that *Leucocytozoon* may be more host-specific than traditionally recognized, challenging the expectation of broad host ranges under generalist transmission. We hypothesized that opportunistic transmission continuously exposes parasites to novel hosts, but selective establishment in compatible hosts filters which infections persist.

We constructed bipartite host-parasite networks at the host family level using 2,732 infection records of *Leucocytozoon* lineages in passerine birds from the MalAvi database, analyzing the Palaearctic-Afrotropical and Nearctic-Neotropical systems separately as an independent test of consistency. Singleton lineages, representing over half of lineage richness but only ~15% of infection records, were excluded to retain lineages with evidence of sustained transmission.

Networks were highly modular (Q = 0.58-0.67) and specialized (H2' = 0.68-0.75) in both systems, with parasite lineages infecting restricted, non-random, and non-overlapping subsets of host families. Paridae, Corvidae, and Turdidae consistently formed isolated, lineage-rich modules, while migratory families played connecting roles: Muscicapidae and Phylloscopidae in the Palaearctic-Afrotropical system, Tyrannidae and Troglodytidae in the Nearctic-Neotropical system. Lineages within modules were phylogenetically closer than between modules (14-17% lower mean pairwise distance; $P < 0.005$) yet were not monophyletic.

Leucocytozoon diversity in passerines appears structured by opportunistic transmission creating continuous exposes to novel hosts and selective establishment restricting persistent infections to compatible host-parasite pairings. Most variants generated through cross-species transmission fail to persist, while those that establish diversify within ecological compartments repeatedly colonized by independent lineages. The consistency of these patterns across two independent biogeographical systems suggests host specificity as a general feature of *Leucocytozoon* diversity, driven by selective filters operating after host exposure.

Keywords: cross-species transmission, host specificity, *Leucocytozoon*, network analysis, Passeriformes

Funding source: ITC Conference Grant - WIMANET COST Action CA22108

Session 1

Host-pathogen interactions & disease dynamics in wildlife, diagnostic methods and wildlife disease control

Poster Presentations

P001. Remote digital necropsy of wildlife

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The national general wildlife disease surveillance in Sweden is based at SVA in Uppsala and relies on citizen science for reporting of dead or diseased wildlife by the public, especially the hunting community. For a necropsy, the carcasses need to be shipped to SVA. Ordinary parcel postal service has a weight limit of 20 kg, so larger carcasses need more expensive transportation, as well as being time consuming. The objective of this surveillance system development is to improve the diagnostics and increase the number of examined large Swedish wildlife.
The principals of the Canadian Digital necropsy manual for cattle were used for inspiration, to be adapted for large wildlife species in Sweden. A visit to the Canadian company that runs the digital necropsy system was done to get hands on practical experience and discussions. A workshop with wildlife pathologists at SVA was done to discuss adaptation and solutions for the Swedish situation.
Experience from field work in Canada provided insight into the applicability in wildlife necropsies. The internal SVA workshop highlighted the need to use a mix of existing networks, adapt a protocol for photo documenting a field necropsy, develop the existing digital tool for reporting for wildlife mortality; rapporteravilt.sva.se, and run a pilot study by educating selected dedicated hunters to test the system. Necropsies in the field, performed by laypersons who have passed a basic course in documenting, opening and sampling carcasses, and easy online reporting to SVA to decide what samples should be shipped for further examination, are necessary steps to increase the number of diagnoses of suitable large wildlife carcasses. Collaboration with the Swedish Association for Hunting and Wildlife Management within their official task of wildlife sampling is a logical start for a practical pilot field study.

Keywords: Wildlife disease surveillance, citizen science, pathology

Funding source or Acknowledgement: Swedish Environmental Protection Agency is acknowledged for funding.

P002. Advancing non-invasive wildlife monitoring: environmental drivers and applications of eDNA in eco-epidemiology.

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The wildlife–livestock–environment interface constitutes a complex system with important implications for biodiversity and disease dynamics. Environmental nucleic acid detection (ENAD) has emerged as a non-invasive tool for monitoring pathogens, microorganisms, and host-related signals in environmental samples. However, the influence of environmental factors on ENAD performance and its relationship with animal population and health indicators remains insufficiently understood.

Here, we present the main findings from two complementary studies applying ENAD to environmental surfaces across different geographic contexts. At broader spatial scales, our results demonstrate that climatic and habitat characteristics are key drivers of ENAD outcomes. Environmental conditions influence the detection, diversity, and richness of pathogen-related molecular markers, with higher marker diversity observed in northern latitudes. These findings highlight the importance of accounting for environmental heterogeneity when interpreting ENAD data.

At a more localized scale, ENAD signals showed variable associations with wildlife population and health indicators depending on the methodological approach. The environmental detection of the IS*6110* marker was significantly associated with tuberculosis seroprevalence in wild boar when sampling was conducted on random surfaces, underscoring the relevance of sampling design in eco-epidemiological inference. Additionally, the detection of *Enterococcus* spp. DNA was positively associated with animal presence signs, supporting its potential use as an indirect indicator of wildlife activity.

Overall, these results highlight the value of ENAD as a non-invasive tool within integrated wildlife monitoring frameworks, while emphasizing the need to consider environmental drivers and methodological strategies to improve its application and interpretation. Further research is required to validate and standardize ENAD approaches across diverse ecological and epidemiological contexts.

Keywords: environmental DNA, One Health, wild boar, *Mycobacterium tuberculosis* complex, natural ecosystems.

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P003. Altitudinal patterns of tick–host–pathogen interactions in a mountain ecosystem: insights from the PyrTick project

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Tick-borne diseases are an increasing public health concern, yet integrated data on tick ecology, host associations, and pathogen circulation remain limited, especially in mountain ecosystems such as the Pyrenees. The PyrTick project aims to address this gap through a multidisciplinary approach combining vector, host, and pathogen data across altitudinal gradients.

May 2024 to March 2026, standardized vegetation dragging was conducted monthly along altitudinal gradients (600–1600 m a.s.l.) in 21 sampling points in four valleys in the central Pyrenees (Aragón, Spain). Host active sampling included small mammals (n=152), lizards (n=137), and birds (n=21). Ungulates (n=71) were sampled passively. Ticks were morphologically identified, and selected samples were screened for pathogens using PCR methods.

A total of 5,128 questing ticks were collected, the majority of which were *Ixodes ricinus*. The remaining ticks belonged to seven additional species, including *Dermacentor marginatus*, *Haemaphysalis punctata*, *H. inermis*, *Ixodes acuminatus*, *Ixodes frontalis*, *Rhipicephalus sanguineus* s.s., and *Hyalomma* spp. Tick activity peaked at intermediate elevations (1000–1400 m), with the highest abundance at 1400 m. Seasonal dynamics of *I. ricinus* showed a spring peak in all life stages, with nymphs peaking in May and larvae and adults in May–June. Tick prevalence reached 75% in small mammals, 95% in lizards, and 24% in birds. The majority of ticks were identified as *I. ricinus*. Immature stages, mainly larvae, predominated in small mammals, lizards, and birds, whereas adults parasitized ungulates. Pathogen screening is currently ongoing, and initial analyses of ticks collected from lizards identified *Rickettisa helvetica*, *R. monacensis* and *Babesia divergens/capreoli*-like.

These results highlight the dominant role of *I. ricinus* and a clear altitudinal and seasonal pattern of tick activity in the Pyrenees. High infestation levels across multiple host taxa underscore the key role of local host communities in driving tick–host–pathogen dynamics. By integrating vector, host, and pathogen data along a shared altitudinal gradient, PyrTick provides a relevant framework for understanding and anticipating tick-borne disease risk in mountain ecosystems.

Keywords: disease ecology, mountain ecosystems, tick-borne diseases.

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P004. When Parasites Shape Predators: Investigating *Toxoplasma gondii* infections in free-ranging Wolves

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Numerous pathogens are known to manipulate host behaviour to enhance their own transmission or survival. Classic examples include the fungus *Ophiocordyceps unilateralis* or the trematode *Dicrocoelium dendriticum*, both of which alter ant behaviour to their advantage. The protozoan parasite *Toxoplasma gondii* represents another well-documented manipulator, inducing increased risk-taking and a loss of fear of felids in infected rodents. In contrast, the effects of *T. gondii* on carnivorous species remain poorly understood. Existing evidence is limited to a few studies, including observations of hyena cubs displaying unusually bold – and often fatal – behaviour toward lions, and wolves from the Greater Yellowstone Ecosystem making high-risk decisions when infected with *T. gondii*. The aim of our work was to determine *T. gondii* seroprevalence in gray wolves in Switzerland and elaborate on the potential implications an infection might have on a highly social species such as the wolf, taking into account different types of demographical, social and ecological characteristics.
In Switzerland, long-term wolf (*Canis lupus*) health monitoring provides an opportunity to investigate the prevalence and potential risk factors for *T. gondii* infection. We conducted a serological survey complemented by PCR testing of tissue samples. We then fitted a generalized linear model with *T. gondii* serostatus as response variable and sex, health status, body condition score, altitude, lynx density and risk behaviour, as explanatory variables.
The estimated seroprevalence was 36.8% (35/95), while no samples tested positive by PCR. Health status (disease), local lynx density and risk-taking behavioural traits such as leading a pack, dispersing, predation amongst others were significantly associated with *T. gondii* seropositivity.
These findings align with results from the wolves in the Yellowstone Ecosystem. They also suggested interactions between wolves and concurrent free-ranging felids, which might go far beyond the classical concurrence among large carnivores. This opens a broad field for future research, which should include behavioural studies of live individuals, ideally combined with clinical monitoring.

Keywords: *Canis lupus*, protozoa, toxoplasmosis, behaviour

P005. Retrospective analysis of possible associations between Pneumocystis spp. and five viral pathogens in three wild carnivore species

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Fungi of the genus Pneumocystis colonizes the respiratory tract of numerous mammalian hosts, with their proliferation frequently associated with compromised or altered immune function of the host. Although disease severity is typically associated with underlying immunosuppression primarily in humans, the epidemiological relevance of subclinical infection in wildlife species remains poorly defined. Viral pathogens capable of modulating host immunity have been proposed as potential triggers to Pneumocystis proliferation, yet evidence from natural populations is still limited.
This study investigated the occurrence of Pneumocystis spp. and its possible association with selected viruses in wild carnivores from Serbia. A total of 108 clinically healthy animals, including golden jackals ***(****Canis aureus****)***, Eurasian badgers ***(****Meles meles****)***, and red foxes ***(****Vulpes vulpes****)***, were collected from Veliko Gradište, Stara Pazova, and Ugrinovci during the 2022/2023 hunting season. Conventional PCR and real-time PCR were used for the detection of Pneumocystis spp., canine parvovirus type 2 (CPV-2), suid alphaherpesvirus 1/pseudorabies virus (PRV), canine distemper virus (CDV), canine coronavirus (CCoV), and canine herpesvirus (CHV) from lung samples.
Overall, *Pneumocystis spp*. was detected in 40.7% of examined animals (20/60 golden jackals, 4/9 Eurasian badgers, and 20/39 red foxes). Among the investigated viruses, CPV-2 was identified in three golden jackals (5.0% of tested golden jackals; 2.8% of all animals), while PRV was detected in two golden jackals (3.3% of tested golden jackals) and three red foxes (7.7% of tested red foxes; 4.6% overall). Co-detection of Pneumocystis spp. and PRV was observed in one golden jackal and two red foxes, whereas Pneumocystis spp. was not detected in CPV-2-positive individuals. All samples tested negative for CDV, CcoV and CHV. No statistically significant differences were observed in pathogen distribution across host species, sex, age categories, or sampling locations. Semi quantitative results showed mean threshold cycle (Ct) values of 33.6 for Pneumocystis spp., 24.0 for CPV-2, and 31.3 for PRV. Despite relatively high viral loads in co-infected animals, the fungal burden remained low and consistent with subclinical infection.
These findings do not indicate a major role of the investigated viral pathogens in promoting clinically apparent Pneumocystis infections in the studied wildlife populations. Nevertheless, considering the low prevalence of viral infections and the absence of histopathological confirmation, subtle immune-modulatory effects cannot be excluded. Further integrative studies are required to better understand host-pathogen interactions and the ecological drivers of Pneumocystis dynamics in wild carnivores.

Keywords: *Pneumocystis sp*., golden jackals, badgers, red foxes, Serbia

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P006. Using dogs as a model to identify alternative matrices for canine distemper serology in wildlife surveillance

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Canine distemper virus (CDV) is a major pathogen of domestic dogs and many wild carnivores, with substantial implications for wildlife health and conservation. Serology is a valuable tool to document past exposure, but it usually relies on serum, which is often unavailable in wildlife investigations where carcasses are the main source of material. Before considering alternative matrices in wild species, they should first be evaluated in a biologically relevant model such as dogs for which the commercial kits are designed. We therefore compared CDV serological signals obtained from serum and several alternative matrices collected from dogs, with the aim of identifying matrices that could later be used for wildlife surveillance.

This ongoing study was conducted at the Ecole Nationale Véterinaire de Toulouse. Samples were collected from dogs admitted to the hospital for clinical care and subsequently necropsied. For each dog, serum/plasma, cerebrospinal fluid, urine, serohaemorrhagic effusions, heart-clot fluid, and homogenates from lung, spleen and quadriceps muscle were collected when available and stored frozen. CDV antibodies were screened using a commercial ELISA kit. Statistical analyses comparing matrices and assessing agreement with serum are ongoing.

Preliminary ELISA results show that several non-serum matrices yield measurable CDV antibody signals. Serohaemorrhagic effusions produced the strongest reactivity overall, while lung homogenates and cerebrospinal fluid also generated consistent signals in a substantial proportion of dogs. Urine showed detectable but more variable reactivity. By contrast, muscle homogenates and heart-clot fluids yielded low signals in this preliminary panel. Statistical analyses are in progress to determine which matrices best reflect serum results and to define their diagnostic interest.

These preliminary findings support the feasibility of CDV serological screening from alternative post-mortem matrices. Using the dog as a model is a key strength of this approach, because it allows matrix comparison in the species for which the assay was designed before extrapolating to wild carnivores. This work may help develop practical serological tools for wildlife surveillance when serum is unavailable and only carcass-derived material can be collected.

Keywords: canine distemper virus; serology; alternative matrices; wildlife surveillance; dog model; post-mortem samples

Acknowledgement: Ceva Wildlife Research Fund for its support

P007. Detection of a canine coronavirus in British red foxes (*Vulpes vulpes*)

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Great Britain (GB) has an estimated population of 430,000 red foxes (*Vulpes vulpes*), with an estimated 150,000 of them living in urban environments and cities. Whilst red foxes are predominantly solitary animals and rely on scavenging and hunting small prey, studies have shown that domestic dog DNA from faeces can make up a large part of a fox's diet.
Dogs have known coronaviruses that are transmitted via the faecal-oral route, and coronaviruses have been reported in red foxes internationally. To determine if canine or vulpes coronaviruses are present in GB red foxes, samples were collected from 2021 to 2025 from across England, Scotland and Wales, with 1700 samples taken. The sample types consisted of oronasal and rectal swabs, tissue samples and faecal samples.
RNA was extracted from the samples and screened for coronaviruses using pan-coronavirus PCR primers. PCR-positive samples were then sent for sanger sequencing, followed by Illumina sequencing. PCR positive results have been found in four red foxes across GB in rectal swabs, three of which were in adult male foxes. Further sequencing was conducted on one of the samples, and downstream bioinformatic pipelines identified the sequence as a coronavirus related to other canine coronaviruses circulating in GB found in domestic dogs.
Great Britain's red foxes play an important role in both wild and urban habitats. This canine coronavirus is likely transmitted via coprophagia, specifically through red foxes ingesting infected domestic dog faeces. Determining the presence of coronaviruses within wild foxes and domesticated dogs is critical to our preparedness for the emergence and detection of novel and known viruses in and between animals.

Keywords: Coronavirus, Surveillance, Bioinformatics, Red Foxes, Great Britain

Funding source or Acknowledgement: This work could not have been conducted without the collection of samples from wildlife charity hospitals, the APHA and the students and staff at the University of Nottingham Veterinary Pathology Service, Sutton Bonington, UK.

P008. Selected emerging parasitic diseases in expanding Serbian populations of golden jackal *Canis aureus* and grey wolf *Canis lupus*

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This study concerned selected parasitic pathogens of the golden jackal and the grey wolf in Serbia; *Dirofilaria immitis, Toxoplasma gondii* and *Neospora caninum* in the jackal, and *D. immitis* and *Hepatozoon canis* in the wolf. Spatial, temporal and host parameters were assessed for each, to detect any significant association between them and the diseases. In Serbia, this is the first time embryogenic dynamics are assessed in *D. immits* in the jackal. The aim was to determine what role these species play in these diseases' dynamics, in what measure they are affected, and in the instance of *D. immitis*, whether the jackal may be a reservoir species.
847 golden jackal carcasses were examined for heartworm, the parasites measured and embryogenic dynamics analysed to determine female nematode fertility. 96 jackal muscle tissue samples were subjected to PCR assay for *T. gondii* and *N. caninum*. 150 grey wolf spleen samples were subject to PCR for *H. canis* and hearts examined for heartworm. Data on municipality, year, season, sex and host age were gathered. Fisher's test was performed in RStudio and spatial distributions mapped in QGIS.
Prevalences in the jackal were: 7.56% (5.78-9.34%) for *D. immitis*; 16.67% (9.21-24.12%) for *T. gondii*; 0.00% for *N. caninum*; in the wolf: 1.33% (0.00-17.23%) for *D. immitis*; 26.47% (15.98-36.96%) for *H. canis*. Embryogenic dynamics in *D. immitis* in the jackal showed 15.15% (7.98-22.32%) fertile females and mean intensity 3.45 (SD 0.00-9.04). The statistically significant variables were municipality, year, season, sex and age class for *D. immitis* in the jackal; the year for *T. gondii*; none for *D. immitis* in the wolf; municipality for *H. canis* in the wolf.
For *D. immitis* in the jackal, prevalence was consistent with adjacent countries; evidence is insufficient to call it a reservoir, but high prevalence and other factors warrant further research. In *T. gondii*, prevalence was high as in the only other study in the area, suggesting a possible reservoir role that needs further confirmation. The low prevalence of *N. caninum* was consistent with reports in other species despite high numbers in cattle. As in other studies, prevalence of *D. immitis* in the wolf was low, but the high worm burden (23; SD 17.34-28.65) was noteworthy. The high prevalence of *H. canis* points to the important circulation of this parasite in the area.

Keywords: *Dirofilaria immitis, Toxoplasma gondii, Hepatozoon canis*, golden jackal, grey wolf

P009. Detection and genotyping of tapeworm eggs in faecal samples of grey wolf (*Canis lupus*) in the Czech Republic

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The population of the grey wolf (*Canis lupus*) in Europe has increased significantly in recent years. The Czech Republic represents a crossroads of different wolf populations, and wolf migration and recolonization may facilitate the spread of wolf-associated parasitic fauna, including zoonotic species. This study aims to assess the diversity and species composition of tapeworms in free-ranging wolves using genotyping in combination with sieving and molecular methods, and to determine frequency of their occurrence.
A total of 357 faecal samples from grey wolves from the Šumava National Park were analyzed. Of these, 65 were genetically confirmed as wolf scats, while 292 were identified based on morphology, size, and composition. Samples were examined using a sieving method (with mesh sizes of 105, 38, 21 µm), with taeniid eggs retained on the 21 µm mesh and detected microscopically. DNA was isolated using a modified DNeasy Blood & Tissue Kit protocol, and a fragment of the mitochondrial NADH dehydrogenase subunit 1 (NAD1) gene was amplified, Sanger sequenced and compared with sequences in GenBank using BLAST.
The sensitivity of the sieving technique (21.3%) was slightly higher compared to PCR (19.9%). Overall, tapeworms were detected in 19.3% of samples by genotyping, increasing to 19.9% when passaged tapeworms (from prey) were included. Eight species from six genera were identified, with *Taenia krabbei* and *Taenia hydatigena* being the most common. Less frequent species included *Echinococcus multilocularis* and *Mesocestoides litteratus*, while *Taenia lynciscapreoli*, *Hydatigera kamiyai*, and the passaged species *Eurotaenia* sp. and *Raillietina* sp. were rare. Coinfections occurred in 0.8% of samples. Among the 65 genetically confirmed wolf scats, 18 were positive, showing a similar tapeworm distribution. For genotyped tapeworms with wolves as definitive hosts, the occurrence frequency was 19.33%, increasing to 27.69% in PCR-positive samples genetically confirmed as wolf scats.
The sieving method combined with molecular-genetic analysis appears to be a suitable non-invasive approach for identifying tapeworm species. Based on this study, wolves in the Šumava region host several tapeworm species, including *Taenia krabbei*, *Taenia hydatigena*, *Mesocestoides litteratus*, and *Echinococcus multilocularis*, the latter being a zoonotic species of significant public health concern. *Eurotaenia* sp. and *Raillietina* sp. were interpreted as passaged from prey. Notably, *Hydatigera kamiyai* (typically associated with felids) and *Taenia lynciscapreoli* were also detected.

Keywords: *Taenia krabbei*, *Taenia hydatigena*, *Echinococcus multilocularis*, sieving method, wildlife parasitology

Funding source or Acknowledgement: This work was funded by the IGA VETUNI 103/2023/FVL.

P010. Whole genome sequencing of recent parvovirus from domestic and wild animals in central Italy

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Carnivore protoparvovirus 1 (CPPV-1) belongs to the *Parvoviridae* family, which includes highly adaptable pathogens circulating in both domestic and wild carnivores. The capsid protein VP2 influences the host range and antigenic variability. Within this family, two main groups are recognized: Feline Panleukopenia Virus (FPV) and Canine Parvovirus (CPV). The circulation of these viruses at the domestic–wildlife interface contributes to their persistence, although the genetic diversity of wildlife strains remains poorly understood. The aim of this study is to determine the molecular characteristics of CPPV-1 strains detected in wild carnivores and to compare them with strains identified in domestic animals in central Italy.

A total of 618 samples collected through passive surveillance in Umbria and Marche regions between 2023 and early 2024 were screened for CPV using a targeted PCR approach. Positive samples were further analyzed by whole-genome sequencing using next-generation sequencing (NGS). Phylogenetic analyses were performed to investigate viral diversity and evolutionary relationships among wildlife and domestic strains.

Among wildlife (n = 173), positive samples were detected in wolves (24/47), foxes (15/73), badgers (6/51), and in one golden jackal and one polecat. Domestic animals included dogs (52/102 positive) and cats (171/343 positive). Complete genome sequences were obtained from 15 samples (cats, n = 11; wolves, n = 3; fox, n = 1). After phylogenetic analysis wolf strains were classified as CPV-2a (n = 2) and CPV-2b (n = 1). CPV-2a strains clustered with variants circulating internationally between 2016 and 2021, whereas CPV-2b grouped with previously described Italian strains. The fox-derived FPV strain clustered with those from domestic cats.

This study provides the first molecular evidence of CPPV-1 circulation in wildlife in central Italy, revealing close genetic relationships with domestic strains. The observed phylogenetic clustering supports the occurrence of interspecies transmission, highlighting wildlife as a potential reservoir for viral maintenance and spread. These findings underscore the importance of integrated surveillance within a One Health framework to better understand viral dynamics and support effective control measures.

Keywords: *Carnivore protoparvovirus 1,* Feline Panleukopenia Virus, Canine Parvovirus, wildlife, domestic–wildlife interface, One Health

P011. Dynamics of canine distemper virus circulation in wildlife in Central Italy

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Canine distemper virus (CDV) is a contagious, multi-host pathogen, threatening wildlife, especially endangered species. CDV has been widely reported in wild carnivores across Italy, particularly in northern and central regions. In 2013, an Arctic-lineage CDV outbreak affected dogs, Apennine wolves, and other wild carnivores in the Central Apennines (Abruzzo). In 2016, a European-wildlife CDV strain was detected in a fox in the same area, indicating co-circulation.
Surveillance activities for CDV were activated and between 2013 and 2023 all wild carnivores found dead in Abruzzo and Molise regions have been submitted for diagnostic testing. A total number 1,360 wild carnivores underwent pathological and histological examinations when carcasses were available, whereas diagnostic testing was performed on swab or blood samples collected from live animals. All specimens were tested by real time RT-PCR specific for CDV and samples with the lowest Ct values were selected for whole genome sequencing (WGS), using the combination of SISPA protocol and Illumina DNA Prep kit and then sequenced on a NextSeq1000. Consensus sequences were produced by mapping analysis by iVar 1.3 tool performed within GENPAT platform (https://genpat.izs.it/).
Overall, 137 samples turned out positive. Two peaks of cases occurred in 2013 and 2021–2022, with sporadic reports in other years; the same areas were affected, but the extent of the outbreak expanded. Species involved were Foxes (73/541), Wolves (42/461), Marsican brown bears (2/46), Badgers (18/234), Beech marten (1/34) and Polecat (1/9). Only 28% of animals showing anatomical or histological lesions tested positive for CDV by PCR, likely due to post-mortem decomposition, low viral load, and/or viral RNA degradation. Complete or nearly complete CDV consensus sequences were obtained from 83 samples. Molecular characterization and phylogenetic analysis are ongoing.
Health monitoring of found dead wild carnivores provides a useful tool to track disease dynamics. Data suggest endemic circulation in the wild, posing risks to susceptible endangered species and continuous spillover/spillback to livestock guardian dogs, for which vaccination remains the key preventive measure.

Keywords: canine distemper virus, wildlife

P012. Results from the first years of the Carnivore Diseases Monitoring Program in Navarre (Northern Spain)

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Wild carnivores, closely related to domestic dogs and cats, share various pathogens and parasites, some of which threaten their conservation while, for others, act as reservoirs. Here, we present the initial findings of a monitoring program launched by the Regional Government of Navarre (Northern Spain), which focuses on the collection and analysis of road-killed carcasses from both protected and invasive carnivore species.

Since 2020, 415 carcasses from 11 species within the Mustelidae, Viverridae, Canidae and Felidae families have been recovered and necropsied. A wide range of samples, including thoracic exudate, ectoparasites, and major organs are routinely collected.

Serological screening detected antibodies against *Leishmania* and *Dirofilaria* in 3 and 9 out of 171 animals, respectively, and against FeLV and FIV in 9 and 0 out of 55 European wildcats. Molecular analyses identified Carnivore protoparvovirus 1 in 2 of 171 individuals, specifically FPV in a badger and CPV-2 (Asian lineage) in a wildcat. Amdoparvoviruses were detected in 6 of 171 animals, including four distinct viral strains, one of which represents a novel species found in a stone marten. *Cytauxzoon europaeus, Hepatozoon felis,* and *Babesia vulpes* were detected in 41, 29, and 1 out of 63 wildcats, respectively. *Trypanosoma pestanai* was confirmed in 9 out of 44 Eurasian badgers. Cardio-respiratory nematodes, identified by morphological and molecular methods in wildcats, genets and mustelids, included *Angiostrongylus chabaudi*, *A. daskalovi, Oslerus rostratus, Troglostrongylus brevior, Crenosoma* sp., *Aelurostrongylus abstrusus,* and *Eucoleus aerophilus*. Ticks identified included *Rhipicephalus sanguineus* s.l., *Ixodes hexagonus, I. ricinus, I. ventalloi, and Dermacentor reticulatus*.

Several new records for the Iberian Peninsula and new host-parasite associations were revealed. Other pathogens, such as Distemper and FeLV/enFeLV, are under study. These findings highlight the value of this monitoring program in detecting new or previously unreported pathogens and parasites.

Keywords: Carnivora, epidemiology, passive surveillance.

Funding source or Acknowledgement: This work was supported by Gobierno de Aragón [Grant no. A16_23R].

P013. Surveillance of parvoviruses and canine circovirus in fecal samples of free-ranging carnivores

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Free-ranging carnivores play an important role in the ecology and transmission of infectious diseases, including viruses with potential impact on wildlife, domestic animals, and public health. Non-invasive sampling such as fecal collection represents an effective tool for monitoring pathogen circulation in wildlife populations. The aim of this study was to investigate the occurrence of *Bocaparvovirus carnivoran1*, *Protoparvovirus carnivoran1* and *Circovirus canine* in fecal samples of free-ranging carnivores in the Czech Republic.

Approximately 400 fecal samples were collected from free-ranging carnivores, including wolves (*Canis lupus*), red foxes (*Vulpes vulpes*), and Eurasian lynx (*Lynx lynx*). The sampling area covered primarily the Czech Republic, with additional material obtained from border regions with Slovakia and Poland. Specimens were collected within ongoing monitoring programs of large carnivores and stored in sampling tubes for further processing.

Each sample was subsequently subsampled for virological analyses, while genetic analyses were performed separately. All specimens were screened using quantitative PCR (qPCR) assays targeting *Bocaparvovirus carnivoran1*, *Protoparvovirus carnivoran1,* and *Circovirus canine*. Molecular characterization of qPCR-positive samples is currently ongoing.

Preliminary results indicate a low prevalence of the viruses investigated in the sampled carnivore populations. Viral DNA was detected in a small proportion of samples using qPCR. Further analyses will focus on molecular characterization of positive cases and their genetic context within free-ranging and pet carnivores.

This study demonstrates the feasibility of non-invasive surveillance of viral pathogens in free-ranging carnivores. Although viral prevalence in fecal samples appears to be low, continued monitoring is essential to understand the circulation of pathogens in wild animal populations and the potential risk of transmission between domestic and wild animals.

Keywords: carnivores, fecal samples, parvoviruses, circovirus

P014. Breaking the cycle: Eliminating urban *Echinococcus multilocularis* in Uppsala, Sweden

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Echinococcus multilocularis, the etiological agent of alveolar echinococcosis, is established in Central and Eastern Europe and continues to expand geographically, particularly northward and westward. Surveillance in Sweden has identified three distinct areas with established infection over time: Uddevalla and Gnesta (detected in 2011), and more recently Uppsala (2025). Targeted surveillance in 2025 showed that positive fox fecal samples in Uppsala were confined to a small urban area of approximately 3 × 2 km. This limited spatial distribution presents a unique opportunity for local elimination of the parasite through targeted deworming of red foxes, the definitive host. Testing intervention in Uppsala—the smallest of the affected areas—allows for systematic evaluation and refinement of the deworming methodology under Swedish conditions. The aim is to break the transmission cycle between red foxes and small rodents (intermediate hosts), with the objective of eliminating *E. multilocularis* from the Uppsala area and thereby removing the associated zoonotic risk. Deworming will be conducted using ready to use praziquantel baits. Manual, spatially targeted bait distribution, informed by red fox ecology and movement patterns, enables efficient deployment within the confined urban area while minimizing labor and operational costs. Surveillance of parasite presence will be performed through PCR analysis of fox fecal samples collected throughout the intervention period. Activities will be to: acquire permits, equipment, pharmaceuticals, personnel and baseline data; communicate with researchers, landowners, the public, relevant organizations, human and veterinary health sectors; develop staff training and standardized operational protocols; document bait uptake, efficacy and logistical performance; and finally, to evaluate feasibility and effectiveness of the intervention strategy.
Persistence is essential. The project will commence in 2026; however, multiyear deworming is required to disrupt the parasite's transmission cycle. Continued baiting during 2027–2028 is anticipated, potentially with extended intervals between bait distributions as the parasite pressure declines to reduce labor requirements. The primary objective is to protect public health. Successful elimination of *E. multilocularis* from Uppsala would remove the local zoonotic risk and reduce public concern among residents and recreational users of the area.

Keywords: eradication, parasite, surveillance, wildlife, zoonosis

Funding source or Acknowledgement: The Swedish Board of Agriculture is funding the project.

P015. Ancylostomatidae in carnivores from Romania: new host associations, haplotype diversity and presence of *Ancylostoma caninum*

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Hookworms (Ancylostomatidae) are important parasites of domestic animals and humans worldwide, with some species having zoonotic potential. Although hookworm infections are frequently reported in Europe, molecular data remain limited. This study investigated the diversity, prevalence, and distribution of hookworms in domestic and wild carnivores from Romania using morphological and molecular methods.

Between 2011 and 2025, 319 wild carnivores belonging to six species were examined: gray wolves (*Canis lupus*), golden jackals (*Canis aureus*), red foxes (*Vulpes vulpes*), raccoon dogs (*Nyctereutes procyonoides*), European wildcats (*Felis silvestris*), and Eurasian lynxes (*Lynx lynx*). Animals were collected as roadkills or legally hunted specimens. Hookworms recovered during necropsy were morphologically identified and analyzed by PCR targeting the ITS-2 region, followed by sequencing. In domestic carnivores, coproscopically positive samples were confirmed molecularly.

The overall prevalence of hookworms in wild carnivores was 14.1%. Infections were detected in wolves (17.4%), golden jackals (16.8%), European wildcats (15.7%), red foxes (5.1%), raccoon dogs (100%), and lynxes (12.5%). Three species were identified: *Uncinaria stenocephala*, *Ancylostoma caninum*, and *A. tubaeforme*. Molecular analyses revealed 14 unique sequences, including nine haplotypes of *U. stenocephala*, three of *A. caninum*, and two of *A. tubaeforme*. Additionally, *A. caninum* and *U. stenocephala* were confirmed in domestic dogs from Romania.

This study provides the first comprehensive molecular assessment of hookworm diversity in Romanian wild carnivores and the first molecular evidence of *A. caninum* in domestic dogs from Romania, highlighting the role of wild carnivores as reservoirs of infection.

Keywords: hookworms, carnivores, *Ancylostoma*, *Uncinaria*

P016. An ELISpot-based methodology for characterizing IFN-γ responses to *Mycobacterium bovis* in European badgers (*Meles meles*)

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Tuberculosis (TB), caused by *Mycobacterium bovis (M. bovis),* remains a major issue for the cattle husbandry industry in France and in particular in the south-west despite the implementation of extensive control measures in both livestock and wildlife. Among the latter badgers (*Meles meles*) occasionally act as maintenance hosts and spill the infection back to cattle. Badger vaccination is a promising strategy to reduce TB prevalence in badgers and thereby in cattle. TB infection is currently assessed in badgers by direct detection of *M. bovis* in tissues from animals culled for surveillance (under national programme Sylvatub) around infected farms or found dead (road-killed animals). Alternative immunological tests would allow a larger proportion of Sylvatub badgers to be tested. This would provide a more accurate picture of TB prevalence and support the targeted deployment of vaccination. In TB infected or vaccinated rodents, splenic monocytes (SM) can respond to mycobacterial antigens similarly to peripheral blood mononuclear cells (PBMCs). In badgers, fresh spleen samples can be collected at post-mortem more widely through Sylvatub than fresh heparinised blood (for PBMCs isolation) which requires animal anaesthesia. This proof of principle study aimed to measure badger specific interferon-gamma (IFN-γ) responses in stimulated SM and PBMCs, by ELISpot assay, a sensitive method for detecting this cytokine. The tested hypothesis was that badger stimulated SM can produce IFN-γ at similar levels to PBMCs and ELISpot IFN-γ with SM to be proposed as a potential diagnostic test on dead animals.
Heparinised blood was collected from 26 live anaesthetised badger (under badger vaccination study in Dordogne and Sylvatub). Within 1-4 hours following euthanasia, spleens were removed at post-mortem. PBMCs/SM were extracted and stimulated for 16h with mycobacterial antigens. IFN-γ responses were measured using ELISpot assay (Spot Forming Units (SFU) and Relative Spot Volume (RSV)), removing background from antigenic responses. *M. bovis* presence in tissues was tested by PCR and culture for all animals.
In this study (20 PCR negative and 6 PCR positive badgers), IFN-γ responses measured by ELISpot in TB infected badgers can be similar by stimulated splenocytes and PBMCs in the same TB confirmed badgers. The higher background responses were occasionally produced by SM than by PBMCs were included in the analysis.
Final cut-off points for ELISpot PBMCs and SM will be calculated following access to more field PCR-confirmed TB positive and negative samples. ELISpot IFN- γ in SM is a promising alternative to blood-based diagnostic tests for TB surveillance in targeted infected sites.

Keywords: *Mycobacterium bovis*, European badger, splenocytes, wildlife tuberculosis, ELISpot

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017. Culling-induced changes to individual movement behaviour in an intensively studied badger (*Meles meles*) population.

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In the UK, European badgers (*Meles meles*) have been culled with the aim of reducing badger-to-cattle transmission of bovine tuberculosis (bTB). However, questions persist about the efficacy of this approach since culling-induced perturbation of badgers is hypothesised to drive increased prevalence of bTB in badgers and higher incidence in adjacent cattle herds, likely due to an increase in badger movement following culls.
We investigated the short-term impacts of industry-led culling (2018-2021) on movements in a badger population in the high-risk area for bTB in the UK. As part of the study, 87 adult badgers were fitted with GPS collars, generating over 40,000 locational fixes. As predicted, badgers increased their ranging behaviour following culling but in contrast to previous research, such changes did not occur immediately. Instead, perturbation effects were only observed in 2021, after four years of successive culls. Analysis of estimated marginal means revealed that badgers travelled further from their setts, covered larger distances nightly and travelled further between GPS fixes post-culling in 2021, equivalent to an increase in movement behaviour of 44-70%. We show that industry-led culls can induce changes in badger movement patterns, supporting the social perturbation hypothesis. Such behavioural changes among surviving badgers had the potential to increase bTB transmission amongst badgers and between badgers and cattle. Our study therefore highlights the need for considered management decisions for controlling bTB, as culling may take multiple years to generate a perturbation effect but once a tipping point is reached, the effects may be induced rapidly and strongly.

Keywords: bovine tuberculosis, cull, movement behaviour, perturbation, wildlife disease management

P018. Fenbendazole treatment for gastrointestinal nematodes in captive bison (*Bison bonasus*) in Slovakia

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Parasitic diseases can cause serious health problems and play a crucial role in the preservation and restoration of the European bison (*Bison bonasus*). Traditionally, broad-spectrum benzimidazole anthelmintics are widely used to control parasitic infections in wild and domesticated ruminants in veterinary medicine.
The aim of this study was to determine the parasitic status of captive European bison (*Bison bonasus*) kept in Topoľčianky Bison Park, Slovakia, to identify the species/genera of gastrointestinal (GI) nematodes based on the morphological characteristics of infective third-stage larvae (L3), and to evaluate the efficacy of anthelmintic therapy.
Twenty-three bisons were used for the study. The McMaster coprological method was used to examine bison for GI parasite infection. Ten bison with the highest level of GI parasitic infection were treated with fenbendazole (Helmigal 50mg/ml oral suspension, PharmaGal, Slovak Republic) *per os* at a dose of 7.5 mg/kg body weight. The efficacy of fenbendazole was evaluated using the *in vivo* faecal egg count reduction test (FECRT) at 10 days after therapy.
Prior to treatment, the parasite fauna of the captive bison population showed that lung nematode *Dictyocaulus viviparus* had the highest prevalence (60.90%), followed by GI nematodes of the family Trichostrongylidae (56.50%), *Trichuris* spp. (47.89%), *Nematodirus* spp. (39.19%), and *Toxocara* spp. (17.40%). Eggs of the liver fluke *Fasciola hepatica* were not detected. Morphological identification of GI nematode L3 revealed that before therapy, *Haemonchus contortus* had the highest prevalence (51%), followed by *Ostertagia* spp. (35%) and *Cooperia* spp. (14%). After fenbendazole treatment, only *H. contortus* L3 larvae were detected. The FECRT showed a 90.5% [95% CI: 85.50; 94.10] reduction in strongylid faecal egg counts. Therefore, our data indicated doubtful efficacy of fenbendazole therapy (FECRT < 95%, 95% CI < 90%) for GI nematodes in the captive bison herd.
Fenbendazole showed reduced efficacy against the GI nematode *H. contortus*. Regular parasitological monitoring and appropriate management strategies are, therefore, necessary to control parasitic infections in captive European bison populations.

Keywords: bison, parasites, EPG, fenbendazole treatment, Slovakia

Acknowledgement: The study was supported by the Grant Agency VEGA, Grant No. 2/0028/26.

P019. First detection of Small Ruminant Lentivirus in a roe deer (*Capreolus capreolus) in Italy*

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Small ruminant lentiviruses (SRLVs) infect sheep and goats worldwide and represent one of the most insidious viral infections affecting these species. SRLVs antibodies were detected in several wild ruminants in the United States and Europe, while molecular detection has been described only in French ibexes and in red deer in Poland. These findings may suggest a potential role of wild ruminants in the epidemiology of SRLVs. In Italy, a passive surveillance study was conducted from 2023 to 2025 in wild ruminants to investigate the occurrence and circulation of SRLVs.
The monitoring program was based on the analysis of carcasses originated from road-killed animals and individuals that died in wildlife rescue centers in two central Italian regions, Umbria and Marche. Organs were collected and analyzed at the National Reference center for Ruminant retroviruses. All samples were tested by a nested RT-PCR targeting the gag-pol region and positive samples were subsequently Sanger sequenced.
Between 2023.01.01 and 2025.12.31, total 179 roe deer (*Capreolus capreolus*) were sampled. Overall, 245 samples were collected, including 132 spleens (53.87%), 56 lungs (22.85%), 43 pooled organ samples (17.55%), and 14 blood clots (5.71%). One road-killed female from Marche region tested positive in spleen for SRLV by PCR. Sanger sequencing of the gag-pol region revealed that the SRLV belonged to the A23 subgenotype, and clustered with strains previously identified in domestic small ruminants in southern Italy.
Data reported herein showed that cervids may be naturally susceptible to SRLV. This is the first detection of SRLV in roe deer in Italy and Europe, and belonging to the A23 genotype, genetically related to SRLV from domestic animals. The paucity of data on SRLV in wild ruminants globally hampers robust conclusions on the most likely origin of such virus. Wildlife health monitoring programs are essential to clarify the epidemiological relevance of these findings and to better define the potential role of wild ruminants in the maintenance and transmission of SRLVs. Systematic screening for infectious agents, regardless of the apparent cause of death, is essential to ensure a comprehensive assessment of population health and to improve early detection of emerging or spillover infections.

Keywords: Lentivirus, SRLV, Roe deer, wild ruminants, PCR

P020. A metagenomic study of the European bison microbiome

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The European bison is the largest wild terrestrial mammal in Europe. After the total population was reduced to fifty-four individuals, today several wild and semi-wild populations are established across Europe. Health and biology of these populations are closely monitored to ensure their wellbeing. Insights into the microbiota of this species, however, are limited. Especially in ruminants, the gut microbiome plays an essential role in metabolic processes and may protect against pathogens. On the other hand, pathogens or pathogenic genes can be harboured by the microbiome. An example are antimicrobial resistance (AMR) genes, which, are relevant especially in an anthropogenic context where wildlife can serve as reservoir. In the present study, we used metagenomic sequencing to characterize the microbiome and resistome of European bison across multiple populations.
A total of 78 samples were collected from wild herds in Poland (rectal sampling) and a semi-wild herd in Döberitz, Germany (faecal droppings). DNA was extracted and subjected to metagenomic shotgun sequencing. Reads were taxonomically annotated and analysed for resistance genes. Both, microbiome and resistome were tested for group differences between locations and individual factors. Microbiome composition was relatively homogenous across populations. Oscillospiraceae (17.14 ± 4.07%), Lachnospiraceae (9.24 ± 2.06%), Clostridiaceae (8.73 ± 11.69%) and Bacteroidaceae (6.29 ± 2.61%) were the most abundant families. Samples collected from Droppings showed the highest compositional divergence. The resistome was dominated by genes conferring resistance to the classes of aminoglycosides and macrolide-lincosamide-streptogramine antibiotics (MLS).
Metagenomic sequencing revealed a stable microbiome and resistome across European bison populations, supporting their potential use as baseline indicators for wildlife health monitoring. These findings demonstrate the value of metagenomic approaches for wildlife health research.

Keywords: European bison, microbiome, resistome, metagenomic sequencing

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P021. Evidence of Bluetongue virus circulation in wild ruminants and its relationship with livestock outbreaks in Central Italy

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Bluetongue (BT) is a vector-borne disease of ruminants caused by bluetongue virus (BTV), transmitted by Culicoides spp. In Italy, BTV surveillance has been implemented since 2001, with circulation of multiple serotypes over time. Recent epidemic waves were associated with BTV-1 in 2014, BTV-4 in 2016–2017, and BTV-8 in 2025. While outbreaks in livestock are well documented, the role of wild ruminants remains poorly understood. This study investigated BTV circulation in wild ruminants in central Italy (Abruzzo and Molise regions) and assessed their potential role in virus maintenance and early detection.
Between 2013 and 2025, 1.331 wild ruminants were tested, including mouflon (*Ovis musimon*), fallow deer (*Dama dama*), red deer (*Cervus elaphus*), and roe deer (*Capreolus capreolus*). Animals from both captive and free-ranging populations were collected as road-killed or found dead. Spleen tissues were analysed by PCR for BTV detection and serotype identification. Prevalence and 95% confidence intervals were estimated. Differences among species were assessed using the chi-square test, and odds ratios (OR) were calculated. Wildlife data were compared with outbreaks in domestic ruminants.
Between 2013 and 2025, 631 outbreaks and 3.699 cases of BT were reported in domestic ruminants, with peaks in 2014, 2016 and 2025, associated with BTV-1, BTV-4 and BTV-8, respectively. Overall, 48 wild ruminants tested positive (3.61%; 95% CI: 2.73–4.75), with the same serotypes as domestic animals. Cases were observed in red deer (n=36), followed by mouflon (n=7), fallow deer (n=3) and roe deer (n=2). PCR positivity was not detected every year, and wildlife cases generally did not precede virus circulation in domestic animals. BTV positivity was associated with species ($p < 0.05$; OR = 34.52, red deer vs all other species, 95% CI: 8.09–147.11; $p < 0.0001$). Positive mouflon and fallow deer were sampled in captive settings and detected over limited periods, suggesting localized outbreaks. Red deer accounted for most cases among free-ranging animals and showed consistent detection across epidemic years. Positive wildlife cases occurred in areas with and without reported livestock outbreaks and were not clearly associated with high-density farming areas (81–85 animals/km^2).
This study provides the first data on BTV circulation in wild ruminants in central Italy. BTV circulation in wildlife may occur independently of livestock outbreaks. Detection in captive species appears linked to localized outbreaks, whereas red deer may act as an indicator of virus circulation. Passive wildlife surveillance can complement official systems, supporting early detection and improving understanding of BT epidemiology.

P022. Sixteen years of endemic circulation of Border Disease Virus after a severe outbreak in a Pyrenean chamois population from Andorra

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In 2001, Border Disease Virus (BDV), a pestivirus primarily affecting small ruminants, emerged in Pyrenean chamois (*Rupicapra pyrenaica pyrenaica*) populations across the Pyrenees, leading to population declines of up to 80% in some areas. In chamois, this virus has shown to produce reproductive failure, immunosuppression, and high mortality.
Twenty-five years after the initial outbreaks, BDV continues to circulate and affect some chamois populations, while others have shown signs of recovery. However, recent data from Andorra, a small country in the eastern part of the Pyrenees, have remained unpublished until now. This study describes the long-term epidemiological situation of BDV in the Enclar hunting reserve, a 2,300-ha protected area established in 2000 in southwestern Andorra, where hunting is strictly regulated.
In late 2009, the first chamois carcasses attributed to BDV were detected in the reserve. Between 2009 and 2010, the population declined by 58% (from 415 to 173 individuals). Hunting was suspended for two seasons and the population recovered to approximately 300 individuals by 2012 and has remained relatively stable since, with recruitment rates (births per adult) ranging from 0.18 to 0.32. In 2012, the government decided to resume hunting, with a quota below 10% of the population.
Between 2012 and 2025, serum (n = 205) and spleen (n = 259) samples were collected from harvested chamois in the contest of a disease surveillance program. Serum samples were tested for BDV antibodies using ELISA, while spleen samples were analysed for viral detection using ELISA and RT-PCR depending on the period. Antibodies against BDV were consistently detected throughout the study period, including in young animals (< 2 years), indicating continuous viral circulation. Viral RNA was detected in one clinically healthy individual in 2018 and in two individuals in 2025.
These findings suggest an endemic and asymptomatic circulation of BDV in this population, similar to patterns described in some areas of the eastern Pyrenees. Despite the severe initial impact, the host population appears to have reached a stable equilibrium with the virus. Next steps would be to assess the viral strain of the circulating virus as recent studies has shown the existence of at least two strains, with different pathological and epidemiological implications.

Keywords: Chamois, Border Disease virus, Pestivirus, epidemiology.

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P023. Impact of short-term freezing on morphology and hatchability of *Fascioloides magna* eggs

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Digenean trematode *Fascioloides magna* is originally a parasite of North American deer species. It was introduced to Europe at least twice, forming three natural foci of disease. Definitive wild hosts (red deer, fallow deer and recently in some areas roe deer) are shedding eggs via the faeces. In this study we aim to analyse the potential impact of short-term freezing on morphology and hatchability of *F. magna* eggs. *F. magna* eggs were collected from fresh faecal samples of wild red deer. Faecal samples were frozen for 7, 14, 21 and 28 days, and eggs were isolated (successive washing and sedimentation to remove debris). Isolated eggs were analysed morphologically under a stereomicroscope, quantified and distributed into Petri dishes. Number of eggs per sample varied due to differences in the faecal sample. Only intact eggs were selected. The embryonation process was conducted within incubator, in deionized water under constant temperature of 25 °C. Development of the eggs was monitored under a microscope (40x and 100x magnification). Hatching rate was calculated as percentage of embryonated eggs (empty shells vs total number of eggs in the Petri dish (at the beginning of observation). Developmental stages were classified as unembryonated eggs, formation of the central embryo, appearance of characteristic eye spots and active miracidia.
Following the periods of 7, 14 and 21 days of freezing we did not observe changes in the eggs morphology. In the sample frozen for 28 days some of the eggs were broken, and granulated content was partially outside of the egg. Embryonation process lasted between 28 and 32 days. In the first three groups hatching rate was around 90% (89%, 92%, 90% respectively). Last group of eggs is still under monitoring.
F. magna eggs can survive in deep frozen red deer faeces for at least 21 days. During this period no alterations in eggs morphology were observed and development of miracidia was successful. However, time required for miracidia to complete development was slightly longer with the duration of freezing. Following the 28 days of freezing occasional disintegration of the eggs was observed. Further monitoring is required to obtain more reliable conclusions.

Keywords: *Fascioloides magna*, eggs, freezing, morphology, hatchability

Funding source: Croatian Science Foundation Project No. IP-2024-05-8056.

P024. Across Italian ecosystems: what shapes parasite dynamics in wild boar?

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Understanding parasite transmission in wildlife requires disentangling the interplay between environmental conditions and host-related factors. In free-ranging ungulates such as wild boar (*Sus scrofa*), these processes operate across multiple spatial and biological scales and are often influenced by the sampling approach adopted. This study explores how environmental gradients and host traits shape lung and gastrointestinal parasite infections in wild boar populations across diverse Italian ecosystems, with implications for wildlife disease ecology.
Two sampling strategies were implemented. Non-invasive faecal samples were collected from the environment in alpine and Mediterranean habitats, enabling spatially explicit analyses based on geographic coordinates and environmental predictors (e.g., elevation, temperature, land-use classes). In parallel, rectal faecal samples were obtained from culled individuals across multiple study areas (alpine, appennine and Mediterranean habitat), allowing the integration of host-level variables, including age, sex, body mass, and mean group size. All samples were analysed using the Mini-FLOTAC technique. Generalized linear (mixed) models were applied to investigate ecological and host-related relationship with parasite occurrence and abundance.
Parasite communities were dominated by *Eimeria* spp., gastrointestinal strongyles (GIS), and *Metastrongylus* spp. Across both sampling approaches, parasite occurrence showed weak and inconsistent associations with explanatory variables, whereas abundance-based analyses revealed clearer ecological signals. GIS abundance was consistently negatively associated with open natural habitats, suggesting reduced survival of free-living stages under more exposed environmental conditions. Host-level analyses highlighted age as a key driver of infection, with juveniles and subadults exhibiting higher parasite burdens both for GIS and *Metastrongylus* spp. At the landscape scale, *Metastrongylus* spp. abundance declined significantly with increasing elevation, likely reflecting constraints on intermediate host availability. In contrast, *Eimeria* spp. did not display consistent environmental or host-related patterns.
Despite differences in sampling strategy (field-collected vs. rectal samples), both approaches converged on consistent ecological patterns, particularly for GIS, reinforcing the robustness of key findings across methodological frameworks. Importantly, they captured complementary aspects of parasite dynamics: host traits, such as age, shape infection heterogeneity at the individual level, while environmental gradients constrain transmission processes at broader spatial scales. Integrating non-invasive and host-based approaches provides a more comprehensive framework for investigating host–parasite–environment interactions in wildlife, supporting improved understanding of disease ecology in wild ungulate populations.

Keywords: Wild boar; parasite community; helminths; protozoa; environmental associations

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P025. Molecular survey of *Calodium hepaticum* in small mammals in Serbia

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Small mammals represent important hosts of various parasites, including species of zoonotic relevance, and may act as reservoirs, or in some cases as intermediate or definitive hosts in parasite life cycles. *Calodium hepaticum* is a parasitic nematode primarily found in rodents, but also reported in a wide range of mammalian species, while in humans it can cause hepatic calodiasis. The aim of this study was to perform the first molecular investigation of this species in Serbia.
A total of 286 small mammals were analyzed from seven sampling locations in the urban and peri-urban areas of Belgrade. The sampling was conducted over the period 2020–2024. Eight small mammal species were examined (*Apodemus flavicollis, Apodemus sylvaticus, Apodemus agrarius, Crocidura leucodon, Myodes glareolus, Microtus spp., Microtus subterraneus,* and *Crocidura suaveolens*). Additionally, individuals of *A. flavicollis* were age-classified into appropriate age groups based on lens weight measurements.
Macroscopic liver lesions were observed in 21 individuals (7.34%) out of 286 examined small mammals. Of these, *C. hepaticum* was confirmed in 20 individuals by morphological egg identification and PCR amplification of the 18S rRNA gene, all of which occurred exclusively in *A. flavicollis* (20/220; 9.09%). In *A. flavicollis*, no significant difference in infection prevalence was observed between males and females (χ^2 = 0.260, df = 1, p > 0.05). In contrast, a significant difference among age groups was detected, with the highest proportion of positive individuals recorded in the older age group (20%) and the lowest in juveniles (3.2%) (χ^2 = 10.316, df = 4, p = 0.035). As an isolated finding, *C. leucodon* (1/7; 12.5%) was confirmed to be infected with *Capillaria plica* based on morphological egg identification and PCR analysis.
These results indicate the presence of *C. hepaticum* in small mammal populations in Serbia, with *A. flavicollis* acting as a key host in the studied area, highlighting the importance of further epidemiological and molecular investigations regarding its zoonotic potential.

Keywords: zoonotic, nematode; rodents; *Capillaria*; parasite

Acknowledgement This study was supported by the Ministry of Education, Science and Technological Development of the Republic of Serbia, Contract No. 451-03-33/2026-03/ 200007

P026. Prevalence, Genetic Diversity, and Landscape Associations of *Orthohantavirus puumalaense* in Bank Voles (*Clethrionomys glareolus*) from Northern Sweden

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Puumala hantavirus (PUUV, *Orthohantavirus puumalaense*) is a zoonotic pathogen maintained in bank vole (*Clethrionomys glareolus)* populations within vast areas of its reservoir's distribution range in Europe. Its transmission dynamics are shaped by host demography, environmental, community, and spatial factors. Following the detection of PUUV in Swedish bank voles by metatranscriptomic analysis, this study investigated PUUV prevalence, landscape associations, and genetic diversity in bank voles from two sites in Västerbotten County, northern Sweden, representing inland (Vindeln) and coastal habitats (Coast), during a complete vole cycle (2020-2023).
Sample sizes for both study areas were based on previously published serologically estimated PUUV prevalences. In total, 519 bank voles (Vindeln, *n*=339; Coast, *n*=180) were screened for PUUV RNA by S-segment-specific RT-PCR from lung-derived RNA. Infection probability was analysed using logistic regression including host and temporal factors and their interactions. Viral genetic diversity was assessed from a 685-nucleotide S-segment using phylogenetic reconstruction, ADMIXTURE, and principal component analysis. Landscape composition was quantified from Swedish National Land Cover Database (NMD) data at two spatial scales (2.5×2.5 km and 200×200 m), and associations with PUUV occurrence were tested using generalized linear mixed models.
Eighty-three individuals tested positive for PUUV, corresponding to an observed prevalence of 16.8% (57/339) in Vindeln and 14.4% (26/180) in the coastal area. Model-based predicted prevalence differed significantly with host and temporal factors, being higher in a) adults (16.5%, 95% CI:12.3–21.9%) than juveniles (1.5%, 95% CI:0.4–4.8%) and b) males (8.9%, 95% CI:4.9–15.5%) than females (2.9%, 95% CI:1.3–6.2%) and increased during the population cycle with highest prevalences during the peak phase. A significant Season×Area interaction indicated site-specific seasonal dynamics. Genetic analysis of 68 sequences identified 48 haplotypes, all clustering within the North-Scandinavian PUUV lineage. Multivariate analyses showed clear genetic structuring, suggesting local transmission and limited viral dispersal. At the landscape scale, PUUV RNA presence was negatively associated with artificial land (β=-0.38, p=0.048) and mixed forest (β=-0.09, p=0.014), whereas coniferous forest showed only a weak, non-significant negative trend. No significant habitat effects were detected at the local scale, and variation among trapping plots suggested fine-scale ecological heterogeneity.
Our findings suggest that PUUV prevalence in bank voles is associated with host, temporal, and landscape factors, while viral genetic diversity is more strongly linked to spatial structuring. Integrating ecological and molecular data can improve our understanding of hantavirus transmission dynamics in endemic regions.

Keywords: PUUV, bankvole, zoonosis, land-use, phylogenetics, Sweden

Funding source: This research was supported by the European Union, grant agreement no. 101060568, project: BEPREP.

P027. Preliminary findings on ha-MYXV infections in European Brown Hares (*Lepus europaeus*) in Lower Saxony, Germany

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The emergence of the recombinant myxoma virus strain ha-MYXV in Iberian hares (*Lepus granatensis*) in 2018 marked a shift in the epidemiology of myxomatosis. Since 2024, outbreaks have also been reported in European brown hares in Germany, indicating further host expansion and a spatially heterogeneous spread. Local population declines of up to 80 % have been reported, yet epidemiological dynamics and effects at the population-level remain unclear.
To assess the occurrence of ha-MYXV in European hares in Lower Saxony, a survey was conducted in two consecutive years in November 2024 and December 2025, respectively. Based on the survey, 12 hunting grounds were selected (10 classified as affected, 2 as unaffected of ha-MYXV cases) for sampling in December 2025. A total of 131 animals were sampled. Eyelid tissue was analysed by real time PCR, and serum samples were tested using serum neutralization test, immunofluorescence assay, and ELISA.
Ha-MYXV genome was detected in 6/129 (4.7 %) hares, all originating from previously affected areas. All samples from regions assigned as unaffected tested negative. None of the animals showed clinical signs. Serological evidence of exposure amounted to 15 of the 128 samples (11.7 %). Five individuals were positive in both PCR and serology, while 10 were sero-reactive without detectable viral DNA, suggesting prior exposure. Additionally, 12 samples yielded discordant or inconclusive results across the three serological tests. Overall, most animals were negative in both PCR and serology.
Our findings demonstrate circulation of ha-MYXV in apparently healthy hares. However, low detection rates, lack of validated diagnostics, and inconsistent serological results highlight uncertainty in interpreting infection status and immune responses. It remains unclear whether ha-MYXV will cause sustained population declines or follow dynamics like myxomatosis in rabbits. Expanded sampling is urgently needed to assess temporal trends, immunity development, and impacts on population dynamics.

Keywords: myxomatosis, ha-MYXV, European brown hare, *Lepus europaeus*, wildlife disease

P028. Pathological Features of Fulminant Leptospirosis in a Zoo-Housed Red-Necked Wallaby (*Notamacropus rufogriseus*): A Case Report

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Leptospirosis is a globally distributed zoonotic disease caused by pathogenic Leptospira spp., affecting domestic and wild animals. Reservoir hosts, including rodents and marsupials, often shed the bacteria asymptomatically via urine. Infection occurs through contact with contaminated environments, with bacteria entering through mucous membranes or damaged skin. Following leptospiremia, organisms localize in renal tubules, enabling persistent shedding. Disease pathogenesis is associated with vascular injury, thrombocytopenia, and hemorrhagic diathesis. Although marsupials are typically subclinical carriers, infection with virulent strains may result in severe systemic disease. This report describes pathological findings in a fatal case of leptospirosis in a zoo-kept red-necked wallaby.

A captive red-necked wallaby (*Notamacropus rufogriseus*) underwent a complete necropsy. Tissue samples were fixed in 10% neutral buffered formalin, processed routinely, and embedded in paraffin. Sections (4–6 µm) were stained with hematoxylin and eosin (H&E). Selected sections were stained using Warthin–Starry (WS) silver stain for spirochete detection.

Gross examination revealed multisystemic lesions, including ulcerative hemorrhagic gastritis, necrohemorrhagic enteritis, and a congested, mottled liver. Hemorrhages were present in the pancreas and mesenteric lymph nodes. Kidneys showed diffuse cortical and tubular degeneration, and the myocardium exhibited multifocal pale areas. Histopathology confirmed severe tissue damage: diffuse hepatic necrosis, acute tubular necrosis, extracapillary glomerulonephritis, and mild lymphocytic interstitial nephritis. Additional findings included pancreatic and myocardial necrosis and ulcerative gastritis. WS staining demonstrated numerous argyrophilic spirochetes in the liver and kidneys, consistent with *Leptospira* spp.

This case demonstrates that species considered reservoir hosts can develop fulminant, fatal leptospirosis when infected with virulent strains. The disease was characterized by acute onset, systemic vascular injury, and marked hemorrhagic diathesis. Diagnosis was supported by combined histopathology and silver staining. Leptospirosis should be included in the differential diagnoses of sudden death in zoo-kept macropods. Due to its zoonotic nature, strict biosecurity, environmental management, and occupational safety measures are essential in zoological settings.

Keywords: leptospirosis, red-necked wallaby, zoo-animal, acute tubular necrosis

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P029. Antimicrobial Resistance of Indicator Commensal *Escherichia Coli* in Wild Animals and Birds in the Territory of the Republic of Serbia

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The presence of multidrug-resistant isolates in wild animals and birds indicates the circulation of resistant bacteria in the environment, with migratory bird species playing an important role as bioindicators of their presence in ecosystems. The aim of this study was to determine the prevalence of resistance in commensal *E. coli* isolated from rectal and cloacal swabs of wild animals and birds collected in the territory of the Republic of Serbia during the period 2023–2025. A total of 57 samples were analyzed, including beaver (*Castor fiber*, n=2), badger (*Meles meles*, n=3), swan (*Cygnus olor*, n=3), grey heron (*Ardea cinerea*, n=1), white-tailed eagle (*Haliaeetus albicilla*, n=8), pigeon (*Columba livia*, n=9), green woodpecker (*Picus viridis*, n=1), hooded crow (*Corvus cornix*, n=7), saker falcon (*Falco cherrug*, n=1), common buzzard (*Buteo buteo*, n=3), sparrowhawk (*Accipiter nisus*, n=1), turtle dove (*Streptopelia turtur*, n=1), harrier (*Circus sp.*, n=1), rook (*Corvus frugilegus*, n=1), roe deer (*Capreolus capreolus*, n=2), tawny owl (*Strix aluco*, n=6), white stork (*Ciconia ciconia*, n=2), goshawk (*Accipiter gentilis*, n=1), and blackbird (*Turdus merula*, n=1).
Isolation of indicator commensal *E. coli* was performed on Tryptone Bile X-glucuronide (TBX) agar, while identification was carried out using the automated biochemical identification system AUTOMIC-I-600. Antimicrobial susceptibility testing was performed using the disk diffusion method on Mueller–Hinton agar, and interpretation of inhibition zones was conducted according to the guidelines of the European Committee on Antimicrobial Susceptibility Testing (EUCAST).
The results showed that 40.35% of isolates exhibited resistance to one or two classes of antibiotics, while multidrug resistance (to three or more classes) was detected in 52.63% of isolates. Resistance to β-lactam antibiotics was detected in all 57 isolates, while 87.71% showed resistance to macrolides. The lowest resistance rates were observed for aminoglycosides and cephalosporins. Resistance to clinically important antibiotics in human medicine (amikacin, azithromicycin, tigecycline, cefepime, piperacillin, tazobactam, and nitrofurantoin) was detected in the 12 isolates.
Detection of resistance to these antimicrobial agents in wild animals indicates their potential role as reservoirs and bioindicators of the spread of antimicrobial resistance in the environment. These findings further confirm the importance of applying the "One Health" approach in monitoring and controlling antimicrobial resistance. Continuous monitoring of wild populations can contribute to early detection and a better understanding of transmission pathways of resistant strains between the environment, animals, and humans.

Keywords: white-tailed eagles, environmental pollution, fluoroquinolones, resistance, virulence

Funding source / Acknowledgement: This work was funded by Ministry of Science, Technological Development and Innovation of Republic of Serbia by the Contract of implementation and funding of research work of NIV-NS in 2026, Contract No: 451-03-33/2026-03/200031.

P030. Shifts in the Microbial Core: Does Avian Influenza Alter the Faecal Bacteriome of Mallards?

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Waterfowl, particularly mallards, constitute an important natural reservoir of Avian Influenza viruses (AIVs), which are primarily transmitted via the faecal–oral route. Increasing evidence suggests a bidirectional interaction between IAV infection and the host gut microbiota in wild birds. The aim of this study was to assess the impact of low pathogenic AIVs on the faecal microbiome of wild mallards and to contextualize these findings within previously reported patterns.
The 16S rRNA gene was sequenced from 55 faecal samples collected from mallards across three Spanish wetlands over a 16-year period (2008–2024). In an initial analysis we evaluated the influence of ecological variables on bacterial community composition. Subsequently, we compared H3N8 positive (N=7) and negative (N=4) samples from a specific wetland at a specific sampling date in order to detect microbiome changes associated to AIV presence.
Across the full dataset, a greater proportion of the variance in microbiome composition was explained by the year (R^2=0.337), phenology (R^2=0.098) and the bioregion (R^2=0.137) than AIV presence (R^2=0.035). In the subset analysis, no significant differences were detected in alpha or beta diversity between positive and negative samples. However, differences in core microbiome composition were observed: AIV-positive samples showed a higher prevalence and relative abundance of *Cetobacterium* and a decreased relative abundance in *Psychrobacter*. In addition, five genera (*Serratia*, *Bacillus*, *Candidatus_Arthromitus*, *Peptoclostridium* and *Carnobacterium*) were significantly associated with AIV-positive samples.
Overall, our results support the notion that ecological factors exert a stronger influence on the gut microbiome of wild mallards than AIV presence. Nevertheless, the observed shifts in core microbiome composition and the emergence of specific bacterial genera in AIV-positive samples suggest a potential association between AIV presence and faecal bacteriome structure. These patterns should be further investigated in studies with larger sample sizes and controlled conditions to better disentangle ecological and infection-driven effects.

Keywords: influenza, mallard, faeces, bacteriome

Funding source MCIN/AEI/10.13039/501100011033, FSE+ (PID2020-114060RR-C31 and PRE2022-101762); Basque Government.

P031. Presence and Tissue Tropism of Avian Coronaviruses in Wild Birds in the Netherlands

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Avian coronaviruses (AvCoVs), including Gammacoronaviruses (GCoVs) and Deltacoronaviruses (DCoVs), have been detected in wild birds and domestic poultry. GCoVs are associated with infectious bronchitis in chickens and are detected mostly in wild waterfowl, while DCoVs are present more extensively in wild birds, poultry and mammals. DCoVs spillover events to humans and domestic pigs have been documented, resulting in acute enteric clinical signs. The virus circulation, transmission and tropism of AvCoVs in wild birds in the Netherlands is unknown. This study investigated the presence and tropism of AvCoVs in tissues of 150 wild birds from the Passeriformes, Pelecaniformes, Anseriformes, and Charadriiformes orders that were found dead in the Netherlands between 2019 and 2024. Tissues collected during necropsy and stored in the biobank of the Dutch Wildlife Health Centre were tested by PCR using PanCoV primers targeting the RdRp gene. Positive samples were confirmed by sequencing. Coronaviruses were detected in 10 of the 150 birds (6.7%). DCoV were detected in the intestines of three song thrushes (*Turdus philomelos*), and two Eurasian spoonbills (*Platalea leucorodia*), one of these spoonbills was also found positive in the lungs. Five birds from the Anseriformes group were found positive for Gammacoronaviruses in their intestines. All samples from the Charadriiformes group tested negative. These findings highlight the circulation of AvCoVs in wild birds in the Netherlands and underscore the need for further research into their pathogenic role and potential for interspecies transmission.

Keywords: coronaviruses, wild birds, RT-PCR, virology

Session 2

Health and diseases of bats and rats

Oral Presentations

Insights into Bat Health, Mortality, and Pathogen Surveillance: Findings from the Interdisciplinary Project 'Bat Health in Central Germany – From Pathology to Protection'

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Bats are unique mammals that increasingly depend on conservation measures due to ongoing habitat destruction. The interdisciplinary project 'Bat Health in Central Germany – From Pathology to Protection', initiated in 2025, aims to link bat conservation with environmental, animal, and human health within a One Health framework.
The project includes macroscopic and histopathological investigations, identification of parasitic, bacterial, and viral pathogens, and analyses of the immune system. In addition, a tissue biobank has been established, providing material to support future research questions. Furthermore, the results are actively being integrated into the project's communication strategy and education initiatives.
A total of 29 bats representing 11 species were examined. Additionally, 24 bats underwent necropsy but have not yet been subjected to detailed analyses. Preliminary findings indicate the following causes of death: 24.1% (n = 7) trauma, 17.2% (n = 5) predation, 17.2% (n = 5) combined infection and trauma (co-morbidity; order unclear), 17.2% (n = 5) infection, 10.3% (n = 3) starvation, 10.3% (n = 3) undetermined causes, 3.4% (n = 1) circulation failure. Trauma cases were predominantly classified as blunt force trauma, consistent with collision events. Predation cases were mainly associated with reported cat contact. Additionally, endoparasite screening detected infections in 19 of 29 bats, resulting in an overall prevalence of 65%, with trematodes as the dominant taxonomic group. Furthermore, one Daubenton's bat tested positive for EBLV-2. Further examinations are ongoing.
Trauma was the leading cause of mortality, which is consistent with previous reports. Also, the high prevalence of endoparasites corroborates earlier findings. Additionally, the detection of EBLV-2 highlights bats as reservoirs for zoonotic pathogens, as demonstrated in previous studies, underscoring the need for continuous surveillance in Germany. Although detection rates are low, the presence of lyssaviruses in bat populations represents a relevant public health risk, especially for individuals with frequent bat contact, such as researchers, veterinarians, wildlife rehabilitators, and conservationists. Accordingly, the German Standing Committee on Vaccination recommends pre-exposure rabies vaccination for these groups. Thus, this study provides valuable data on bat health in Central Germany, a region with well-documented bat populations but limited information on their health status. Continued sampling and comprehensive analyses will improve understanding of bat health and host–pathogen dynamics, contributing to the broader objectives of the One Health approach.

Keywords: bat health, conservation, veterinary pathology, surveillance, One Health

Molecular Characterization and Haplotype Analysis of *Neoehrlichia mikurensis* in Bat-Associated Ticks in Serbia

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Neoehrlichia mikurensis has been documented in questing ticks and *Apodemus flavicollis* mice in Serbia, however the role of bats and their specialized ticks in its natural cycle of this pathogen remains poorly defined. Therefore, this study aimed to identify and genetically characterize *N. mikurensis* strains circulating in bat-associated ticks and to determine their phylogenetic relationship with known global lineages.

A total of 221 tick specimens (*Ixodes simplex* and *Ixodes vespertilionis*) were collected from 112 bats belonging to five species (*Miniopterus schreibersii*, *Myotis myotis*, *Rhinolophus ferrumequinum*, *Rhinolophus hipposideros*, and *Rhinolophus euryale*) in Serbia. Ticks were analyzed in 19 pools using PCR targeting the 16S rRNA gene. Two overlapping 16S rRNA datasets were constructed: Dataset I (743 bp, n=93) for initial phylogeny and haplotype detection, and Dataset II (169 bp, n=104) for comparison with global bat-associated sequences.

Four representative *N. mikurensis* sequences were obtained from the positive samples and were further used for detailed molecular analysis. Bayesian phylogeny of Dataset I revealed four clusters (A–D). Serbian sequences clustered within the cosmopolitan Cluster B but remained clearly distinct from all other sequences in that group. Analysis of Dataset II showed that Serbian sequences group specifically with other bat-derived sequences, forming a separate, highly similar cluster. Analysis of Dataset I revealed 13 haplotypes (H1–H13), with Serbian sequences forming a unique, separate haplotype. Additionally, haplotype continent-based analysis displayed that Asian sequences have higher genetic diversity (six haplotypes) compared to European (four) and Australian (two) ones. Haplotype network analysis of Dataset II confirmed that Serbian sequences group with previously reported bat-associated strains into a single, highly similar haplotype, distinct from other global sequences.

The study implies the presence of a unique, bat-specific genetic lineage of *N. mikurensis* in Serbia. The discovery of a separate phylogenetic cluster and a distinct haplotype suggests that this pathogen has been adapted to a specialized bat-tick cycle and indicates the importance of including bats in zoonotic surveillance and provide new insights into the genetic diversity of the genus *Neoehrlichia*.

Keywords: *Neoehrlichia mikurensis,* bats, haplotype analysis, phylogeny

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The Calm City? Landscape Drivers of Cortisol in Urban Pipistrelles

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Urbanization constitutes an intense habitat transformation that creates new habitats, promoting the establishment of species capable to adapt to these conditions, including some chiropterans. However, urban bats might be negatively affected by anthropogenic pollution such as exposure to contaminants, noise, or artificial light. In this study, we studied intrinsic and extrinsic factors related with fecal cortisol metabolites (FCM) in Soprano's pipistrelles (*Pipistrellus pygmaeus*) captured in urban and periurban areas of Zaragoza (NE Spain). We hypothesize that the less natural the habitat of each individual, the higher the stress level.

Ninety adult pipistrelles were captured in artificial roots located in three urban parks and in one abandoned building about 8 km from the city. Animals were sexed, weighted and measured, wing mites counted, and a fecal sample obtained. FCM was measured by a cortisol-21-CMO enzyme immune assay. Landscape composition was quantified around each roost at three spatial buffers (500, 1500, and 3000 m), using five land-cover variables: urban, vegetation, barren, water, and agricultural. Landscape composition was summarized using separate principal component analyses (PCA) for three spatial buffers around the capture site (500, 1500, and 3000 m). We tested 12 candidate models that varied in the inclusion of locality, body mass or body condition, and landscape PCA axes from the three buffers, and selected the best-supported model using AIC.

The best-supported model included sex, body weight, mite load, and the first two PCA axes at the 3000 m scale. FCM levels tended to be higher in more open and agriculturally influenced landscapes, and lower in more vegetated, water-rich habitats. Sex, weight and mite load was not related with FCM levels. Contrary to our hypothesis, individuals inhabiting more open, agriculturally influenced landscapes exhibited higher FCM levels. This pattern suggests that the challenges associated with urban environments may be counterbalanced by specific advantages of these habitats, including lower predation risk or increased access to resources, such as insects attracted by city lights.

Keywords: urban wildlife, chiropterans, stress.

Funding source or Acknowledgement: This work was supported by the University of Zaragoza [Grant no. UZ2021-BIO-03] and Gobierno de Aragón [Grant no. A16_23R].

Wild rats as carriers of disease

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Rats can carry many pathogens, several of which can cause disease in humans if transmitted. Knowledge about the disease status and the pathogens carried by wild rats in Sweden is limited. Therefore, the aim of this study was to assess their health status and identify which pathogens rats carry in two urban and suburban areas in Sweden.
A total of 249 wild rats were collected through regular pest control using non-baited electrical cages between February and September 2024. The rats were collected from areas in and around Uppsala and Malmö and transported to the Swedish Veterinary Agency for postmortem examination.
All rats were visually examined for ectoparasites and a full necropsy was performed on each rat. Samples were collected for analysis of *Leptospira* spp. (kidney), Hepatitis E virus (HEV) (liver), *Bartonella* spp. (liver), *Salmonella* spp. (liver, spleen, and colon), Seoul hantavirus (lung), Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (lung) and tick-borne encephalitis virus (TBEV) (liver). Specific real-time PCR protocols for each pathogen were used for detection.
The rats were overall healthy and had an average body weight of 75 g (range: 25–348 g). Ectoparasite findings included fleas (n=47 rats), ticks (n=19 rats) and lice (n=7 rats). One rat had a servere pneumonia caused by *Corynebacterium kutscheri*. One rat carried *Salmonella enterica* subsp. *enterica* serovar *Bareilly*, and five rats carried *Leptospira* spp. in their kidneys with one sample confirmed in Warthin-Starry silver staining. No rats tested positive for hantavirus, HEV, *Bartonella* spp., TBEV, nor SARS-CoV-2.
Wild rats in the study were generally healthy and carried a limited number of pathogens. However, the study is limited by the sample size and by the young age of the rats. The potential transmission of leptospirosis from rats to humans and dogs is of particular importance and warrants further investigation to better understand its prevalence and distribution among wild rat populations in Sweden.

Keywords: rat, disease, pathology, wildlife

Funding source or Acknowledgement: Swedish Environmental Protection Agency, European Union's EU4Health programme under Grant Agreement Nr 101132473 OH4Surveillance

Session 2

Health and diseases of bats and rats

Poster Presentations

P032. Active Railway Tunnels as a little investigated cause of mortality in bats

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Bat populations in Great Britain have declined significantly over the last century. GB has 18 species of bats, all protected by law and four of these are IUCN red listed. This decline is due to anthropogenic causes rather than disease. Here the significance of bats mortality in tunnel is investigated.
There were reports in late 2018 of about 70 dead bats in a railway tunnel in Southern England, none were examined. A single natterer's bat (*Myotis nattereri*) was submitted in December 2019 as part of a Natural England Survey to investigate possible barotrauma in bats involving railway tunnels and roads. Gross findings of subcutaneous haemorrhage and extensive pectoral muscle haemorrhage indicated this bat died due to direct trauma. In September 2020 a further three were submitted. It is very time consuming and costly to regularly visit active railway tunnels to collect any dead bats, so carcases are often markedly autolysed when picked up.
Visits were made in September 2021 to inspect work on the renovation of bat roost sites in another tunnel in East Anglia. 20 dead bats were found during an inspection visit on 14th September. These included five brown long-eared bats (*Plecotus auritus*), seven Daubenton's bats (*Myotis daubentonii*), three common pipistrelles (*Pipistrellus pipistrellus*), four Natterer's bats and one of unknown species. All had gross evidence of traumatic injuries. On a further visit on 23rd, 12 more bats were found; four brown long-eared bats, one Daubenton's bat, one common pipistrelle, four Natterer's bats, one *Myotis* spp. and one unknown species. All these were dead except one of the brown long-eared bats, which was grounded. This was taken to the tunnel entrance and after a short while it flew away.
Anecdotally there is a spike in mortality as the result of late summer/early autumn leking and swarming in tunnels. Mitigation could be put in to substantially reduce mortality but it is costly, e.g. such as a lighting system tripped before trains arrive combined with 'bat shelters' (tiles on walls) to flush bats into hiding. This has been used successfully in one tunnel in Oxfordshire and recently no dead bats have been found. Also to improve collection of dead bats in target tunnels dogs are being trained to locate them as is done at wind turbine sites. This initial work suggests that trains in railway tunnels could also cause high levels of bat mortality and has prompted similar research in Germany.

Keywords: Bats, trauma, railway tunnels

P033. EBLV-1 confirmation and clinical behavioral patterns in *Cnephaeus serotinus* from Ukraine

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European bat lyssavirus type 1 (EBLV-1) is a zoonotic pathogen of public health concern, yet data on its clinical manifestation in naturally infected bats remain scarce. Bat rehabilitation centers, which receive injured and debilitated animals reported by the public, offer a unique opportunity to detect lyssavirus infections that would otherwise remain undiagnosed. The Ukrainian Bat Rehabilitation Center (UBRC) is a specialized facility staffed by biologists and veterinarians, focused on bat rescue and rehabilitation across Ukraine. The management of cases involving potentially dangerous pathogens is carried out under the institutional framework of the National Scientific Center 'Institute of Experimental and Clinical Veterinary Medicine' (NSC IECVM). Here we report cases of EBLV-1 detected among bats handled by the UBRC in 2024–2025.

Eleven *Cnephaeus serotinus* that died or were euthanized due to neurological signs or poor prognosis were selected for lyssavirus screening. Animals originated from six localities across Ukraine. Clinical signs were documented by trained rehabilitators through video recordings and standardized text protocols prior to euthanasia or natural death. Brain tissue and five additional organs (liver, kidney, lungs, intestine, spleen) were collected. After nucleic acid extraction, reverse transcription nested PCR targeting the lyssavirus nucleoprotein gene was performed. Metagenomic sequencing on the Illumina platform was performed after viral enrichment and sequence-independent single-primer amplification.

Lyssavirus RNA was detected in brain tissue of 7/11 individuals (63.6%), all confirmed as EBLV-1 by sequencing. Multi-organ screening revealed viral RNA in extraneural tissues (liver, lungs, kidney, intestine, spleen) in most positive cases, with variable dissemination patterns. Clinical signs in confirmed cases included aggression, disorientation, pharyngeal spasm with inability to swallow, hypersalivation, hypertonia, and cyanosis of the oral mucosa. Two individuals presenting with neurological signs (axial circling, progressive weakness) were negative for lyssavirus, highlighting the importance of laboratory investigation to rule out lyssavirus in cases with nonspecific neurological symptoms.

Bat rehabilitation centers represent effective passive surveillance nodes for lyssavirus detection in regions with limited diagnostic infrastructure. Detailed behavioral and clinical observations in rehabilitation settings complement conventional surveillance and provide valuable data on EBLV-1 pathogenesis. Enhanced diagnostic capacity and awareness are needed in Ukraine, particularly under the constraints of the ongoing conflict.

Keywords: EBLV-1, lyssavirus, *Cnephaeus serotinus*, bat rehabilitation, passive surveillance, Ukraine

Session 3

Vectors and vector-borne diseases in wildlife

Oral Presentations

Invited lecture

The role of wildlife and the consequences for wildlife health of vector-borne diseases

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The evolutionary history of blood-feeding arthropods is closely linked to the wild vertebrates with which they established parasite-host interactions millions of years ago. These long-standing interactions have been instrumental in shaping the diversity of microorganisms that have co-evolved with arthropods and vertebrates. The rapid changes—often abrupt from an evolutionary perspective—that human activities have caused in most terrestrial ecosystems and the climate have driven numerous pathogens transmitted by blood-feeding arthropods into new ecological settings where they can have serious consequences for the health of animals and humans.

There are numerous examples illustrating how environmental changes caused by human activities alter the demographic dynamics of wild vertebrate communities, blood-feeding arthropods and their pathogens, changing their spatial distribution patterns, displacing them to entirely different ecosystems or facilitating their adaptation to new parasite-host systems. Using various examples, we will analyse the role that environmental or host community changes have played in the (re)emergence of vector-borne pathogens with consequences for the health of humans and wildlife.

In the Northern Hemisphere, the explosion in wild ungulates has, in part, influenced the (re)emergence of tick-borne encephalitis, Crimean-Congo haemorrhagic fever, Louping ill and Lyme borreliosis, with serious consequences for human and animal health. At the same time, environmental changes have affected a multitude of blood-feeding arthropods associated with wildlife and, consequently, the dynamics of certain pathogens and the diseases they cause, e.g. West Nile fever, bluetongue, epizootic haemorrhagic disease, leishmaniosis or avian malaria.

Understanding the causes and consequences of these changes on known diseases is essential to predicting the impact of current or potential changes on the dynamics of these and other vector-borne diseases, both known and unknown. Preparedness can mitigate the consequences of the (re)emergence of vector-borne pathogens on human and wildlife health, and facilitate the ecological transition towards modern, healthier, biodiverse societies.

Keywords: biodiversity, landscape immunity, resilience, ticks, mosquitoes

Funding source or Acknowledgement: MCIU/AEI & EU, European Wildlife Disease Association (EWDA), Sara Savić and Tamaš Petrović.

Open-access training videos for arthropod vector identification and wildlife sampling to support wildlife disease surveillance

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Reliable identification of arthropod vectors and standardized wildlife sampling are critical for surveillance of vector-borne pathogens affecting wildlife and domestic animals. However, practical training materials accessible to field veterinarians, researchers and official veterinary labs remain limited in many regions. A series of IAEA-funded projects aimed to develop and disseminate standardized visual training resources to support capacity building in vector and wildlife disease surveillance. The Joint FAO/IAEA Centre (Animal Production and Health Section) produced a series of teaching videos covering key procedures used in surveillance of vector-borne diseases. Three complementary modules were developed: (1) identification of major arthropod vectors of veterinary importance, including mosquitoes, biting-midges, sand flies, and ticks; (2) standardized methods for collection, sorting, and storage of vectors; and (3) field techniques for capturing and sampling wildlife groups relevant for pathogen surveillance, including wild ruminants, small rodents, carnivores, and bats. The videos were designed as practical demonstrations aligned with written Standard Operating Procedures available on the iVetNet training platform. All materials were made freely accessible through the official IAEA YouTube channel and the IAEA ZODIAC training portal. The resulting training package consists of multiple short instructional videos covering vector collection and handling, vector identification, and wildlife capture and sampling techniques. The materials combine visual demonstration with harmonized SOP-based procedures, facilitating standardized training across laboratories and field teams. Open-access distribution through online platforms enables broad international accessibility and integration into training programmes for medical and veterinary parasitology, entomology, and wildlife health, including a One Health vision. These openly accessible training resources contribute to harmonization of field and laboratory practices in vector-borne disease surveillance. By supporting standardized identification and sampling methods, they strengthen capacity for wildlife disease monitoring and integrated surveillance at the wildlife-livestock-human interface.

Molecular screening of wild carnivores in Israel uncovers widespread *Babesia negevi* and *Hepatozoon canis* prevalence

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Hemoparasite species of the genera *Babesia* and *Hepatozoon* are transmitted by arthropod vectors and infect domestic and wildlife animals. The aim of this study was to detect piroplasm and *Hepatozoon* infection is wildlife carnivores from Israel.
Animal samples were collected from wildlife carnivores trapped by the Israel Nature and Parks Authority, brought to the wildlife hospital at the Safari zoological center, or submitted for necropsy at the Kimron Veterinary Institute. PCR for the 18S *rRNA* gene of piroplasmids and *Hepatozoon* was followed by DNA sequencing.
Samples from 344 animals were collected between 2019 and 2025. These included 260 golden jackals, 35 Eurasian badgers, 22 red foxes, 8 striped hyena, 6 grey wolves, 4 porcupines, 4 Egyptian mongooses, 3 stone martens, 1 Fennec fox, and 1 caracal. In total, 137/344 (39.8%) carnivores were positive for at least one infectious agent and 11 different pathogen species were detected. Eighty-three carnivores (24.1%) were positive for *Hepatozoon canis*, including 79 jackals, 3 red foxes and 1 wolf. Twenty carnivores (5.8%) were positive for *Babesia negevi* (14 badgers, 4 jackals, 1 red fox), 8 for *Babesia banethi* (5 red foxes, 2 jackals and one grey wolf), 6 badgers for *Babesia* sp. badger type A, 3 badgers for *Babesia* sp. badger type B, 3 badgers for *Babesia* sp. badger type C, 3 jackals and 1 caracal for *Hepatozoon felis*, 3 red foxes for *Babesia vulpes*, one mongoose for *Babesia* sp. 2 BCS-2013, one stone marten was positive for *Hepatozoon martis*, and one hyaena was positive for a *Babesia* sp. which could not be fully determined. A high infection rate of 74% was found for *Babesia* in badgers, mostly with *B. negevi* (40%) which causes clinical disease in dogs. It is likely that badgers constitute a reservoir for *B. negevi*. Red foxes were infected by three *Babesia* spp. (*B. banethi* 22.7%, *B. vulpes* 13.6% and *B. negevi* 4.5%). The prevalence of *H. canis* in jackals was 30.4% and in red foxes it was 13.6%, and its probable that they serve as reservoirs for domestic dog infection. Interestingly, *H. felis* infection, was detected in jackals (1.2%) and a caracal.
Wildlife carnivores in Israel are infected with a variety of piroplasmid and *Hepatozoon* spp. and are likely to be reservoirs for domestic pet infection.

Keywords: *Babesia*, *Hepatzoon*, Badger, Golden Jackal, Red fox

Detection of zoonotic *Bartonella* species in wild canids from Israel

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Bartonella are Gram-negative bacteria transmitted by blood-feeding arthropods and carried by mammalian hosts worldwide. They are emerging pathogens at the interface of domestic, livestock and wildlife, and their occurrence among host species may serve as sentinels of zoonotic interactions in nature. In this study, we evaluated the eco-epidemiological traits of *Bartonella* infection and diversity in wild canids from Israel.

Blood samples of wild canids were collected between 2018-2025 by the Israel Nature and Parks Authority from 158 sampling sites. DNA samples were extracted and screened for *Bartonella* spp. using three loci by real-time and conventional PCR (ITS, *gltA* & *ssrA*). Each sampled individual was characterized by species, sex, season and climate zone. Climate zones were defined by hot-summer Mediterranean (Csa), hot semi-arid (BSh), and hot desert (BWh).

In total, 473 blood samples were analyzed, including golden jackals (*Canis aureus*; n = 454; 96.0%), grey wolves (*Canis lupus*; n = 7; 1.5%) and red foxes (*Vulpes Vulpes*; n = 12; 2.5%). The overall *Bartonella* prevalence was 24.9% for the golden jackals (113/454) and 33.3% for red foxes (4/12). No samples of grey wolves were found positive for *Bartonella*-DNA. Five species of *Bartonella* were detected: '*Candidatus* B. merieuxii'(*C. aureus*, 52/454, 11%; *V. vulpes*, 3/12, 25%), *B. rochalimae* (*C. aureus*, 33/454, 7.2%; *V. vulpes*, 1/12, 2.6%), *B. henselae* (*C. aureus*, 18/454, 3.9%), *B. vinsonii* subsp. *berkhoffii* (*C. aureus*, 12/454, 2.6%) and *B. bovis* (*C. aureus*, 1/454, 0.2%). Co-infection with at least two *Bartonella* spp. was detected in *C. aureus* (12/454, 2.6%). Due to the limited sample size among wild canid species, eco-epidemiological patterns related to *Bartonella* infection were primarily based on the grey jackal records. The grey jackals exhibited stable prevalence across seasons, ranging from 22.7% in winter to 30.4% in summer. The Csa zone showed more infection rate of positives (97/375, 25.9%), followed by BSh zone (14/62, 22.6%), while BWh zone did not show any positive samples (0/6, 0%). Among the golden jackals, *Bartonella* prevalence was slightly higher in females (27.3%) compared to males (22.0%).

Three zoonotic *Bartonella* species (*B. henselae*, *B. rochalimae* and *B. vinsonii* subsp. *berkhoffii*) were detected in wild canids from Israel. Similar *Bartonella* prevalence was detected in the jackals across sex, season and climate zones. The dominance of the golden jackal in both sampling and infection rates highlights its importance as a key host species for *Bartonella* circulation in the study area.

Keywords: *Bartonella*, wild canids, jackals, Israel

Babesia banethi in red foxes: description of a novel species with epidemiological and clinical data

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Red foxes represent important reservoirs of ticks and tick-borne pathogens. In this context, *Babesia vulpes* is the most commonly detected piroplasm in foxes, although key aspects of its life cycle and associated pathological abnormalities remain unknown. A second small *Babesia* sp., previously reported by PCR in foxes from the Middle East as "*Babesia* sp. MML-2014", is herein described as *Babesia banethi*. In addition, this study investigates the epidemiology of this novel species and its clinical relevance in alive red foxes from southern Italy.
The description of *B. banethi* was based on morphometric assessment of intraerythrocytic stages, coupled with sequencing of two nuclear and one mitochondrial gene targets and phylogenetic analyses. In addition, 54 red foxes were clinically examined, sampled for hemato-biochemical analyses, and screened for *Babesia* spp. by light microscopy and PCR. In addition, necropsies were performed on 20 animals. Ticks were collected from foxes and dissected for cytological detection of *Babesia* spp., as well as by PCR. Finally, disease evolution over more than one year was evaluated in a red fox naturally infected by *B. banethi*.
Sequence comparison, phylogenetic analyses and the unique morphological features (Maltese cross) confirmed that *B. banethi* is differentiated from *B. vulpes* and represents a new species. Overall, 46.3% foxes were positive for *Babesia* spp., with *B. vulpes* (42.6%) predominating and *B. banethi* detected in two sick animals (3.7%). Light microscopy showed high agreement with PCR results. Most infected foxes were juveniles and presented clinico-pathological alterations, although interpretation was limited by trauma-related conditions. In necropsied foxes, *B. vulpes* DNA was most frequently detected in brain, with merozoites observed within cerebral capillaries. Among 67 ticks collected, five species were identified, including *Ixodes kaiseri*, reported for the first time in Italy. While no stages of *Babesia* spp. were observed in tick organs, *B. banethi* DNA was detected in one *I. kaiseri*. One *B. banethi*-infected fox had debilitation, anemia and hemoglobinuria. While the imidocarb dipropionate treatment resulted in transient clinical improvement, two treatment rounds of atovaquone and azithromycin led to stable clinical recovery and PCR negativity.
These findings confirmed *B. banethi* as a distinct and clinically relevant *Babesia* species in red foxes, co-circulating with *B. vulpes* in southern Italy. The detection of *B. vulpes* in brain suggests possible tissue tropism, while the presence of *B. banethi* DNA in *I. kaiseri* raises questions regarding its vector competence. Overall, data underscore the need for integrated surveillance of fox and tick populations to better assess potential host-switching at the wildlife–domestic interface.

Keywords: *Babesia banethi*; red foxes; hematobiochemical findings; cytology

Ectoparasite Specialization Shapes *Bartonella* Circulation in Armenian Bats: Evidence from High-Throughput Pathogen Screening

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Bats and their ectoparasites form complex host-vector systems capable of maintaining diverse bacterial pathogens, yet these interactions remain poorly characterized in the Caucasus. We conducted the first high-throughput molecular survey of bacterial and protozoan pathogens in bat ectoparasites in Armenia. A total of 450 ectoparasites (mites and ticks) collected from 72 bats were pooled into 189 samples and screened using microfluidic real-time PCR targeting 43 bacterial and protozoan pathogens. The ectoparasite community was dominated by *Spinturnix myoti* and *S. psi*, showing strong host specificity to *Myotis blythii* and *Min. pallidus*. *Bartonella* DNA was detected in 34.4% of pools, whereas *Rickettsia* spp. was rare (1.1%). At the bat level, 62.5% of individuals carried *Bartonella*-positive ectoparasites. *Bartonella* prevalence varied significantly among ectoparasite taxa, with *Spinturnix* mites showing approximately 4-5-fold higher odds of infection than *Macronyssus granulosus*. Life stage was a strong predictor of infection, with adult mites far more frequently positive than immature stages. Host species, region, and sex did not significantly influence pooled prevalence. These findings highlight the dominant role of spinturnicid mites in *Bartonella* circulation within Armenian bat colonies and provide essential baseline data for understanding the ecology of vector-borne bacteria in the Transcaucasia.

Keywords: Bartonella, Bat ectoparasites, *Spinturnix mites*, Vector–host specialization, High-throughput pathogen screening

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Vector-Borne RADAR project: investigating *Orthoflavivirus* infections of wild birds in the United Kingdom

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The first mosquito-borne zoonotic virus detected in the United Kingdom (UK) was Usutu virus (USUV), in 2020. Recurrent identifications in subsequent years led to the establishment of the **V**ector-**B**orne **R**eal-time **A**rbovirus **D**etection **A**nd **R**esponse project in 2023, with the objective of investigating the emergence, transmission and impact of orthoflaviviruses affecting wild birds in the UK.
National passive surveillance of wild birds for USUV and West Nile virus (WNV) was enhanced through collaboration with wildlife rescue centres using Blackbirds (*Turdus merula*) as a sentinel species for USUV. Active surveillance was conducted on mosquitoes and migratory and resident passerines across England, supported by antibody and antigen testing including next generation sequencing for lineage characterisation. Data from avian population monitoring schemes were used to investigate possible USUV-mediated impact on susceptible host species.
Combined, results revealed a northwestern expansion of USUV range in England. However, a significant decline in the Blackbird population attributed to the virus was only observed in Greater London. Phylogenetic analyses revealed endemicity of USUV in Southeast England together with additional incursions into the UK. USUV RNA was detected in a variety of mosquito species; competence studies are required to understand their role in transmission. WNV RNA was detected for the first time in the UK, in *Aedes vexans* collected in 2023, with no subsequent detection in host or vector to date.
Integrated surveillance of host and vector improved understanding of *Orthoflavivirus* occurrence and impact in the UK, which informed government risk assessments and policy. The collective findings of USUV persistence and multiple *Orthoflavivirus* introductions into the UK in recent years highlight the growing threat from vector-borne disease in Northern Europe.

Keywords: Usutu virus, West Nile virus, Blackbird, mosquito, *Orthoflavivirus*

West-Nile virus in Red-footed falcons (*Falco vespertinus*) and Common kestrels (*Falco tinnunculus*) at the start of breeding season and pre-migratory Autumn roosting

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Red-footed falcons (RFF) and Kestrels represent migratory raptor species, sharing both breeding and foraging habitats in Eastern Hungary with high aggregation of both species at mixed breeding colonies and Autumn roosts. By comparing the seasonal infection rates of West-Nile virus (WNV) in a trans-Saharan migrant (RFF) and a short-range migrant (Kestrel) we aimed to assess their epidemiological roles, and overall potential for the transmission and spread of WNV and additional infectious agents.
WNV infection prevalence was assessed in birds at pre-migratory roosts and after their return to breeding grounds in spring. Adult birds were captured and sampled at the beginning of their breeding season at nesting sites and in September at Autumn roost sites. Blood samples were tested for WNV by qPCR and for Plasmodium and Haemoproteus infections by nested PCR. On-site WNV circulation was monitored through the testing of mosquitos captured near Autumn roost sites.
From the 28 Kestrels and 31 Red-footed falcons sampled at the 2023 Autumn roost 2 and 3 tested WNV positive, while 10 and 4 were infected with haemoparasites respectively. At the 2025 Autumn roost we sampled 1 infection free Kestrel and 37 Red-footed falcons detecting 5 WNV infected birds and demonstrating 72.7% haemoparasite prevalence. The 24 Kestrels and 15 Red-footed falcons sampled at the beginning of the 2025 breeding season all tested negative for WNV and showed 85.7% and 78.6% haemoparasite prevalence respectively. All mosquitoes captured at the study site in September 2023 and 2024 tested WNV negative.
High amplitude fluctuations in weather conditions and prey base at the steppe habitat caused extreme yearly variations in host and mosquito vector populations at our study site effectively hindering the 2024 roost. Nevertheless, WNV infections emerged at the Autumn roosts of 2023 and 2025 indicating the potential of seasonal, mixed species avian population aggregations for local WNV amplification. However, the absence of WNV at the beginning of the breeding season suggests the lack of high distance WNV introductions by these two small falcon species. Our study also demonstrates the direct and indirect epidemiological effects of environmental and climatic fluctuations on pathogen emergence.

Keywords: Red-footed falcon, Kestrel, West-Nile virus, haemoparasite, mosquito

Funding source / Acknowledgement: This research was funded by the Grant for Wildlife Health Research and Education in Eastern Europe, research grants TKP-2021-EGA-01 and the National Laboratory for Health Security grant RRF-2.3.1-21-2022-00006.

An overlooked ectoparasite at the urban human-avian interface: pathogens in the Common House Martin Bug

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The Common House Martin Bug (*Cimex hirundinis,* homotypic synonym: *Oeciacus hirundinis*) is a haematophagous ectoparasite primarily of the Common House Martin (*Delichon urbicum*), a migratory bird frequently nesting on human dwellings. This close association creates a direct interface between wildlife and humans, yet the role of this ectoparasite in pathogen maintenance remains poorly understood. We investigated host-feeding patterns and pathogen carriage in *C. hirundinis*.
Parasites (n=80) were collected from four nests in two urban locations in Hungary. Insects were morphologically and molecularly identified and analyzed in pooled samples. Blood-meal sources were determined using PCR targeting vertebrate mitochondrial DNA. Samples were screened for avian haemosporidians (*Plasmodium*, *Haemoproteus*), *Trypanosoma* spp., and selected arboviruses (West Nile, Usutu, Sindbis) using PCR assays and Sanger sequencing.
Blood-meal analysis revealed consistent feeding on both Common House Martins and humans across all nests, providing molecular evidence of opportunistic host use at the human-avian interface. Haemosporidian DNA was detected in all pools, with three *Plasmodium* lineages identified: *Plasmodium elongatum* (GRW06), *Plasmodium relictum* (SGS1), and a lineage (ACCTAC01) likely associated with African transmission cycles. Additionally, *Trypanosoma culicavium* was detected in two pools. All samples tested negative for West Nile, Usutu, and Sindbis viruses.
We provide the first molecular evidence of avian *Plasmodium* and *Trypanosoma* in *C. hirundinis*, including the first report of *Plasmodium* in the *Cimicidae* family and the first confirmation of human blood-feeding by this species. These findings suggest a previously unrecognized role of nest-dwelling ectoparasites in pathogen maintenance at the human-avian interface.

Keywords: avian ectoparasites, Haemosporidians, *Trypanosoma*

Funding source P.K.'s work is supported by the NKKP_STARTING-152282 project (with the support of the Ministry of Culture and Innovation from the National Research Development and Innovation Fund) and the Bolyai János Research Grant of the Hungarian Academy of Sciences.

Mosquito vectors of *Setaria tundra*: an emerging threat to wildlife health in Serbia

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Parasitic nematodes that adversely affect animal health in Serbia have been documented in numerous studies and clinical reports, with primary attention given to two *Dirofilaria* species (*D. repens* and *D. immitis*). During surveillance aimed at detecting these parasites in mosquito vectors in the Vojvodina Province (northern Serbia), *Setaria tundra*, previously unrecorded in Serbia, was identified incidentally. This parasitic nematode was detected at two sites, Mali Iđoš (North Bačka County) and Iđoš (North Banat County), in two mosquito vector species: *Aedes caspius* (collected in late July 2021 at Mali Iđoš) and *Aedes vexans* (collected in mid-August 2021 at Iđoš). Animal species of the Cervidae family serve as the primary hosts of *S. tundra*. Considering its documented presence in neighboring countries on one side and its impact on cervid populations, an increased attention to this parasite, its hosts and vectors in Serbia, is warranted. Clinical manifestations of setariosis typically include fever, weight loss, and general weakness, but severe outcomes such as fibrinous perihepatitis and peritonitis may occur, especially in calves, which are particularly susceptible. Despite its veterinary importance, available data on *S. tundra* remain scarce in Serbia.

Therefore, the aim of this study is to provide a more comprehensive understanding of the key elements involved in the transmission cycle of *S. tundra*. The results of mosquito monitoring obtained at 65 locations in Vojvodina Province from 2014 to 2025 with the special focus to the distribution and abundance of *Ae. vexans* and *Ae. caspius* will be presented. Both species are floodwater mosquitoes whose life cycles are closely related to river water levels. They are native to Serbia and particularly abundant in spring, when flooding of main lowland rivers occurs.

This research also examines the overlap between mosquito vectors and cervid hosts distribution, highlighting areas of co-occurrence. The findings emphasize the importance and need of continual surveillance and further epidemiological and ecological investigation of *S. tundra* in Serbia.

Keywords: *Aedes vexans, Aedes caspius,* cervids, mosquitoes, parasitic nematodes

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Vector tick species and mammal reservoirs for emerging tick-borne Yezo virus

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Yezo virus (YEZV) is an emerging tick-borne orthonairovirus first reported in 2021 from Hokkaido, the northernmost region of Japan. YEZV infections causing acute febrile illness are reported in Hokkaido and northeastern China. Despite its public health significance, the maintenance mechanism of YEZV in nature remains largely unknown. To anticipate disease occurrence, we aimed to reveal the high-resolution spatial distribution of YEZV and the natural vertebrate reservoirs.
In 2024, ticks were collected with a constant effort at 171 sites in the central part of Hokkaido (an east-west length of 124 km and a north-south length of 209 km, approximately), followed by screening for YEZV. Potential suitable habitat of YEZV was predicted with a resolution of 1 × 1 km using generalized linear model. In 2025, we selected eight sites from areas where the presence of YEZV was predicted to be highly likely and performed small mammal trapping. In addition to the animals captured in 2025, a retrospective screening was performed on small mammals collected across Hokkaido in 2023.
In 2024, a total of 9,908 ticks were collected and YEZV was primarily detected in *Ixodes persulcatus* and *Ixodes ovatus* ticks. The model based on the environmental variables successfully predicted areas of high infection risk with acceptable predictive performance. A total of 420 small mammals (284 from 2025 and 136 from 2023) were screened, consisting of 252 mice, 121 voles, and 47 shrews. Anti-YEZV antibodies were detected in 14 of 198 rodent serum samples. YEZV RNA was detected in 11 mice and five shrews, while all voles tested negative. Infectious virus was detected from multiple organs and serum of *Apodemus speciosus* mouse and *Sorex gracillimus* shrew, indicating that these mammals serve as a source of infection for feeding ticks. Phylogenetic analysis revealed close relationships among YEZV isolates from mammals, ticks, and those from previously reported human cases.
Our intensive tick collection revealed the high-resolution (1 × 1 km) distribution of emerging tick-borne YEZV. The detailed distribution data enabled us to prioritize sites for wild animal surveys. Subsequent investigations demonstrated that wild mice and shrews serve as natural reservoirs. This study highlights the effectiveness of comprehensive field observation and ecological analysis for the epidemiological understanding of emerging tick-borne infectious diseases.

Keywords: tick-borne orthonairovirus, emerging infectious disease, *Ixodes* tick, small mammal, ecological niche modelling

Integrated biodiversity monitoring in a Crimean-Congo hemorrhagic fever virus circulation zone in the South of France

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For a few decades, One Health movement has been emphasizing the need to open epidemiology to environmental dimensions. In the scope of (re)-emerging diseases, the ecological study of host-vector-pathogen interactions in their environment became crucial. Crimean-Congo hemorrhagic fever virus (CCHFv) is a vector-borne virus for which ticks of the *Hyalomma* genus are considered the main vectors. In mainland France, this virus was first detected in *Hyalomma marginatum* ticks in 2023. Infected non-human animals are asymptomatic, yet they may act as virus or tick population amplifiers and thus are of particular interest for CCHFv circulation monitoring. *Hyalomma marginatum* is a two-host tick species whose adult stages are well known to largely feed on domestic ungulates, especially cattle. However, there is a gap of knowledge regarding the role played by other wild ungulates in CCHFv or tick population dynamics in France. In the context of CCHFv spread in the Mediterranean basin, there is a need to understand CCHFv circulation mechanisms on a fine scale, as it seems to be highly dependent on local environmental features. To this end, we deployed a combination of different methods to monitor animal host and vector populations in the South of France (Pyrénées-Orientales) with the objective to better understand the ecology of the disease and to identify "at risk conditions/zones" for the virus to emerge/spread. We investigated the locally available host communities for the larvae and nymphs of *Hyalomma* ticks (birds) as well as for the adults (large mammals). Bird species abundance and density were estimated with the point-count method during spring and autumn. In addition, wild ungulate densities were assessed through the systematic deployment of camera traps, following the Random Encounter Model method. Moreover, a sampling network with hunter associations was engaged to widely collect blood and tick samples from wildlife. Furthermore, we assessed the tick community with the dragging method to monitor *Hyalomma marginatum* population and its representativity among other tick species. Finally, in order to study host-vector interactions, we simultaneously collected ticks from locally captured birds, from cows grazing on the site, and from game species thanks to our collaboration with hunters. The combination of the diverse methods we employed, coupled with close collaboration with hunters and other local stakeholders, has enabled us to establish an integrated working network based on "One Health" principles that could be replicated in other areas of CCHFV circulation.

Keywords: Crimean-Congo hemorrhagic fever, *Hyalomma marginatum*, ticks, biodiversity monitoring, hosts

Session 3

Vectors and vector-borne diseases in wildlife

Poster Presentations

P034. Does biodiversity buffer tick-borne pathogens? A systematic review of empirical evidence

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Unprecedented rates of biodiversity loss and infectious disease (re)emergence have prompted an upsurge of research in disease ecology. The dilution effect theory (DET) was developed to describe the relationship between biodiversity and infectious disease dynamics; higher biodiversity is expected to reduce pathogen transmission among competent hosts. Despite over two decades of research on the DET, conflicting evidence makes it difficult to reach a consensus. With Lyme borreliosis (LB) being the primary case study for DET, studies have largely focused on North American and European ecosystems, often overlooking other host-tick-pathogen systems. This review seeks to systematically gather existing empirical evidence on the DET effect on tick-borne pathogen (TBP) dynamics, with an emphasis on multi-pathogen systems and the effect of methodological differences on result validity.

A systematic review was conducted following the Collaboration for Environmental Evidence (CEE) guidelines and standards. Searches were conducted in May 2025, without temporal or spatial restrictions. The search string consisted of three concept blocks: community metrics, TBPs and tick genera. Consulted databases included Web of Science, Pubmed and Scopus. A strict quality appraisal was performed in accordance with CEE guidelines.

Of 30,149 records, 31 passed both screening stages, of which 18 met quality criteria for analysis. Studies were conducted in the United States (12), Canada (4), Belgium (1) and Germany (1). Of 15 studies which reported sampled tick species, *Ixodes* sp. predominated, with *Ixodes scapularis* (8), *Ixodes pacificus* (5) and *Ixodes ricinus* (2) being the most frequent. Pathogens assessed included *Borrelia burgdorferi* sensu lato (15 studies), *Anaplasma phagocytophilum* (4), *Babesia* spp. (3), *Borrelia miyamotoi* (1) and *Rickettsia* spp. (1). Seven studies investigated multiple pathogens and/or genotypes. Evidence of dilution was reported in 8 cases (3 weak), amplification in 7, no effect in 10, and mixed effects in one. Outside of LB, only two instances of dilution were identified, both classified as weak, whereas amplification was observed once and no effects in 7 cases. All dilution events were recorded in northeastern North America.

Evidence remains inconsistent, with dilution and amplification reported for LB, whereas other TBPs show no clear relationships. Importantly, all dilution events were geographically clustered, limiting the generality of the DET. In addition, methodological heterogeneity challenges comparisons and the validity of results. Our findings suggest that focusing on community-level traits may be more informative than biodiversity *per se*.

Keywords: dilution effect, tick-borne pathogens, biodiversity, disease ecology

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P035. Circulation of Tick-Borne Pathogens in wildlife-derived ticks form North-Eastern Italy

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Tick-borne pathogens represent a growing concern for both animal and human health, yet their circulation within wildlife communities remains partially understood. This study describes the occurrence of main tick-borne pathogens in ticks collected from wild animals in northeastern Italy between 2024 and 2025.
Ticks were collected in Veneto and Trentino Alto Adige regions, from wildlife submitted for necropsy by local authorities. Ticks were morphologically identified and then processed for molecular detection of *Anaplasma phagocytophilum*, *Rickettsia* spp., *Borrelia* spp., *Babesia* spp. and tick-borne encephalitis virus (TBEV).
A total of 536 ticks were collected from 8 wild host species, including ungulates, carnivores, and wild boar. Ticks were predominantly identified as *Ixodes ricinus* (99.3%), with a marginal presence of *Ixodes hexagonus* (2 ticks), *Haemaphysalis punctata* (1 tick) and *Rhipicephalus sanguineus* (1 tick). Hosts included wolves (151 ticks), alpine chamois (117 ticks), red deer (84 ticks), roe deer (82 ticks), golden jackal (70 ticks), red fox (25 ticks), alpine ibex (4 ticks) and wild boar (3 ticks).
Anaplasma phagocytophilum was the most prevalent pathogen (41%; 159/388), detected across seven host species, showing positive results in ticks from wolf (15%; 21/140), golden jackal (57.9%; 33/57), chamois (62.4%, 63/101), roe deer (39.1%; 18/46), red deer (86.4%; 19/22), ibex (100%; 4/4) and wild boar (33.3%; 1/3). *Rickettsia spp*. (16.3%; 63/387), *Borrelia spp*. (4.6%; 19/415) and *Babesia spp.* (7%; 27/387) were also detected in ticks from 7, 4 and 6 host species respectively. Notably, TBEV was identified only in a single tick collected from a golden jackal (0.24%; 1/420), although TBE is considered endemic in this area.
These findings describe a complex multi-host epidemiological context, evidencing a heterogeneous distribution of tick-borne pathogens in ticks across wildlife species. Data on pathogen distribution among host species, combined with information on host population dynamics and management, can provide valuable insights into which species are most effective for early detection and surveillance, as well as which may play a key role in the epidemiological cycle.

Keywords: *Anaplasma phagocytophilum*, *Rickettsia* spp., *Borrelia* spp., *Babesia* spp., TBEV

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P036. Composition and geographical distribution of wild ungulate-associated tick species in Catalonia, northeastern Spain

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Ticks are hematophagous arthropods that parasitize terrestrial vertebrates and transmit pathogens, representing a growing public health concern. Although numerous studies have been conducted across Europe, information on the distribution and composition of tick species in Catalonia remains limited. Given the role of wild ungulates in sustaining tick populations and facilitating pathogen circulation, this study aimed to characterize tick species, spatial patterns, and host associations across Catalonia to guide surveillance and management strategies.

The study was conducted in Catalonia (41° 35' 28.172'' N, 1° 31' 15.105'' E), north-eastern Spain. Between March 2023 and December 2025, 998 wild ungulates that were hunted were sampled for ticks, including *Cervus elaphus*, *Capreolus capreolus*, *Capra pyrenaica*, *Dama dama*, *Ovis aries musimon*, *Rupicapra p. pyrenaica*, and *Sus scrofa*. Geographic distribution maps were generated using QGIS software to depict the occurrence of each tick species at the county (*Comarca*) level.

A total of 5,888 ticks were collected, of which 5,640 were identified to the species level. Eight species from five genera were detected: *Dermacentor marginatus*, *Haemaphysalis punctata, Haemaphysalis sulcata*, *Hyalomma lusitanic*um, *Hyalomma marginatum*, *Ixodes ricinus*, *Rhipicephalus bursa* and *Rhipicephalus sanguineus*. Tick species exhibited heterogeneous spatial patterns across Catalonia. *I. ricinus* was widely distributed across northern and central counties, particularly in mountainous areas, while *D. marginatus* occurred across most sampled regions. In contrast, *Haemaphysalis* and *Hyalomma* species were more localized, primarily restricted to northwestern and central coast areas, and some southern counties. *Dermacentor marginatus* and *R. sanguineus* were predominantly collected from wild boar, accounting for most infestations in this host. *Ixodes ricinus*, *R. bursa*, and *H. punctata* were more frequently associated with cervids and other ruminants. *Hyalomma spp. and H. sulcata* were detected only sporadically, with low prevalence across hosts.

This study provides the first comprehensive assessment of tick species composition, spatial distribution, and host associations on wild ungulates across Catalonia. The heterogeneous distribution of ticks and differences in host associations highlight the ecological complexity of tick–host interactions in the region. These findings provide baseline data to assess the potential risk of tick-borne pathogens and support targeted management strategies aimed at reducing tick exposure at the wildlife-domestic-human interface.

Keywords: ticks, wild ungulates, Catalonia, host associations, spatial distribution.

P037. An overlooked hotspot of *Babesia/Theileria* circulation in deer from the Western Balkans

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Wild cervids play a central role in tick-borne pathogen (TBP) ecology, yet protozoan TBPs in wildlife from the Western Balkans remain largely unexplored. This study reveals a strong epidemiological signal in deer populations from northern Serbia (Western Balkan region).
A total of 99 samples (blood, spleen, ticks) collected from deer (*Cervus elaphus*) across three regions of Vojvodina (Bačka, Banat, Srem) were analyzed using PCR targeting the 18S rRNA gene of *Babesia/Theileria* spp.
Babesia/Theileria DNA was detected in all regions, with a strikingly high prevalence in Banat (31/36; 86.1%), compared to Srem (14.1%) and Bačka (10.3%). Positive findings were predominantly detected in blood samples, while ticks showed minimal detection and spleen samples were negative. Several randomly chosen samples were Sanger sequenced and the nucleotide sequences have shown 90-100% identity to *Theileria capreoli* isolates from GenBank database.
These findings identify Banat as a previously unrecognized hotspot of *Babesia/Theileria* circulation in wild cervids. The high percentage of positive findings in blood suggests active infections rather than incidental exposure. The exceptionally high prevalence detected in Banat suggests a localized and potentially stable wildlife transmission system, with deer likely contributing to the maintenance of *Babesia/Theileria* circulation. From a One Health perspective, this hotspot may represent an underappreciated source of tick-borne pathogen circulation with potential implications for domestic animals and humans.

Keywords: *Babesia/Theileria*, deer, wildlife reservoir, tick-borne pathogens, One Health, Western Balkans

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P038. Co-circulation of epizootic haemorrhagic disease virus and bluetongue virus in wild ruminants in Catalonia (NE Spain)

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Epizootic haemorrhagic disease virus (EHDV) and bluetongue virus (BTV) are closely related Culicoides -borne orbiviruses of major veterinary importance. We investigated temporal and spatial patterns of EHDV and BTV in wild ruminants from Catalonia, northeastern Spain.
A total of 2,936 wild ruminants were-analyzed between 2023 and 2025 through active and passive surveillance across Catalonia. Serum samples were screened using competitive ELISAs for antibodies against BTV (n = 2,834) and EHDV (n = 2,095), while lymph node and spleen tissues were tested by RT-qPCR for molecular detection of both viruses (n = 551). Sampled species included-all wild ruminant species present in Catalonia.
Molecular and serological evidence confirmed co-circulation and co-infection of BTV-8 and EHDV-8 across the study period. Viral RNA was detected in several host species, with the highest PCR positivity observed in red deer (*Cervus elaphus*) (30.2% BTV; 24.4% EHDV) and fallow deer (*Dama dama*) (16.2% and 10.8%, respectively). Co-infection was detected in red deer (16.86%) and fallow deer (5.4%). On the other hand, PCR positivity was only detected sporadically in mouflon (*Ovis a. musimon*), roe deer (*Capreolus capreolus*), and Pyrenean chamois (*Rupicapra pyrenaica*). Temporal analyses revealed an initial absence followed by a steady rise in molecular detection from 2024, peaking in the second semester of 2024. Serological results indicated broader exposure for both viruses, again highest in red deer (22.6% for EHDV; 32.5% for BTV), followed by fallow deer (13.9% and 20%, respectively). Passive surveillance confirmed characteristic orbiviral lesions associated with EHDV and BTV in red deer (n=2) and mouflon (n=1) found dead in summer 2024.
Wild ruminants in Catalonia were broadly exposed to and infected by both EHDV-8 and BTV-8 from late 2023 to 2025, consistent with orbivirus co-circulation in livestock and widespread regional circulation. EHDV positivity represents the first detection of EHDV in wild ruminants from Catalonia. Notably, EHDV seropositivity was detected as early as November 2023, supporting silent circulation in wildlife in the previous vector season of 2023-2024. Red deer emerged as the most informative and sensitive sentinel species for tracking BTV and EHDV circulation. These findings highlight the need for further studies to improve understanding of EHDV-8 epidemiology to inform surveillance, control, and vaccine development strategies.

Keywords: EHDV, BTV, arbovirus, wildlife, Spain

P039. Using amplicon-based next-generation sequencing for detection of vector-borne bacteria and parasites in Danish roe deer (*Capreolus capreolus*)

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Climate change is expected to alter the distribution and activity of arthropod vectors, potentially increasing the emergence, spread and impact of vector-borne pathogens in wildlife populations in northern regions. Danish roe deer (*Capreolus capreolus*) have experienced prolonged increased mortality associated with a "roe deer diarrhea and wasting syndrome", characterized by severe emaciation, chronic diarrhea, and population decline, although the etiology remains unclear. Hunting yield data indicate that populations at the national level peaked around 2009–2010, followed by a marked decline, particularly in eastern Denmark. Notably, the decline has not stabilized over time but instead appears to be spreading geographically.

The aim of this study was to apply amplicon-based next-generation sequencing (NGS) to detect vector-borne bacteria and parasites in Danish roe deer, to evaluate temporal patterns in pathogen occurrence, and to investigate potential associations between pathogen presence and "roe deer diarrhea and wasting syndrome".

Spleen samples from 270 roe deer were collected as part of the Danish Passive Wildlife Disease Surveillance Program during the period of 2014-2023. The samples were screened using amplicon-based NGS for detection of pathogenic vector-borne bacteria and parasites.

Genes for six vector-borne pathogens - *Bartonella* spp., *Anaplasma* spp., *Babesia* spp., *Treponema* spp., *Setaria* spp., and *Hepatozoon* spp. were identified in the roe deer spleen samples. Results were analysed together with animal data to assess associations between pathogen presence and "roe deer diarrhea and wasting syndrome", including analyses of impact of co-infections with multiple pathogens.

The results provide insight into the occurrence and prevalence of vector-borne pathogens in Danish roe deer and establish a baseline for future investigations into their pathogenic potential. The multi-pathogen detection approach will help clarify whether vector-borne pathogens are associated with "roe deer diarrhea and wasting syndrome" and local population decline and whether they act as primary, contributing, or secondary agents. Furthermore, the approach can be applied for screening for emerging and zoonotic vector-borne pathogens in deer.

Keywords: vector-borne, wildlife disease surveillance, NGS, roe deer diarrhea and wasting syndrome

Funding source: This work was supported by The Danish Hunters' Nature Foundation (Jægernes Naturfond) and The Danish Environmental Protection Agency and The Danish Agency for Green Land Use and Water Environment.

P040. Seroprevalence of West Nile infection in wild mammals: wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*) populations just before the emergence of the first WNV epidemic in Serbia

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West Nile virus (WNV) is a neurovirulent mosquito-borne *Flavivirus* with zoonotic potential, maintained in nature in an enzootic transmission cycle between avian hosts and ornithophilic mosquitoes. The virus occasionally infects other vertebrates, including humans and horses, in which it may cause sporadic disease outbreaks with potentially fatal outcomes. In Europe, WNV has been present for decades. Until 2004, only lineage 1 strains circulated, whereas lineage 2 subsequently emerged in multiple countries, became locally endemic, and spread rapidly across the continent. Consequently, the number, frequency and severity of outbreaks with neurological consequences for birds, humans and horses increased dramatically throughout Central and Southern Europe, including Serbia, posing a significant veterinary and public health problem.

In Serbia, WNV was detected in mosquitoes in 2010 and subsequently in humans and birds in 2012. Evidence of WNV circulation had previously been demonstrated through serological investigations in healthy backyard pigs sampled during 2006/2007 and horses sampled during 2009/2010. To assess WNV circulation in Serbia, the presence of WNV specific antibodies was tested among free living mammals geographically widely distributed during the 2011/2012 hunting season, coincidentally one season before the first human clinically evident WNV epidemic. Serum samples were obtained from 333 wild boars from 53 hunting grounds located on the territory of 13 (6 at north, 2 at central and 5 at south part of Serbia) out of 25 districts of Serbia and from 91 roe deer in 30 hunting grounds located on the territory of 5 districts of Serbia (all located at the northern part of country) that were tested for the presence of WNV antibodies by ELISA and viral neutralization test (VNT). The specificity of their reactivity was assayed against Usutu virus (USUV). Seropositive ELISA results were obtained in 56 (16.82%) wild boars and 20 (21.98%) roe deer. Most of the samples positive for WNV antibodies were detected at the northern or central north part of the country. Of these, 33 (59%), and 4 (23.5%) respectively, neutralized WNV. Cross-neutralization analysis demonstrated that all roe deer neutralizing sera were WNV specific. Among wild boar sera, 84.4% were WNV specific and in 15.5% were nonspecific. Four wild boar sera showed USUV specificity of detected antibodies. These data confirmed the intensive circulation of WNV and USUV in Serbia just a season before the first human WNV epidemic in 2012 in Serbia and was one of the triggers for the establishment of an integrated WNV surveillance program.

Keywords: West Nile, wild boar (*Sus scrofa*), roe deer (*Capreolus capreolus*), WNV serology, prevalence, zoonosis, Serbia

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P041. Serological survey of West Nile virus antibodies in domestic donkeys in Vojvodina, Serbia

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West Nile virus (WNV) is an important mosquito-borne zoonotic pathogen and is one of the most spread arboviruses in the world. Humans and equids are susceptible to WNV infection and act as dead-end hosts. Equids are frequently used as indicators of virus circulation. Donkeys may represent a useful sentinel population, especially in areas where continuous monitoring of WNV activity is needed. The objective of this study was to evaluate WNV IgG seropositivity in a donkey population sampled over three consecutive years, from 2022 to 2024, and to describe serological patterns in relation to year, age group, and repeated sampling.

A total of 164 serum records from donkeys sampled between 2022 and 2024 were included in the analysis, corresponding to 112 unique animals. Repeated samples were available for 52 animals tested in more than one year. Samples were classified according to year, sex, age group, and final WNV IgG ELISA result. Age was categorized into three groups: ≤6 months, >6 months – <5 years, and ≥5 years. Animals aged ≤6 months were considered separately because maternally derived antibodies may influence IgG serological interpretation.

WNV IgG antibodies were detected in all three study years. In 2022, 39 animals were IgG-positive and 14 were negative. In 2023, 27 animals were positive and 14 were negative, while in 2024, 30 animals were positive and 40 were negative. Seropositive animals were present in all age groups, but most positive results were recorded in animals aged ≥5 years. Among animals aged ≤6 months, both positive and negative results were observed. Several animals that were IgG-positive at age of 6 months later tested negative at age of 12 months, suggesting transferred maternally derived antibodies and that seropositivity in this age group should be interpreted cautiously. Longitudinal observations showed that many adult animals remained IgG-positive across repeated samplings, while a smaller number changed from WNV IgG-positive to negative or remained WNV IgG-negative.

Hight seroprevalence rate detected in the examined donkey population throughout the three-year consecutive period, indicating previous exposure and endemic presence of WNV in the region. The observed seroprevalence and persistent IgG seropositivity in repeatedly sampled adult animals supports the value of donkeys as sentinel animals for WNV circulation and relevance for WNV surveillance. However, the seropositivity in young animals emphasize the importance of considering age and possible maternal antibodies presence when interpreting serological findings.

Keywords: West Nile virus, donkeys, IgG, serology, surveillance

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P042. West-Nile virus circulation and impact monitoring of hosts and vectors at Northern Goshawk (*Astur gentilis*) breeding habitats

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West Nile virus (WNV) lineage 2 strains have been persistently circulating in Hungary over the past two decades. During this period, we documented the high susceptibility of Northern Goshawks (*Astur gentilis;* formerly *Accipiter gentilis*) to lineage 2 WNV infection, resulting in significant numbers of both clinical disease and mortality cases. High fluctuations in Hungarian breeding Goshawk populations were also registered simultaneously. However, the extent to which WNV circulation and vector activity contribute to these population changes remains unclear. In order to obtain direct evidence on the effect of vector activity and WNV circulation on the Goshawk population, we devised a pilot study in an area used by a comparatively high number of Goshawk breeding pairs during the 2026 Goshawk breeding and WNV transmission season.
A study area was designated around the village of Piliscsaba, North-West of Budapest, in a hilly, wooded area with multiple Goshawk breeding pair home ranges. A centrally located mosquito trapping site has been set up, with a May to August biweekly trapping regimen. Identified and pooled mosquitoes are tested for WNV by qPCR. Multiple Goshawk breeding pairs were identified, and nestlings are ringed with both standard ornithological and colour-coded rings. Active surveillance includes cloacal and pharyngeal swabbing and blood sampling of nestlings for WNV testing by molecular and serological methods. Passive monitoring of Goshawk mortality and clinical cases has been organized in the wider study area, through two regional wildlife rescue-centres. All clinically and post-mortem processed Goshawk cases are also to be sampled and tested for WNV. Integrated epidemiological analysis of population and WNV surveillance data obtained from Goshawks and mosquitos will be performed.
Ongoing data collection will continue until the end of the 2026 Goshawk breeding and WNV transmission season. WNV infection prevalence in mosquitoes and the WNV exposure rate of the Goshawk population will be evaluated. Combined analysis of reproductive success, population monitoring, vector activity, and virological data is expected to improve understanding of the impact of WNV circulation on Goshawk populations and the in-situ population effects of WNV, supporting future surveillance, risk mitigation, and conservation efforts.

Keywords: Goshawk, mosquito, West-Nile virus, monitoring, risk

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P043. Longitudinal serological dynamics of Bagaza virus in red-legged partridges from southern Portugal: insights from integrated analyses at population and individual level

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Bagaza virus (BAGV) emerged in southern Portugal in 2021, associated with an outbreak (September-October) in red-legged partridge (*Alectoris rufa*). Taking advantage of an ongoing capture-mark-recapture program initiated in 2019, we generated a unique longitudinal dataset on virus-specific antibody dynamics at both population and individual levels. Here, we integrate these data to better understand exposure dynamics, antibody trajectories and the persistence of this emerging virus in a wild bird population in Europe.
Red-legged partridges were captured every two months from 2021 to 2025. All individuals were ringed, and blood samples collected. Seroneutralization assays were performed to detect BAGV specific antibodies. To estimate population-level seroprevalence, around 40 randomly selected individuals per sampling period were analysed. Additionally, individuals with at least one recapture event (n=265) were selected for longitudinal monitoring to reconstruct antibody trajectories, including seroconversion/seroreversion, antibody waning and potential reinfection events.
Overall population-level seroprevalence was 9.98% (107/1072), peaking after the outbreak in November 2021 (28.9%; 24/83) and remaining at low levels thereafter. Among recaptured individuals, 45 showed at least one BAGV antibody detection. Longitudinal analysis of antibody titres revealed multiple seroconversion and/or reinfection events following the 2021 BAGV outbreak. In contrast, only one individual showed evidence of seroreversion after a two-year interval. Additionally, two individuals exhibited a shift from BAGV-specific to West Nile virus-specific antibodies. In 21 cases, antibody responses became indistinguishable from other orthoflaviviruses and were classified as undetermined flavivirus.
Despite the decline in population-level seroprevalence, evidence of ongoing seroconversion and reinfection in captured individuals indicates continued low-level BAGV circulation and likely overwintering in Portugal. Whether this circulation is sufficient to maintain herd immunity and prevent future outbreaks remains unclear. Orthoflavivirus co-circulation, and in turn potential cross-reactivity and cross-protection between WNV and BAGV, warrants further long-term monitoring and possibly in vivo studies to better understand virus evolution and host immunity dynamics of this emerging pathogen in Europe.

Keywords: *Orthoflavivirus bagazaense*, *Alectoris rufa*, Serological surveillance, Capture-Mark-Recapture

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P044. Haemosporidian infections in alpine bird communities of the Cantabrian Mountains, Spain

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Vector-borne haemosporidian parasites (*Plasmodium*, *Haemoproteus*, and *Leucocytozoon*) are important threats to wild bird populations. Among them, avian malaria caused by *Plasmodium* spp. has been associated with severe population declines and extinctions of ecologically important species. Mountain ecosystems are particularly vulnerable to global change, as they host highly specialized and sensitive species, with bird populations declining across European ranges. Climate-driven shifts in vector distribution and seasonal activity may increase pathogen transmission risk in these systems. Here, we assessed the presence of haemosporidian parasites in alpine bird communities of the Cantabrian Mountain Range (northern Spain).

Between 2012 and 2025, we collected 220 blood samples from seven passerine and one corvid species across Picos de Europa National Park, Las Ubiñas-La Mesa Natural Park, and Babia y Luna Natural Park. Detection of parasite DNA was performed using real-time PCR followed by nested PCR assays and Sanger sequencing to differentiate haemosporidian genera and species.

Of the 220 samples analyzed, 33 yielded positive results, corresponding to an overall prevalence of 15.0% (95% CI: 10.9-20.3). The highest prevalence was observed in *Prunella collaris* (33.3%; 23/69), followed by *Oenanthe Oenanthe* (14.3%; 1/7), *Phoenicurus ochruros* (12.5%; 2/16), *Montifringilla nivalis* (5.1%; 6/117), and *Monticola saxatilis* (5.0%; 1/20). Significant differences in prevalence were detected among *P. collaris* and *M. nivalis* (Fisher's exact test, $p < 0.001$). Most infections corresponded to *Haemoproteus* spp. (n = 30), detected across multiple hosts species and study sites. *Leucocytozoon* spp. was identified in one *M. nivalis,* whereas *Plasmodium relictum* was detected in one *P. ochruros* and one *O. oenanthe*.

This study provides a first assessment of haemosporidian infections and the first report of *P. relictum* in alpine bird communities of the Iberian Peninsula. Differences in prevalence and parasite composition among species may reflect variation in host ecology, particularly altitudinal and latitudinal movements that increase exposure to vectors, as well as differences in susceptibility. These findings raise concern about the potential establishment of avian malaria in fragile high-altitude systems and its possible implications for the conservation of already declining alpine bird species.

Keywords: alpine birds, avian malaria, Cantabrian Mountains, Haemosporidians, *Plasmodium*.

P045. Genomic content in avian haemosporidian parasites suggests co-regulation of apicoplast and mitochondrial nucleoids

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Precise quantification of the parasitic load during infections is necessary for the deep understanding of parasite-host interactions. Haemosporidians, an order of intracellular blood parasites, including agents of avian malaria and their closer relatives, have two organelles, remnants of endosymbiosis: the mitochondrion and the apicoplast, which have their own extranuclear genomes (nucleoids). While the number of organelles per parasitic cell appears to be stable, the number of their nucleoids is not, but the dynamics and factors affecting them remains to be elucidated.
We used a set of 71 blood samples of migratory birds infected by haemosporidian parasites to quantify relative DNA quantities of these two organelles through real-time quantitative PCR (qPCR). We investigated the congruence of these two parameters with the microscopically detected number of parasites, for all samples measured and for the subset of those with moderate to high parasitaemia.
We found that apicoplast DNA content was a better predictor for intermediate infection intensities, while mitochondrial DNA content was a better predictor when considering all stages of infection. The difference may result from the regulation of parasite intra- and inter-organellar genomic content throughout the infection stages in vertebrate hosts. When used together, they could explain 89% of the variation of microscopically detected parasitaemia.
Avian haemosporidian seems to regulate mitochondrial and apicoplast replication in a coordinated fashion and in a non-linear way. Our work contributes to the established and new methods for quantification of blood parasites in wildlife and to the understanding of their development and conservation relevant consequences for the avian hosts.

Keywords: avian malaria, qPCR, organellar regulation, real-time PCR, genomic quantification

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P046. Low Prevalence of Haemosporidian Parasites in *Phylloscopus* Warblers in Armenia

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Haemosporidian parasites are widespread blood parasites of wild birds, with prevalence varying significantly across host species and geographic regions. Previous studies from the Caucasus region indicate that infection rates in *Phylloscopus* warblers differ among species, suggesting that host identity is a key determinant of parasite prevalence. This study aimed to assess the prevalence and diversity of haemosporidian parasites in *Phylloscopus* warblers in Armenia.

A total of 69 individuals were examined, including 65 *Phylloscopus collybita menzbieri* and 4 *Phylloscopus nitidus*. Blood samples were analyzed using light microscopy of blood smears and molecular screening methods (PCR and sequencing) to detect and identify haemosporidian infections. Microscopy detected four infected individuals: two *P. c. menzbieri* and two *P. nitidus*. Molecular analysis successfully yielded three positive sequences, while one microscopy-positive sample did not produce a usable sequence. Sequencing identified *Plasmodium* and *Haemoproteus* lineages in *P. nitidus*, and a *Leucocytozoon* lineage in *P. c. menzbieri*. The infection prevalence was 3.1% (2/65) in *P. c. menzbieri* and 50% (2/4) in *P. nitidus*, although the latter estimate is based on a very small sample size.

Overall, haemosporidian prevalence in Armenian *Phylloscopus* warblers was notably low compared to previously reported data from the broader Caucasus region. This discrepancy may be explained by local ecological factors such as vector availability, altitude, or limited sample size. Despite the low prevalence, multiple haemosporidian genera were detected, indicating parasite diversity within the studied host species.

Keywords: haemosporidia, *Phylloscopus*, prevalence, Armenia, birds

Funding source / Acknowledgement: The research was supported by the Higher Education and Science Committee of MESCS RA (projects' numbers 24AA-1F032)

P047. Molecular detection of avian haemosporidians in Norwegian tawny owls (*Strix aluco*)

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Haemosporidian parasites, including *Leucocytozoon* spp., *Plasmodium* spp., and *Haemoproteus* spp., are vector-borne pathogens that can negatively affect avian fitness. Climate change is expected to alter haemosporidian transmission dynamics, particularly in northern regions, through shifts in vector distributions and extended transmission seasons.

This study screened tawny owls (*Strix aluco*; n = 27) from central Norway for haemosporidian infections using polymerase chain reaction (PCR). To assess potential co-infections, samples were also screened for herpesvirus and *Chlamydia spp*. using PCR-based methods.

Ten individuals (37%) tested positive for *Leucocytozoon* spp. Sequencing identified two parasite lineages, STAL3 and STAL1, both previously reported in raptor hosts. Seven individuals (26%) were positive in the *Haemoproteus/Plasmodium* screening PCR; however, sequencing was unsuccessful, and infections could not be confirmed. No samples tested positive for herpesvirus or *Chlamydia spp.*

This study provides the first molecular evidence of haemosporidian infections in Norwegian raptors. Long-term monitoring of haemosporidian prevalence in resident raptor populations, such as tawny owls, may help identify climate-driven changes in parasite distribution, transmission dynamics, and potential impacts on host health.

Keywords: *Leucocytozoon*, *Haemoproteus*, *Plasmodium*, avian malaria, vector-borne disease

Funding source: This study is a part of project funded as a PhD scholarship for IBK at Nord University (224000–166) and as two masters scholarships at Nord University (ASI and SCS). This work was supported by the Fundação para a Ciência e a Tecnologia grant number UI/BD/154770/2023 to RS.

P048. Diversity and Distribution of Psychodidae in Armenia

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The Caucasus is one of the most important hotspots in the world, characterized with high habitat heterogeneity and species richness. Such environmental diversity creates favorable conditions for a wide range of insect taxa, including vector species of ecological and veterinary importance. However, the diversity, distribution, and genetic structure of many insect groups, including the family *Psychodidae*, remain poorly studied in Armenia. This study aimed to assess the species composition, spatial distribution, and genetic diversity of *Psychodidae* in Armenia, with a focus on taxa relevant to wildlife and vector-borne disease ecology.

Specimens were collected from multiple locations across Armenia and identified using morphological and molecular approaches. DNA barcoding (COI) was performed for selected specimens, and sequence data were compared with reference databases. Several key species were identified, including *Psychoda alternata*, *Phlebotomus papatasi*, *Phlebotomus sergenti*, and *Phlebotomus halepensis* (aff. halepensis).

A total of 1845 Diptera specimens (two-winged insects) were collected, of which 132 were identified and 82 underwent genetic analysis. *P. alternata* was recorded in Armenia for the first time. Species composition analysis revealed the following distribution*: Psychoda alternata* — 35.29%, *Psychoda sp.* — 5.88%, *Phlebotomus papatasi* — 29.41%, *Phlebotomus sergenti* — 17.65%, *Phlebotomus aff. halepensis* — 11.76%. Phylogenetic analyses indicated close genetic relationships between Armenian populations and those from neighboring regions, suggesting possible regional connectivity and dispersal.

Overall, our findings provide new insights into the diversity and genetic structure of *Psychodidae* in Armenia and underline their relevance in wildlife ecology and vector-borne disease systems in the region.

Keywords: Psychodidae, Armenia, barcoding, vector-borne, diseases

Funding source or Acknowledgement: This study was conducted within the framework of Research Project No. 25AA-1F045 and was financially supported by the Higher Education and Science Committee of Armenia. We also express our gratitude to the French Agency for Food, Environment and Occupational Health and Safety (ANSES) for their cooperation.

P049. Molecular detection of vector-borne pathogens in wild felids from Poland

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European wildcats (*Felis silvestris*) and Eurasian lynx (*Lynx lynx*) are strictly protected species in Poland, for which data on vector-borne pathogens (VBPs) are scarce or absent. The objective of this study was to investigate the presence and distribution of the most important VBPs in wild felids from Poland and to assess their potential role in pathogen circulation at the wildlife-domestic interface.
A total of 24 wild animals were included in the study: 19 Eurasian lynx and five European wildcats, originating from different regions of eastern Poland. Tissue samples were collected post mortem and examined for selected VBPs using real-time and conventional polymerase chain reaction (PCR) assays. DNA of at least one VBPs was detected in 87.5% (21/24) of felids, including *Hepatozoon felis* and *Hepatozoon silvestris* (62.5%), *Anaplasma phagocytophilum* (45.8%), *Cytauxzoon europaeus* (12.5%), *Bartonella henselae* (8.3%), and *Mycoplasma haemofelis/haemocanis*, *Candidatus* Mycoplasma haemominutum and *Candidatus* Mycoplasma turicensis (79.2%).
The detection of multiple VBP in wild felids from Poland highlights their role as ecological sentinels and potential contributors to pathogen circulation at the wildlife–domestic interface. These findings emphasize the need for continued surveillance of VBPs in wildlife within a One Health framework to improve understanding of transmission dynamics and potential spillover risks to domestic animals and humans.

Keywords: *Anaplasma phagocytophilum;* Eurasian lynx; European wildcat; *Hepatozoon silvestris*; molecular diagnostics

P050. Assessment of the exposure to *Phlebotomus perniciosus* in red foxes and wolves using lung extract as a sample matrix

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Phlebotomine sand flies transmit *Leishmania* parasites through the bite of infected females, with *Phlebotomus perniciosus* representing the main vector in south-western Europe. During blood feeding, sand flies inoculate salivary components that induce host anti-saliva antibodies, which have been validated as biomarkers of vector exposure in endemic areas of *Leishmania infantum*. While domestic dogs are the main reservoir in anthropogenic settings, wild canids may contribute to parasite persistence in sylvatic cycles. However, serological studies in wildlife are often limited by the difficulty of obtaining blood samples.

To overcome these constraints, this study evaluated lung tissue extracts as an alternative matrix to assess exposure to *P. perniciosus* in red foxes (*Vulpes vulpes*) and wolves (*Canis lupus*).

From January 2024 to December 2025, lung tissue samples were collected from carcasses of red foxes (n = 40) and wolves (n = 40) in the Piedmont region of north-western Italy. Lung extracts were prepared and screened for the presence of anti-*P. perniciosus* antibodies using an ELISA based on whole salivary gland homogenate (SGH). In parallel, samples were screened for *Leishmania* antibodies using a commercial ELISA plate designed for dog serum, adapted through an in-house protocol for use with lung extracts from wild canids. All samples were tested in duplicate, and lung extracts from non-bitten dogs were used as negative controls. For both tests, the obtained OD values were adjusted, and the cut-off was defined as the mean OD of the negative controls plus three standard deviations (SD). Overall, 26/40 (65%) foxes and 30/40 (75%) wolves were positive for antibodies against *P. perniciosus* saliva. Eight wolves and two foxes tested positive for *Leishmania* antibodies, and all were also positive for anti-*P. perniciosus* saliva antibodies, showing concordance between exposure and infection markers. This study provides the first evidence of exposure to *P. perniciosus* bites in both wolf and fox populations, supporting the involvement of wild canids in the epidemiology of *L. infantum*.

Given the ongoing expansion and recolonization of these species across Europe, their epidemiological role in the maintenance and spread of infection should be considered in surveillance and control strategies. This is particularly relevant in the context of climate-driven changes facilitating the northward and altitudinal expansion of sand fly vectors. Additionally, our findings support the use of lung extracts as a reliable alternative to serum in ELISA-based assays, offering practical advantages for wildlife studies.

Keywords: Wild carnivores; vector-borne diseases; anti-saliva antibodies

Funding source: This research was supported by EU funding within the NextGenerationEU-MUR PNRR Extended Partnership initiative on Emerging Infectious Diseases (Project no. PE00000007, INF-ACT).

Session 4

Challenges in wildlife health, conservation, climate change and biodiversity

Oral Presentations

Invited lecture

Between hope and terror: visions for a just and sustainable society in the face of global warming and biodiversity loss

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Human society, and particularly its middle- and high-income classes, is causing increasing ecological disruption at a world-wide scale. This includes global warming, loss of biodiversity, and emergence of wildlife diseases — such as chytridiomycosis and highly pathogenic avian influenza — that threaten nature conservation. As wildlife health professionals, we are faced with several challenges to deal with this polycrisis. One is that these ecological problems cannot be solved along current trajectories, but require transformative change to a sustainable society. It means revising our activities to support this transformation. A second challenge is the questionability of solving these ecological problems if we cannot both reduce inequity and establish a standard of justice acceptable to a majority of the world's people. Therefore, we should account for socioeconomic justice and equity in our work. A third challenge is not to sink into apathy and despair because of being overwhelmed by the terror of a darkening future. One way of dealing with this is so-called hopeful pessimism: to strive for change without expecting anything other than the knowledge that each effort for healthy wildlife is one worth making.

Keywords: global warming, biodiversity loss, emerging diseases, transformative change, hopeful pessimism

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Development of National Wildlife Health Surveillance

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Using our experiences from 27-years working in the APHA (Animal and Plant Health Agency)- Diseases of Wildlife Scheme (DoWS) we reviewed the concept and aims of wildlife health surveillance at the national level, and building on the characterisations published by Leighton (1995) and Kuiken et al (2011) we suggested a definition of national wildlife health surveillance (NWHS) as: - surveillance (scanning and targeted) of vertebrate wildlife (all taxa and species) for all forms of disease (e.g. infectious, non-infectious, toxicities) in all regions of a country, on an on-going basis with a view to informing measures to improve the overall health of that nation's wildlife (Duff et al 2026). Networks of specialist organisations are required in the delivery of this comprehensive coverage, while prioritisation and triage are needed to conserve resources. The GB Wildlife Health Partnership, comprising seven organisations, has for more than 15 years successfully delivered this surveillance in Britain. We describe how we closely followed published guidance from the UK government, the European Wildlife Disease Association (EWDA) and the WOAH (World Organisation for Animal Health) on disease surveillance. England is one of the few countries in Europe where the government has produced a wildlife health strategy (the England Wildlife Health Strategy) and we would commend to others working with government to encourage them to publish a description of their interest in NWHS.
We will discuss the challenges that we faced developing NWHS in Great Britain and highlight the actions that were successful in this development.

Keywords: National wildlife health surveillance

Funding source or Acknowledgement: Funding from Defra UK government.

References.

Duff, J.P., Barlow, A., Delahay, R. Holmes, J.P., Martindale, L., Smith, G. and Drewe, J.A. (2026) Lessons learnt from the history and development of a national wildlife health surveillance scheme in England and Wales. *Eur J Wildl Res* **72**, 56 . https://doi.org/10.1007/s10344-026-02085-9

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WildEpi: A New Path for Global Information Sharing on Wildlife Health

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Emergence of diseases at the wildlife–livestock and companion animals–human interfaces, together with the accelerating biodiversity crisis, underscore the need for improved management and sharing of health-related information. When it comes to wildlife, gaps in global health intelligence systems persist. While the World Organisation for Animal Health harnesses transparency for listed animal diseases, reporting pathways for other wildlife health events have remained fragmented. Addressing this gap requires innovative systems capable of capturing both diagnosed and undiagnosed wildlife health events. WildEpi was developed as a next-generation solution to enhance the collection, sharing, and use of wildlife health data within a trusted global network.

WildEpi builds on the specifications designed through an iterative and consultative process involving WOAH Members, technical experts, and international partners. Central to this process was the contribution of an international *ad hoc* expert group, which defined core relevant epidemiological data and key functional and technical specifications. The development followed an Agile approach evolving through final users' feedback to ensure usability and relevance. A risk mitigation strategy for global wildlife data sharing was initiated with a consortium of experts. The Open Data Institute's ethical data framework guided data use to promote responsible data stewardship.

WildEpi is conceived as a centralised, open-source, and mobile-first platform enabling authorised users to report core epidemiological information on wildlife morbidity and mortality events in real time. WildEpi enables the standardised reporting of both diagnosed and undiagnosed wildlife health events across free-ranging or captive wild species. Integrated dashboards allow users to visualise, filter and download data. Importantly, the system complements existing reporting pathways while allowing non-official information sharing and requests for support on risk assessment. WildEpi integrates controlled vocabularies, with taxonomy provided by the Global Biodiversity Information Facility and is associated with a wildlife disease ontology. Access to the platform is restricted to authorised users within a defined community of practice, ensuring controlled data sharing while maintaining trust among contributors.

WildEpi represents an advancement in wildlife health intelligence by operationalising a scalable, user-driven approach to data sharing. By enabling timely reporting and analysis of wildlife health events, it strengthens early warning capacities and supports upstream risk prevention with a One Health, All-hazard approach. As implementation progresses, WildEpi has the potential to enhance coordination, improve understanding of wildlife disease dynamics, and contribute to more effective management of health risks at the wildlife–livestock and companion animals–human interfaces.

Keywords: Global wildlife health reporting, information sharing

WOAH's Global Wildlife Health Strategy: A Strategic Framework to Strengthen Wildlife Health Systems Worldwide

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The accelerating biodiversity loss and the increasing emergence of diseases at the human–animal–environment interfaces are closely linked to anthropogenic pressures, including land-use change. Tackling these dynamics requires robust wildlife health governance, surveillance, and cross-sectoral coordination. With limited resources and capacity, the role of Veterinary Services in these multisectoral coordination plans is often unclear.

The World Organisation for Animal Health has updated its Global Wildlife Health Strategy, grounded in a comprehensive theory of change, aimed at strengthening systemic capacities and coordination. The strategy was developed following an external and independent review of the 2021-2026 wildlife health framework strengths and weaknesses, stakeholder mapping and needs assessment, as well as a three-horizon scanning with experts from different backgrounds, including the WOAH Permanent Working Group on Wildlife.

The 2026-2031 Global Wildlife Health Strategy focuses on three interrelated objectives: (i) establishing effective wildlife health governance systems supported by robust legislative, regulatory, and scientific frameworks; (ii) promoting the systematic application of scientific knowledge and risk analysis to enhance wildlife health management and ecosystem resilience; and (iii) institutionalising sustainable, integrated, and multisectoral wildlife health surveillance systems. To achieve these objectives, the strategy leverages key operational goals, including the development of science-based normative guidance, the dissemination of advocacy and communication tools aligned with the One Health approach, and the strengthening of workforce capacities within Veterinary Services and partner networks. Emphasis is placed on fostering functional partnerships that enable data collection, analysis, and knowledge generation, thereby supporting evidence-based decision-making and early risk mitigation.

This updated strategy provides a structured operational framework to strengthen wildlife health systems globally and to better integrate wildlife into national and international health agendas. By enhancing governance, capacity, and multisectoral coordination, it enables earlier detection and more effective upstream prevention of health threats at the human–animal–environment interface. Its implementation is expected to contribute to more resilient ecosystems.

Keywords: Global wildlife health strategy, capacity building, veterinary services, multisectoral collaboration

Threats to Biodiversity from Disease Outbreaks Associated with Non-Native Parasites in Europe

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Non-native species have negative effects on biodiversity through changing the ecological structure of ecosystems. One way in which such ecological changes occur is through incursion of non-native parasites harboured by the introduced species, where 'parasites' are defined in the ecological sense as viruses, bacteria, fungi, protozoa, helminths and ectoparasites. Native species can be susceptible to non-native parasites because they lack appropriate immune responses and outbreaks of disease may result.

There are many recorded instances of epidemic disease in free-living, wild animals in Europe associated with the incursion of non-native parasites. Examples include outbreaks of fascioliasis in European ungulates following the introduction of wapiti (*Cervus canadensis)* and the giant liver fluke (*Fascioloides magna)* into central Europe; crayfish plague (caused by non-native strains of the oomycete *Aphanomyces astaci)* in white-clawed crayfish (*Austropotamobius pallipes*), following the introduction of signal crayfish (*Pacifastacus leniusculus*) into many European countries; and squirrelpox epidemics in red squirrels (*Sciurus vulgaris*) induced by the non-native squirrelpox virus in the UK. In all three examples, disease outbreaks have had effects on native populations, and yet, in the case of white-clawed crayfish and red squirrels, the catastrophic effects have been surprisingly difficult to detect. Wildlife disease surveillance systems may not be sufficiently robust to demonstrate epidemics, especially in small, secretive species which can be rapidly 'removed' from ecosystems due to the activities of predators, scavengers and through decomposition. Where declines of native species occur, the influence of non-native parasites should be considered a possible factor.

Once a novel parasite becomes established in a new ecosystem, controlling its effects is extremely challenging, especially when the non-native reservoir of infection remains. Where wildlife health professionals are investigating native species declines, disease risk analysis can be conducted to examine the possible role of non-native parasites, and epidemic outbreaks of disease, as a potential factor. Where evidence shows non-native parasites have a role in declines, disease risk analysis will provide indicators for future investigation and surveillance.

Keywords: ecosystem health; epidemic disease; surveillance

Systematic mammal abundance estimates across Europe

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Mammal populations have been changing a lot in recent years, with some increasing in numbers and range (wild boar, deer and wolves) and some remain threatened. For management (of disease and biodiversity) it is important to understand where different species are established, and the densities they obtain in different regions. There has, to date, been no Europe-wide systematic approach to determine abundance and density of mammals.

Using two approaches with occurrence data, and hunting data, we produced independent Species Distribution Maps (SDMs). These are then matched with systematic density estimates made by the European Observatory of Wildlife using the REM camera trapping method. Estimates have been made at more than 100 locations.

Predicted distribution maps were created using both approaches, and these converted into local densities, and the population size estimated for each country. These are predicted density estimates for the average habitat and management in any location, assuming the species is present and fully established. Thus, local issues such as areas with no hunting, unusual local features, regional disease outbreaks or areas bordering expansion are not accounted for.

Systematic approaches to estimating mammal abundance across Europe have been performed for various species, which can act as the denominator for risk assessments, disease modelling, invasive species monitoring and biodiversity monitoring.

Keywords: carnivore, GLM, MaxEnt, ruminant, wild boar

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Mitigating disease risks in conservation translocations through a proportionate approach to disease risk analysis (DRA)

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Conservation translocations are one of the many tools used to help to recover and restore vulnerable or extinct species of wildlife. IUCN guidelines advise that translocation projects should be subject to disease risk analysis (DRA) in order to assess, prevent and mitigate the risks of disease outbreaks in animals being moved, or spillover from those animals into new species, including humans, or new geographic areas. Crucially, the IUCN advises that DRA should be proportionate to the likely risk associated with a project. However, some potentially high-risk projects proceed without sufficient formal disease risk analysis because the process is perceived as costly and time-consuming, while potentially low-risk projects expend considerable resource on commissioning DRAs that may be more comprehensive than they need. Using a decision flow chart helps project managers and wildlife disease experts identify the likely risks in their project early on. Consequently, those leading higher-risk projects have an opportunity to modify translocation plans before they are fully committed in order to reduce the likely risks; conversely, low-risk projects can progress at speed and without incurring unnecessary costs. This approach should result in better compliance with IUCN guidelines, fewer risky translocations and an increase in low-risk, well-managed projects that contribute to efforts to restore wildlife and biodiversity.

Keywords: disease risk analysis, DRA, translocation

Badger vaccination as a complementary tool for controlling bovine tuberculosis in France: eco-epidemiological analyses of a 4-year trial

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In areas surrounding bovine tuberculosis (TB) outbreaks in cattle, European badgers (*Meles meles*) can significantly contribute to *M. bovis* circulation within multi-host systems (Delahay et al. 2001). In France, despite a national TB-free status, the prevalence in badger population may be quite high in some bovine infected areas (Calenge et al. 2024), and control measures include reducing badger densities around pastures from affected cattle herds. These culling measures have notable epidemiological, operational, ecological and ethical limitations. Thus, vaccination emerges as a promising tool, in addition or as alternative to culling, to reduce the circulation of *M. bovis* in endemic areas, as demonstrated in the Republic of Ireland, England and Northern Ireland (Gormley et al. 2021; Carter et al. 2012; Arnold et al. 2021). From 2023 to spring 2026, a study evaluating the use of injectable vaccination in badger populations was conducted in two endemic areas in the south-west of France (total 130km^2). The final objective was to develop an optimal vaccination strategy to be deployed at a broader scale. Specific objectives included assessing operational feasibility, estimating implementation costs to reach a minimum of 60% vaccination coverage and possibly to measure the effects of vaccination on badgers' infection rates.

After identifying all known setts in the study areas, only active or closely related setts were trapped with cages and/or stop-restraints in spring, with two trapping sessions also organised in autumn. Each badger captured for the first time was identified, tested with a rapid blood TB diagnosis test (Dual Path Platform, Chembio©): the negative animals were vaccinated with injectable IM BCG (Sofia strain SL222) and the positive ones, euthanised. At the end of the third year, detailed procedures were adapted for two main types of handlings: anesthetized and conscious animals. Videos were also produced to train the future operators. Capture rate and vaccination levels were estimated. In the medium population density level (density of 1 active sett / km2), the objective of 60% of a vaccinated population was reached within two years, whereas in the low-density level area (0.5 sett / km2), a vaccination rate of 30% of the estimated population was reached. The estimated capture costs were lower in the medium density area.

Vaccination with an injectable vaccine proved feasible across varying badger population densities, although capture and vaccination rates, as well as the associated capture costs, varied considerably.

Keywords: *Meles meles*, *Mycobacterium bovis*, wildlife vaccination, capture

Session 4a

Challenges in wildlife health, conservation, climate change and biodiversity

Oral Presentations

Capture-related mortality: disentangling individual vulnerability, capture conditions and prior experience in roe deer

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Capture is a key tool for wildlife knowledge and management, providing individual-based data that are essential to understand life-history strategies. However, capture and handling are inherently stressful and may induce both short- and long-term adverse effects, including injury, physiological dysregulation, capture myopathy, and mortality. Despite major practical and ethical implications, the mechanisms driving variation in capture-related mortality remain poorly understood. Here we analyze capture-related mortality in the roe deer *Capreolus capreolus*, using long-term data from three monitored populations in France, to disentangle the roles of intrinsic vulnerability, capture context, and prior experience.

We first hypothesize that intrinsic vulnerability influences mortality risk. Frailty, defined as reduced physiological reserves and increased susceptibility to stressors, is expected to be associated with high mortality risk through a reduced capacity to cope with capture stress, whereas high body mass is expected to have a protective effect. Early-life environmental conditions, age and elevated baseline glucocorticoids may also affect mortality risk. Second, we test the influence of the context and method of capture, including environmental and operational conditions. We expect higher mortality during days with a large number of captures, after longer pursuit or handling and in individuals with elevated physiological indicators reflecting excessive stress. Finally, we assess the role of prior experience, predicting that repeated exposure to capture may reduce mortality risk through habituation. In particular, individuals exposed to capture early in life may exhibit attenuated stress responses and enhanced coping capacity, leading to increased resilience and lower mortality risk.

Based on data from 805 to 11346 captures performed during 28 to 50 years, we estimate that mortality at capture ranges from 3 to 6.3% according to the population considered. Individual factors are a main determinant of mortality with young, senescent and light individuals showing highest mortality risk. External and operational conditions like track surface are also associated to mortality. Strikingly, individuals marked as fawns showed low mortality, suggesting habituation and/or intrinsic differences between individuals captured or not. These variations may have consequences on the data collected during capture-mark-recapture studies, as well as on population dynamics itself. By integrating capture, physiological, and environmental data, this study also helps refining capture protocols to enhance animal welfare.

Keywords: capture protocol, frailty, habituation, 3R

Complex Causes behind Poor Growth and High Mortality among Moose Calves

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The moose (*Alces alces*) is an iconic key species of the boreal forests of Northern Europe. Scandinavia had historically high moose densities twenty years ago, but the population has declined. In large parts of the distribution range, moose calf weights are decreasing, and the number of observed calves per cow is declining. Furthermore, anecdotal reports indicate high mortality of young calves, but very few moose calves have been necropsied. The project "Elgkalven Trampe" was established in 2024 to investigate the cause of disease and death in moose calves during their first year. The current abstract reports the preliminary findings of this ongoing study.

A network of locally based "Trampe Contacts" was established in several counties. These dedicated people were paid to be on call for people observing diseased or dead calves, and either perform field examinations or collect carcasses for necropsy. So far, 124 moose calves have been examined postmortem and sampled according to standardized procedures.

The vast majority of the examined moose calves were small (relative to expected size for the time of year) and cachectic. Their rumen was filled with seemingly normal content, but milk coagulates were rarely observed in the abomasum. Many of them had large lymph nodes and slightly enlarged spleen. Their lungs were often uniformly and mildly hyperemic and edematous. Miscellaneous opportunistic bacteria were cultivated from the spleen and lungs. Clostridial bacteria were also frequently found. Almost all animals were positive for *Anaplasma phagocytophilum*, and about half of them had *Giardia duodenalis* in their feces. The levels of gastrointestinal nematodes in the abomasum, small intestines, and feces were generally low to moderate, though sporadic animals showed more intense infections.

The examined moose calves displayed poor condition, suggesting that the observed decline in slaughter weights is related to malnutrition, while reduced calf-cow ratios reflect increased mortality associated with malnutrition. We are currently not able to decide which factors that drive this development. Potential contributing factors include 1) heat stress leading to decreased food intake and increased metabolic cost in the calves and decreased milk production in their mothers, 2) early spring causing suboptimal synchronization between plant nutritional content and the needs of the calves, 3) overbrowsing due to high densities of wild ruminants, and/or 4) infectious diseases reducing appetite and/or diverting nutrients away from growth. Further analyses are ongoing to clarify the relative importance and interactions of these factors.

Keywords: moose calves; malnutrition; disease; poor growth; Norway

Anthropogenic Drought Leads to Gut Inflammation in Wild and Domestic African Herbivores

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Extreme weather, such as droughts and flooding, are increasing in frequency and intensity due to anthropogenic climate change. These extreme weather events disproportionally impact on vulnerable communities and ecosystems in the global south. Drought affects ecosystems by reducing access to water, decreasing food availability and increasing thermal stress. This imposes increased costs and challenges for managing livestock, and increased vulnerability to disease in both humans and animals. Drought also has wider impacts on wildlife that have been displaced within anthropogenic landscapes. Here we evaluate changes in gut health during a prolonged drought as an indicator of the effect of extreme resource limitation on the ability of animals to regulate nutrient absorption and immune function. We used faecal biomarkers to measure gastrointestinal inflammation, total antibodies, and endocrine metabolites, in combination with diet and microbiome composition (via DNA metabarcoding), and faecal egg counts as a proxy of gastrointestinal nematode egg shedding, to mechanistically evaluate gut health in wild and domestic ungulates during drought in Kenya.

We found cross-taxa evidence of compromised gut function, including increased gut inflammation and gut barrier dysfunction during drought compared to a non-drought year. These changes were not associated with changes in nematode parasitism, and we explore the links between diet changes, microbiome enterotypes, and physiological stress as drivers of gut inflammation.

Disrupted gut function associated with drought could provide an explanation for the increased mortality that was seen in both ruminant wildlife and livestock in Kenya during this period. Identifying the impacts of extreme weather events on animal health can help predict and evaluate resilience to climate change at the individual, population and species scales.

Keywords: drought, inflammation, ecoimmunology, biomarkers, shared landscapes

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Monitoring of *Protoparvovirus carnivoran1* in Eurasian lynx (*Lynx lynx*): implications for disease surveillance and conservation

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Health-risk assessment is essential in wild animal populations, particularly in the context of translocation programmes. Infectious agents, including parvoviruses, may reduce the fitness of translocated individuals and threaten already vulnerable recipient populations, such as small and fragmented populations of the Eurasian lynx. Despite the well-documented impact of parvoviruses on domestic cats and other carnivores, data on their occurrence and genetic diversity in Eurasian lynx remain limited.

Between 1997 and 2026, 67 Eurasian lynxes from Croatia, Romania, Slovakia, Slovenia, and Finland were sampled. Mucosal swabs and blood samples were obtained from live individuals captured for translocation and ecological research, while organ samples were collected from carcasses as part of national mortality monitoring programs. Two lynxes captured in Romania, as well as one lynx captured and one found dead in Croatia, tested positive for *Protoparvovirus carnivoran1* using real-time PCR, which differentiates canine parvovirus type 2 (CPV-2) from feline panleukopenia virus (FPV). Of these, one individual tested positive for FPV and two for CPV-2, all detected in rectal swabs. The fourth lynx showed evidence of co-infection, with CPV-2 identified in a rectal swab and FPV in nasal and ocular swabs.

Our findings suggest that Eurasian lynx are susceptible to FPV and CPV-2 and that parvoviruses co-circulate in the environment, potentially exposing animals to multiple sources of infection. Only one positive animal was sampled post-mortem, raising questions about the typical clinical severity of parvovirus infection in this species and the frequency of subclinical or transient infections. Strict biosecurity measures and well-trained personnel are essential during handling and quarantine to minimise the risk of human-mediated introduction and subsequent transmission of the virus. Furthermore, these findings underscore the importance of continuous monitoring of parvoviruses in Eurasian lynx, particularly in the context of translocation projects, given their high environmental stability, contagiousness, and potential lethality.

Keywords: canine parvovirus type 2, CPV-2, feline panleukopenia virus, FPV

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Surveillance of high-stakes viruses for Eurasian lynx population in France

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The Eurasian lynx (Lynx lynx) is a species of high conservation concern, currently classified as Endangered on the International Union for Conservation of Nature (IUCN) Red List in France.
French lynx populations are threatened by habitat fragmentation and range restriction, small population size, low genetic diversity, as well as by illegal killing and road mortality. In this context, infectious diseases may represent an additional and potentially critical threat, especially under ongoing global changes and increasing interactions with domestic animals.
The Eurasian lynx is susceptible to several viral pathogens shared with domestic carnivores, including canine distemper virus (CDV), feline immunodeficiency virus (FIV), feline leukaemia virus (FeLV), and feline panleukopenia virus (FPV).
Disease surveillance in lynx populations in France is primarily carcass-based and relies on diagnostic investigations. Since 2022, surveillance has been strengthened to include systematic screening for CDV, FIV, and FeLV. In addition, retrospective analyses were conducted using samples from a dedicated biobank.
A total of nearly 200 individuals were collected and analysed between 2016 and 2025. Preliminary results indicate the circulation of CDV (11%, 13/123), FIV (1%, 1/106), FeLV (12%, 12/101), and FPV (40%, 44/110) in French lynx populations. Notably, 41% and 54% of CDV- and FPV-positive individuals, respectively, exhibited high viral loads consistent with active clinical infections that may have contributed to mortality.
Phylogenetic analyses revealed contrasting patterns: FPV strains detected in lynx were closely related to those circulating in domestic carnivores, whereas CDV strains appeared distinct between domestic and wild compartments.
Although preliminary, these findings confirm the circulation of multiple viral pathogens in French lynx populations and raise concerns about their potential impact on species conservation. They highlight the need for further investigation into virus transmission dynamics and the ecological drivers shaping pathogen circulation at the wildlife–domestic interface.

Keywords: *Lynx lynx*, viruses, canine distemper, feline leukaemia, feline panleukopenia, diagnostic

A citizen-science serological survey of myxoma and rabbit haemorrhagic disease viruses in Iberian rabbit populations

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The European rabbit is classified as *Endangered* in its native range in the Iberian Peninsula, and infectious diseases are one of the main threats to this keystone species. Large-scale information on population-level immunity to myxoma (MYX) and rabbit haemorrhagic disease (RHD) viruses is essential to inform their management. We performed a citizen-science-based serological survey of wild rabbit populations across Portugal and southwestern Spain, aiming to identify the relationship of immunity to each virus with rabbit demography.

Between 2019 and 2024, dried blood spot (DBS) collection kits were sent to 198 hunting grounds across Portugal, yielding a response rate of 42.4%. Additionally, DBS were collected from 30 selected hunting grounds in southwestern Spain. In total, hunters collected DBS in *Protein Saver 903 cards* from 1,569 rabbits harvested in 114 hunting grounds (average 12.2 DBS/hunting ground, ranging 1-42). Eluates obtained from the DBS were tested for antibodies to MYX and RHD using previously evaluated indirect ELISA protocols. The average rabbit density at each hunting ground was extracted from the hierarchical abundance model developed by project "Life Iberconejo". From the official harvest statistics, we extracted the growth rate of harvest density from 2015-2017 to 2019-2021, for each of the hunting grounds that contributed DBS.

Overall, 25.2% of the samples were seropositive for RHD (95% confidence interval CI_{95} 23.1 – 27.4%), and 49.8% for MYX (CI_{95} 47.3 – 52.3%), while 18.6% were positive for both pathogens (CI_{95} 16.7 – 20.6%). Generalized linear mixed models showed that rabbit abundance was positively related to the prevalence of immunity to MYX ($p<0.01$) and RHD ($p<0.001$). The harvest density growth rate had no relationship with immunity to MYX ($p=0.145$) or RHD ($p=0.259$).

This study shows that population-level immunity to MYX and RHD and rabbit abundance are significantly related at large scales. It demonstrates that citizen-science approaches involving hunters could be flexible methodologies for large-scale serological surveys of pathogens in harvested wildlife.

Keywords: *Oryctolagus cuniculus*, Iberian Peninsula, dried blood spots, hunters

Funding source / Acknowledgement: LIFE programme of the European Union Iberconejo [LIFE20-GIE ES000731].

Session 4

Challenges in wildlife health, conservation, climate change and biodiversity

Poster Presentations

P051. Aspects of brown bears management in Slovakia and effect of health conditions on behavior changes

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The brown bear (*Ursus arctos*) is an iconic species of mountainous ecosystem of Slovakia. The high number and population in expansion of brown bears is currently an extremely discussed topic. It is very sensitively perceived by both professionals, authorities and public. On the one hand, it is a priority species of European importance from the point of view of the European Union, on the other hand, it is a large predator causing damage or dangerous an counters with humans. The prevailing opinion in society is that bears in Slovakia are overpopulated, which is constantly increasing public pressure to hunt them. The aim of the presented article is to determine whether the health status of individuals has an impact on the occurrence of problem behavior. Based on the hypothesis that problem individuals are forced to limit their presents due to the occurrence of some disease or medical handicap, as a result of which they are unable to secure their needs in natural environment and look for easier ways to obtain food.

Over a two-year period (2024-2026), we studied 120 Brown Bear cadavers from the bear intervention teems at the University of Veterinary Medicine and Pharmacy (UVLF) in Košice, Slovakia. This study integrates our field data, necropsy results, parasitic examinations, and existing literature to assess how health factors influence bears behaviour. Necropsies were conducted on half of the carcasses, mainly those from road accidents, while the other half were examined directly in the field with assistance from local police, hunters, and forest rangers. The carcasses and their organs were weighed and measured. Special attention was given to the liver, kidneys, spleen, heart, and gastrointestinal tract to detect toxins, infectious diseases, and parasites. The results emphasize the importance of including veterinary assessments in management decisions, promoting a One Health approach that balances animal welfare, ecosystem health, and human safety.

The results of the examinations provided us valuable information about the health status of bears, which is essential for understanding changes in their behavior and for proper intervention in cases where behavior becomes dangerous or unpredictable. This comprehensive approach will enable effective management of the bear population and protection of the population from potential risks. The results of the project will be helpful for updating data and creating new plans for the management of large carnivores in Slovakia.The rising frequency of human–bear encounters in Slovakia has led to the emergence of, what is called, "problem Brown Bears" (*Ursus arctos*), creating challenges for wildlife management, public safety, and their conservation efforts. The results will be discussed.

Understanding the underlying causes of such behavior is essential. Are these bears driven into human environments by physiological or pathological conditions such as disease, injury, dental problems, or parasitic infections? Or have they become habituated to anthropogenic food sources through prior conditioning, whether via maternal learning, access to waste, or intentional feeding by humans? Addressing these questions requires a multidisciplinary approach, in which veterinary science plays a central role.

Keywords: brown bear health status, problem behavior, field immobilization

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P052. Veterinary aspects of field capture of European bison

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After succesful reintroduction projects a sustainable population of european bison is present free in north east Slovakia,as well as in few captive breeding centers, This require regular management interventions. A safe immobilization protocol was immportant to introduce with focus on easily accesible drug mixture.
In period of 2020 and 2022 a 3 large translocation and transports were performed from Slovakia to Rumania and Hungary of total 23 animals. Animals of different weight and age were captured by darting and transported by standard catle transport tract.Translocation was on 1500 km distance,lasted over 20hours with stops. In the paper, the authors point out the practical aspects of the immobilization and relocation of 23 European bison *(Bos bonasus)*. It involved the transport of 11 individuals, i.e. three pregnant females with cubs, two bulls and three subadult individuals. In the history of captive bison breeding, this was the largest transport of bison to date. The transfer was carried out in two separate transports. The capture, handling, and release into the acclimatization enclosure itself required a consistent and logistical workflow from the point of view of the staff involved.
Immobilization was performed with disposable Pneudart shots in a volume of 5 ml. The chosen anesthetic was a combination of Zoletil and Domosedan /zolazepam-tiletamine-detomidine/. For an adult individual with an estimated weight of 500 kg, a dose of 5 ml was used, which was obtained by dissolving 750 mg of Zoletil in 4 ml of Domosedan. This dose was sufficient to handle an individual for 40 minutes. The entire transport in two stages took place without complications and the individuals successfully acclimatized in the new environment. Combination of Zoletil and Domosedan was faund as effective and safe drug combination. Recommended dose was calculated Zoletil 50 and +1ml Domosedan/100kg bw as effective drug combination for european bison
The experience with the handling of bison confirmed the following findings: For any handling, the individual must be sufficiently immobilized, because there is a risk of serious injury, especially to the head and eyes. During any handling of an immobilized individual, the assistance of at least 2 people is required to fix the head of the bison. It is so large and heavy that if it is not lifted, there is a risk of serious damage to the eyes, which are located much more laterally in bison than in cattle. The digital scale with which the carrier was equipped showed that we had incorrectly estimated the weight of the largest individual and instead of 350 kg the individual weighed 480 kg. A flat body and heavy bones significantly distort the possibility of correct weight estimation. The protocol we chose was sufficient for manatee bison, which is kept in zoos, but not sufficient for wild individuals. It provides a working, handling time of 40-60 minutes. One of the immobilized individuals woke up after an hour even without the need for antidote application.
In the bison reserve in Topoľčianky, the combination of Zoletil and Domosedan /zolazepam-tiletamine-detomidine/represents a safe, low-volume anesthetic protocol that is partially reversible, has minimal adverse effects on physiological parameters, and provides sufficient duration of anesthesia.

Keywords: **European bison, health status, field immobilization, translocation**

Acknowledgement: This study and work was supported by State environmental agency of SR State forestry department in Topolcianky.Conducted by Life project No. Life 18NAT/RO 001082 by Foundation Conservation Carpathia

P053. Systematic health monitoring in reintroduction and population reinforcement projects – the case of *Chlamydia felis* in Eurasian lynx

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The Eurasian lynx (*Lynx lynx*) is the largest wild cat in Europe and was once widespread across the continent. By the early 20th century, however, the species had been exterminated from most of west-central and southern Europe. The Dinaric lynx population was re-established through a reintroduction program using animals from Slovakia in 1973 and later reinforced by additional translocations from Slovakia and Romania between 2019 and 2024. Like other felids, lynxes are susceptible to infections caused by bacteria of the family *Chlamydiaceae*, which can lead to various clinical diseases in both animals and humans. In domestic cats, chlamydiosis most commonly manifests as conjunctivitis caused by *Chlamydia felis*. While this disease is relatively well studied in domestic cats, its occurrence in wild felids remains largely unknown. As part of health monitoring conducted during the translocation from the Carpathian to the Dinaric lynx population, we assessed the prevalence of *Chlamydiaceae* in the donor and recipient populations. DNA was extracted from 34 conjunctival swabs (21 from Romania, 7 from Croatia, and 6 from Slovakia) collected from animals live-captured in box traps (N=31) or from fresh carcasses (N=3). Bacteria of the family *Chlamydiaceae* were detected by amplifying the 23S rRNA gene using qPCR. One sample tested positive and was further analyzed by amplifying the *pmp9* gene to identify the bacterial species. *Chlamydia felis* was confirmed in adult male lynx captured in Romania. Redness of the right eye accompanied by discharge from the medial canthus manifested only four days after capture, while the animal was in quarantine. A single dose of gentamicin sulphate was administered, after which the clinical signs resolved. These findings emphasize the importance of systematic health monitoring in reintroduction and population reinforcement projects, as infectious diseases may reduce the fitness of translocated animals and pose a risk to recipient populations.

Keywords: *Chlamydiaceae*, *Lynx lynx*, conjunctivitis, Dinaric population, Carpathian population

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P054. From individual care to disease surveillance: how French wildlife rescue centres feel towards this paradigm shift

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Wildlife rescue centres (WRCs) arose in France in the 1970's following severe environmental crises. Their historical mission is to care for and rehabilitate distressed wildlife momentarily unable to satisfy their basic needs. However, population-based approaches to disease management is generally not part of their core mission. Characterising their perception of what epidemiological surveillance is, of their potential contribution to it and of the main practical and ethical challenges is critical to ensure the sustainability of surveillance schemes. Here, we aim (i) to understand the motivations of WRCs are in engaging -or not- in wildlife epidemiological surveillance, and (ii) to identify which typological traits may affect these motivations.
A questionnaire-based survey was conducted between November and December 2025 to characterise the perception WRCs have of disease surveillance, how they can contribute, and whether they are more driven by animal or environmental ethics in their activity. In addition, semi-structured interviews were conducted in February and March 2026 with five French WRCs managers, to have a more in-depth understanding of the motivation and challenges WRCs identify to contribute to disease surveillance. Interviews were transcribed and thematic analyses were applied to identify the main recurring themes. The questionnaire was answered by 34 WRCs, representing approximately a third of the target population. All responding WRCs considered they were legitimate stakeholders in disease surveillance, notably because of the number and variety of species they admit each year. Practical conditions of a surveillance scheme were found to be determinant factors in the continuation of their contribution. Most of WRC managers interviewed expressed a degraded relationship or communication with other local disease surveillance stakeholders such as local animal health authorities or local public agencies dealing with wildlife, particularly in times of crisis involving wildlife. Other aspects were identified as limiting, such as specific training and coordination, staff availability, or the regulatory framework.
WRCs are overall willing to contribute to wildlife disease surveillance, although specific ethical and practical aspects such as time and budget should be considered before implementing a surveillance scheme involving WRCs, to ensure its goals and modalities are aligned with WRCs' practical constraints and ethical values.

Keywords: disease surveillance, wildlife rescue centres, acceptability, feasibility

Funding source: French Biodiversity Agency (OFB) and ENVT PhD grant.

P055. Reliability of arterial oxygen content calculations made by the AVOXimeter-4000 co-oximeter and Enterprise Point-of-Care blood gas analyser in immobilised White rhinoceroses (*Ceratotherium simum*)

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White rhinoceroses (*Ceratotherium simum*) are listed as "near threatened" by the IUCN Red List of Threatened Species[a], prompting conservation interventions that often require chemical immobilisation for dehorning or translocation. A common complication during rhinoceros immobilisation is hypoxaemia, which can be detected by measuring arterial blood oxygen content (CaO_2; ml O_2/dL blood). Reliable portable devices are essential to obtain these measurements in field settings.
This study used 247 blood samples from eight male rhinoceroses to evaluate the reliability of CaO_2 values calculated indirectly by the Enterprise Point-of-Care (EPOC) blood gas analyser[b] and the benchtop AVOXimeter-4000 co-oximeter[c]. These CaO_2 values were compared with the method of Tucker[d], which was used as a gold standard since CaO_2 is measured without assumptions on blood physiology. Statistical analyses were performed using Bland-Altman plots and calculating total observed errors (TE_O) from the method of Tucker CaO_2 measurements. The difference in TE_O and TE_a (total allowable error)[e] of ±1 ml/dL was set as performance goal. Comparison of measurements by the EPOC blood gas analyser with the method of Tucker, revealed the set TE_a was exceeded, making it an unreliable assessment of CaO_2 in rhinoceroses. In contrast, the AVOXimeter-4000 measurements, although imprecise were within the set TE_a, making it a reliable device for assessing CaO_2 in rhinoceroses in the field.

Keywords: *White rhinoceros*, chemical immobilisation, oxygen monitoring, blood gas analyser, arterial oxygen content

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[a] EMSLIE R. (2020) Ceratotherium simum. The IUCN Red List of Threatened Species 2020: e.T4185A45813880. http://www.rhinoresourcecenter.com/pdf_files/158/1589193466.pdf.
[b] Siemens Healthineers AG, Forchheim, Germany. CaO_2 manually calculated as (1.34*[Hb]*SaO_2) + (0.003*PaO_2) where [Hb] is the haemoglobin concentration, SaO_2 the percentage saturation of Hb with oxygen, and PaO_2 the arterial partial pressure of oxygen.
[c] International Technidyne Corporation, NJ, USA. CaO_2 automatically calculated from measured haemoglobin fractions using spectrophotometry.
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P056. Water vole reintroduction in the UK: is it a success without indices of health, welfare, or genetic diversity?

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Growing sociopolitical awareness of biodiversity loss in the UK is motivating many ecological restoration projects, including release of small to medium-sized mammals. Water voles (*Arvicola amphibius*) disappeared from 90% of their UK range by 2000, driven by predation and habitat loss. Wetland restoration and removal of the invasive American mink (*Neovison vison*) have enabled reintroduction of captive-bred water voles at over 250 sites across the UK since 2003. However, outcome monitoring, particularly health and genetic diversity indices, remains limited. Our study aimed to fill these gaps by assessing changes in gut microbiota composition combined with individual genotyping, to assess adaptation capacity, estimate reintroduction success, and compare population genetics of reintroduced and native populations.

Faecal and water samples were collected from three water vole populations and their habitats: two reintroduced populations (est. 2024 and 2014), and one native population. Whole DNA was extracted from each sample, and the 16S rRNA gene (V3–V4) and ITS2 region were amplified and amplicon sequenced using Illumina technology. For the reintroduced populations, bioinformatic analyses included comparison of alpha and beta diversities, temporal changes in taxa relative abundance, source tracking of environmental microbiota, and inference of function. A set of 12 microsatellites were characterized, and sequenced to establish individual identity of samples, and genetic diversity for each population.

The reintroduced population showed higher alpha diversity (Shannon index) than the established population, with no temporal changes in either. Beta diversity (Bray–Curtis dissimilarity) remained stable in the established population, whereas the reintroduced population showed a rapid shift in community composition post-release, converging towards that of the established population. Further analyses, including environmental source tracking, taxonomic shifts, potential pathogens, and functional analyses provided additional insight into microbial dynamics.

Reintroduction of captive-bred water voles results in rapid shifts in gut microbiota, changes not observed over the same time period in the established population, highlighting the impact of reintroduction on microbial communities and providing a novel timescale for microbiota adaptation. This improved understanding of gut flora dynamics will support microbiota-informed conservation practices during ecosystem restoration. Individual-level analyses will further clarify links between microbiota adaptation, survival, and population genetic diversity, raising important questions for health and welfare in ex situ conservation programmes.

Keywords: reintroduction, microbiota, genotyping, outcome-monitoring

P057. Prevalence of tick-borne and rodent-associated pathogens in restored Scottish wetlands

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Human driven habitat degradation and associated biodiversity loss have been widely linked to changes in the distribution and prevalence of host and vector species, and the associated pathogens. While multiple studies have investigated the effects of biodiversity loss on pathogen prevalence and disease incidence, the effects of nature and biodiversity restoration on the abundance of hosts and vectors and the prevalence of pathogens are uncertain. Wetlands are globally endangered ecosystems, that host diverse communities of vertebrates. Wetland restoration projects often examine the effects on the resident animal communities, yet the potential effects on pathogen vectors and hosts are unclear. In this study, we examined how wetland restoration affects abundance of ticks and prevalence of tick-borne and rodent-associated pathogens.

We collected ticks and live trapped rodents in three sites in Scotland, United Kingdom across 2023-2025 with sampling in spring and autumn of each year (only spring in 2025). Our study used a Before-After/Control-Impact design, thus samples were collected at five timepoints in Control-Impact sites, while in the Before-After site at two and three timepoints before and after the restoration, respectively. Pathogen screening was done from 2195 ixodid ticks (adults *n*=217; nymphs *n*=1978), and from tissues of wood mice (*Apodemus sylvaticus*, *n*=5) and field voles (*Microtus agrestis*, *n*=30).

We did not find statistically significant differences in the density of nymphs between the control and impact sites or before and after the restoration. None of the rodents tested positive for *Borrelia* spp. or *Rickettsia* spp., however 34.3% of the rodents were positive for *Leptospira* spp. DNA with no statistically significant differences between the sites.

Wetland restoration did not affect the density of nymphs or prevalence of rodent-borne pathogens. It is likely, that more time is needed for the host and vector communities to potentially resemble those in undisturbed or healthy wetlands.

Keywords: nature restoration, tick-borne pathogens, rodent-associated pathogens, zoonotic disease

Funding source / Acknowledgement: This study is a subproject within BEPREP and has received funding from the European Union (grant agreement No 101060568; project BEPREP).

P058. Comparison of physiologic and acid-base variables in anaesthetised wild muskoxen (*Ovibos moschatus*) herded above the arctic circle by helicopter or by land

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Among large arctic herbivores, the muskox (*Ovibus moschatus*) plays a key role in ecosystem functioning and represents a fundamental resource for the sustenance and economy of some indigenous communities.
As part of a collaborative ecological project, 34 adult female and 15 adult male free-ranging muskoxen were immobilized in West Greenland. Fixed doses of 3.3/2.45 mg etorphine, 53/40 mg xylazine, 0.45/0.43 mg medetomidine, 60/45 mg ketamine and 3/2.25 mg midazolam were used for males and females respectively. Twenty-seven individuals were approached and herded by helicopter whereas 22 were approached by land. Herded oxen were anaesthetised by darting from the ground and physiological and venous acid-base parameters were monitored.
At first vital check, muskoxen herded by helicopter displayed a higher heart (59±22 bpm) and respiratory rate (31±7 bpm) compared to animals herded by land (42±7 and 24±8 bpm respectively, $P<0.01$). All muskoxen displayed both metabolic and respiratory acidosis, which was exacerbated in animals herded by helicopter (pH 7.203±0.089) compared to those herded by land (pH 7.259±0.041, $P=0.002$). The lower venous blood pH in helicopter-herded muskoxen was corroborated by lower values of bicarbonate, base excess and total CO2 ($P<0.02$). Hyperlactatemia was mild in land-herded (2.51±1.7 mmol/L) and moderate in helicopter-herded (4.46±5.2 mmol/L, $P=0.007$) animals.
Anaesthetised wild muskoxen display moderate mixed acid base imbalances, which are more pronounced in animals herded by helicopter, likely due to high-intensity exertion and physiologic stress. Provision of oxygen and minimising herding and anaesthesia time are imperative in wild ungulate immobilisation.

Keywords: muskox, acidaemia, helicopter, hyperlactatemia

P059. Hematology and biochemistry reference values for white-bellied *(Phataginus tricuspis)* and black-bellied *(Phataginus tetradactyla)* pangolins from a rescue center in Cameroon

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Pangolins are the most trafficked mammals globally, with African species increasingly targeted as Asian populations decline. This growing pressure highlights the need for effective health assessment and management of individuals confiscated from the illegal wildlife trade. Blood analysis, including hematology and biochemistry, is a fundamental tool in wildlife veterinary medicine, enabling clinical evaluation, disease detection, and guiding rehabilitation. To date, no baseline reference values exist for three of the four African pangolin species: white-bellied, black-bellied and giant pangolins. The lack of such physiological data limits evidence-based veterinary decision-making in African pangolin conservation programs. Here, we have established reference values for white-bellied (*Phataginus tricuspis*) and black-bellied (*Phataginus tetradactyla*) pangolins retrieved from trafficking in Cameroon, and explore how sex, age, and body mass influence physiological profiles.

Clinically healthy pangolins confiscated from the illegal wildlife trade and admitted at the Tikki Hywood Foundation rescue center, Cameroon, were blood-sampled three days post-admission. Blood collection was standardized and conducted under isoflurane anesthesia. Hematology was assessed via complete blood count, and biochemistry included liver, pancreatic and kidney function markers, electrolytes, glucose and proteins. Statistical analyses combined univariate and multivariate approaches to evaluate associations of sex, age, and body mass with physiological profiles.

The study established hematological and biochemical reference values for both pangolin species, enabling preliminary interspecific comparison. Univariate analyses in white-bellied pangolins revealed limited but significant associations of certain biomarkers with sex, age class, and body mass. Multivariate analysis indicated subtle global differences in physiological profiles. Due to the small sample size for black-bellied pangolins, only descriptive statistics were provided.

This study provides the first comprehensive hematological and biochemical reference data for two African pangolin species. These data will help veterinary clinical assessments and strengthen rehabilitation and conservation initiatives for these threatened species.

Keywords: African pangolins, hematology, biochemistry, *Phataginus tricuspis*, *Phataginus tetradactyla*

Funding source / Acknowledgement: Supported by Ceva Wildlife Research Fund. The authors thank Prima Laboratory (Yaoundé) for their technical collaboration

P060. Heat related mortality in Brown long-eared bat (*Plecotus auritus*) pups in England

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A number of dead BLE bat pups were found during a routine roost check on 9th July 2025 in a bat reserve building in Somerset, England. The dead pups were spread out, with 10 in the attic and five on other floors within the building. No dead adults were found. The previous check was on 14th June when the pups were just born. BLE adults were still in the roost and several greater (*Rhinolophus ferrumequinum*) and lesser (*Rhinolophus hipposideros*) horseshoe bats were also present. The building had multiple cooler areas for the bats to retreat to, but it's suggested that as they were all a similar age and non-volant, the adults were unable to move them due to their size.
The 15 pups were submitted to WNDS for examination. Most fairly desiccated, some with tissue missing probably due to maggot predation and a few maggots were seen. The three "freshest" were selected for more detailed examination and histopathology.
These were two females weighing 3.32g and 3.54g and a male 4.01g. Unfortunately, the organ sections from the females although they could be identified, autolysis and postmortem bacterial invasion precluded any useful examination. The changes in the male were not so marked but even so the tissue autolysis was too marked for examination. Although some content was seen in the remnant intestine indicating this pup had been previously feeding.
The highest temperature recorded in the apex of the roof void was 39.51°C, and presumably a higher temperature underneath the roof tiles, where the bats were likely to be roosting. The clinical history and the probable local environmental temperature would indicate that this is a case of heat stress related mortality. Pruvot and others (2019) reported mass mortality in insectivorous bats during a heat wave in 2016 in Cambodia. This was further confirmed by Russo and others (2025) reporting heat wave related mortality in bats in forests in Northeast Italy during the Summers of 2023 and 2024 mainly affecting common noctules (*Nyctalus noctula*). Great Britain has 18 species of bats, all protected by law and four of these are International Union for Conservation of Nature (IUCN) red listed. Unfortunately, persistent climate change is an increasing danger to British bats.

Keywords: Bats, Heat stress, Climate change

Acknowledgement: APHA Histology section

P061. Increasing Prevalence of Heart Murmurs in Swiss Eurasian Lynx (*Lynx lynx*): Risk Factors and Echocardiographic Insights

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Long-term health surveillance of Eurasian lynx (*Lynx lynx*) in Switzerland has repeatedly identified cardiac pathologies. Cardiomyopathy and subaortic stenosis have been identified postmortem, while heart murmurs are detected at capture. Reintroduction history, limited connectivity, and low genetic diversity in Swiss populations indicate a genetic etiology. Building upon previous work, we reassessed heart murmurs in free-ranging Swiss lynx, adding echocardiographic evaluation, to determine prevalence, risk factors, and diagnostic indicators of cardiac health, and to provide an evidence-based foundation for conservation management.

Cardiac auscultation recordings from 85 free-ranging lynx of both sexes and various ages, captured between 2013 and 2025, were retrospectively evaluated for murmur timing and grade (1–6). Serum samples from all 85 lynx were analysed for the cardiac biomarkers N-terminal pro-B-type natriuretic peptide (NT-proBNP) and cardiac troponin I (cTnI). Since 2017, echocardiographic data have been collected in the field to evaluate cardiac structure and function. We assessed associations between heart murmurs and signalment, population, cardiac biomarker levels, and echocardiographic parameters.

Preliminary analyses confirm that heart murmurs are widespread, affecting over half of the assessed lynx (58.8%). Prevalence is higher in the Alpine (75.0%) than in the Jura population (37.8%). Males are affected more frequently, with increasing prevalence in recent years. Most murmurs are systolic and graded 2–3/6. Echocardiographic analysis revealed aortic and mitral valve insufficiency in several lynx. Cardiac biomarker levels show a wide range and reach values associated with cardiac disease in felids. Reintroductions are a key tool for conservation. However, the persistently high prevalence of heart murmurs in Swiss lynx highlights the need for integrated genetic, demographic, and health monitoring to guide conservation strategies and ensure the successful re-establishment of healthy populations. Identifying risk factors and diagnostic indicators improves cardiac health assessment in free-ranging lynx and supports informed decisions for translocation of individuals as well as genetic rescue of populations.

Keywords: Cardiac disease, echocardiography, cardiac biomarkers, wildlife health, genetic diversity

P062. Inbreeding depression in a reintroduced lynx population: a genetic defect causing fatal disease

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Long-term health monitoring of the Eurasian lynx (*Lynx lynx*) populations in Switzerland revealed a recurring lethal disease characterised by severe organ mineralisation in young individuals from one population. The observed pathology, together with the species' reintroduction history, limited population connectivity, and reduced genetic diversity, suggested a genetic cause for the disease.
Post-mortem examinations and histopathological findings were combined with genomic analyses. Whole-genome sequencing and a genome-wide association study (GWAS) were performed to identify candidate variants, followed by targeted genotyping to assess the spatio-temporal dynamics of the identified recessive allele.
Consistent with the observed pathology, we identified a plausible pathogenic missense variant, p.L13P, in the *FGF23* gene, which encodes a key regulator of phosphate homeostasis. Spatio-temporal analyses showed that the deleterious allele was introduced from a source population and subsequently increased in frequency within the affected population.
To our knowledge, this study provides the first evidence of a specific genetic variant causing a lethal disease that directly affects fitness in a wild population. It highlights the importance of integrating post-mortem examination, biobanking, population monitoring, and genomics to inform conservation management and preserve biodiversity on all levels.

Keywords: Eurasian lynx, wildlife reintroductions, genetic diversity loss, FGF23, organ mineralisation

P063. *Taenia arctos* in European brown bears (*Ursus arctos*): Is moose (*Alces alces*) the sole intermediate host in Slovakia?

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Tapeworms of the genus *Taenia* Linnaeus, 1758 are globally distributed in carnivorous and omnivorous animals, including bears. At present, all taeniid species recorded in bears are attributed to *Taenia arctos*. For this cestode, bears (*Ursus arctos arctos*, *U. a. horribilis*, *U. americanus*) serve as definitive hosts, while moose (*Alces alces*, *A. americanus*) have been identified as the only known intermediate hosts. Across the Holarctic, *T. arctos* has been recorded in brown bears in Finland (prevalence 1.9%), Canada (7.7%), and Romania (1.1%). The **aim** of our study was to examine the distribution of *Taenia* species in the wild brown bear population in Slovakia and to investigate whether the moose is truly the sole intermediate host of this parasite in the country.

In 2024-2026, 120 brown bears (*Ursus arctos*), culled under a government-approved special population control program, were collected across Slovakia and examined using the classical parasitological dissection method. Helminths were collected manually from the gastrointestinal tracts and fixed in 70% ethanol for morphological and molecular examination.

In total, 34 cestode specimens were collected from 12 bears (prevalence=10%). The intensity of infection ranged from 1 to 8 tapeworms (average=2.8±1.9SD). Based on morphological and molecular analyses, all individuals were confirmed as *T. arctos*.

Analysis of published data confirmed that the moose is among the rarest large mammals in Slovakia. In the country, it occurs only sporadically as solitary individuals or small groups (up to 20 animals), primarily in the northeastern region. Therefore, we pose the scientific question of whether such a small and unstable moose population can support effective transmission and a relatively high prevalence of *T. arctos* in Slovakia's bear population. It is also plausible that additional ungulate species, such as red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*), or mouflons (*Ovis gmelini musimon*), may play a role in the life cycle, given that their populations in Slovakia have reached historically unprecedented levels.

Given the absence of recent data on tapeworm larval stages in wild ungulates in Slovakia and the high prevalence of *T. arctos* in the brown bear population, targeted parasitological studies on red deer, roe deer, and mouflon are warranted. Such investigations would elucidate the life cycle of *T. arctos* and potentially identify its additional intermediate host species in central Europe.

Keywords: bears, cestodes, intermediate hosts, moose, Slovakia

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P064. Estimating *Toxoplasma gondii* exposure in Swedish wolverines (*Gulo gulo*) – a retrospective study

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The wolverine (*Gulo gulo*), the largest member of family Mustelidae, is a top predator and scavenger found in circumpolar regions throughout North America and Eurasia. Due to its trophic position and large home range sizes, the species could serve as sentinels for ecosystem health of northern Arctic tundra, taiga, mountain, and boreal forest ecosystems. The species is listed as Vulnerable by the IUCN, still limited information exists on the potential importance of diseases in regulating and/or threatening wolverine populations, especially in the recovering Scandinavian population. *Toxoplasma gondii* is a zoonotic food borne parasite which has been reported in mortality events of various Mustelid species. Exposure to the parasite has been found in Canadian wolverines, but there is no information from Scandinavia, where felids, the final host of the parasite, are less common compared to North America. Using a commercially available multi-species ELISA kit, we tested archived samples (n=108) collected between 1994 and 2003 from Swedish wolverines for the presence of antibodies to *Toxoplasma gondii*. A seroprevalence of 24% was found, which is lower than previously reported from Northwest Territories (62%) or Nunavut (41%), Canada (but see British Columbia (0%)). Surprisingly, there was no significant difference in exposure between sex (18% in males vs. 28% in females) and age (33% in adults vs. 19% in juveniles) groups.
With climate change, a northern expansion of parasites is expected, thus monitoring the population health of Swedish wolverine populations is relevant for both OneHealth and conservation biology.

Keywords: *Toxoplasma gondii*, wolverine, ELISA, seroprevalence, Scandinavia

P065. Visual Syndromic Surveillance of Alpine Chamois (Rupicapra rupicapra) in Écrins National Park, France: A 21-Year Cost-Benefit Analysis and Protocol Optimization

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Wildlife health surveillance is increasingly recognized as a cornerstone of the One Health approach, bridging animal, human, and environmental health. Syndromic surveillance—based on visible symptom description—offers a practical, non-invasive and suitable method for large-scale monitoring of wildlife populations. Since 2003, Écrins National Park (French Alps) has implemented a visual syndromic surveillance protocol targeting the northern chamois *Rupicapra rupicapra*, an iconic alpine species. However, the cost-benefit ratio of this long-term protocol has recently become a subject of debate, prompting a need for evidence-based evaluation. This study aims to (1) analyze 22 years of syndromic surveillance data (2003–2024) to assess demographic and health trends, (2) evaluate the protocol effectiveness in detecting health and reproductive changes, and (3) propose alternative protocols, better aligned with field staff constraints while keeping high effectiveness.

Between 2003 and 2024, visual observations of chamois were performed in 7 areas of the park during 3 seasons, with 2384 observations per year on average, and 7 clinical changes defined. In order to analyze spatio-temporal variations in demographic parameters (reproductive success and sex ratio) and prevalence of each clinical change, we used Generalized Linear Models (GLM) and Generalized Linear Mixed Models (GLMM).

The analysis highlights a marked decline in reproductive success over the 22-year study period, alongside a progressive increase in the proportion of males. Among 52503 chamois observed, 2.09% showed clinical change, the most frequent observations being trauma, lameness, ocular and respiratory changes. Clinical changes showed distinct spatial patterns, suggesting potential influences of environmental factors. Finally, temporal variations in lesion frequency were also detected, particularly for ocular and skin changes, reflecting significant variation in health within the population. Thus, despite the lack of complete diagnostic, the surveillance scheme detects demographic and health changes that can be further investigated or managed. The study also highlights limitations of the current protocol, such as significant observer-dependent bias and the time-intensive nature of data collection.

While syndromic surveillance provides valuable insights into wildlife health and generates a volume of data that is incompatible with conventional health monitoring, its long-term sustainability requires adaptation. Among the alternative protocols tested, decreasing to 2 instead of 3 annual observation periods decreases fieldwork time while maintaining high power to detected variations. By refining protocols to balance scientific rigor, animal welfare, and operational feasibility, Écrins National Park can optimize its contributions to One Health while addressing practical constraints.

Keywords: Wildlife surveillance, syndromic monitoring, non-invasive methods, cost-benefit analysis, alpine ecosystems

P066. Reproductive status of red deer hinds (*Cervus elaphus*) in two hunting grounds in Vojvodina (Serbia) during the 2024/2025 hunting season: a pathomorphological study

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The reproductive capacity of females represents a key parameter for the sustainable management of deer populations. Certain reproductive disorders in cervids can considerably impair fertility; however, the prevalence of such conditions in Serbia remains to be systematically investigated. The aim of this study was to determine the prevalence of reproductive pathologies in red deer hinds culled in two hunting grounds in Vojvodina during the 2024/2025 season, and to assess their association with age and pregnancy status.

The study included two hunting grounds managed by PE "Vojvodinašume" in the Srem District: Bosutske šume (10,080 ha; approximately 450 deer) and Kućine (1,249 ha; approximately 84 deer). Of the total 44 hinds culled during the study period, 24 reproductive tract samples were collected, representing 55% of all culled individuals. Samples were examined immediately after culling. Age was determined by dental analysis and cross-referenced with hunting records. Pathoanatomical examination included assessment of pregnancy status and classification of endometritis based on macroscopic characteristics of the uterine mucosa and contents: catarrhal/haemorrhagic (type 2) and purulent-necrotic (type 4) forms. Results: Endometritis was diagnosed in 8/24 hinds (33.3%), exceeding values reported in the literature (5–15%) for free-ranging deer. Type 2 endometritis was identified in 6 cases (25.0%), and type 4 in 2 cases (8.3%). Further findings comprised intrauterine foetal death and ovarian aplasia, resulting in an overall reproductive pathology rate of 41.7%. Prevalence increased with age, reaching 57.1% in hinds aged 7–9 years and 60.0% in those aged 10–13 years. Pregnancy was recorded in 9/24 females (37.5%), of which 8/9 showed normal pregnancy without associated pathology (88.9%), while one case involved a macerated foetus (11.1%).

The high prevalence of endometritis and its strong negative association with pregnancy indicate a considerable burden of reproductive pathology in the studied populations. The findings indicate a positive correlation between age and the prevalence of endometritis. Regular pathomorphological monitoring of reproductive organs in culled females is recommended, while future studies should include bacteriological analyses and evaluation of nutritional factors.

Keywords: *Cervus elaphus*, endometritis, reproductive pathology, Vojvodina, Serbia, wildlife health

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P067. Modeling future distributions of zoonotic helminths in *Apodemus* mice

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Helminths in mice of the genus *Apodemus* were studied in Vojvodina, Serbia (2019–2025), with 242 individuals examined. Nematodes, tapeworms and flukes were recovered from the hosts, including species with zoonotic potential. The aim of the study was to model the potential distribution of the zoonotic species *Rodentolepis fraterna* and *Calodium hepaticum* in Vojvodina Province for the year 2050. Species distributions were predicted using presence data and a set of bioclimatic variables from the WorldClim v2.1 database. Habitat suitability was modeled using the MaxEnt (Maximum Entropy) model implemented in the R program. The models were trained on current climate conditions and projected under the BCC-CSM2-MR climate model with the SSP2-4.5 scenario.

Analysis of the importance of bioclimatic variables revealed differences in ecological requirements between the two species. For *R. fraterna*, average daily temperature variation was the most important factor. The mean temperature of the wettest quarter, the minimum temperature of the coldest month and precipitation seasonality also had a significant impact. As for *C. hepaticum*, the average temperature of the wettest quarter was the most important predictor with the highest contribution to the model. Precipitation in the wettest month and seasonality of precipitation also had significant effects.

The results indicate a relatively narrow climatic niche, defined by a combination of temperature and humidity. Generated heat maps visualized the potential distribution data of both species in Vojvodina Province, providing insight into potential changes in ecological requirements over time. The projections indicate possible changes in spatial patterns of habitat suitability compared to current conditions, including potential changes in range within the region. Research on zoonotic species is especially important in the context of climate change, as it can shift their distribution ranges, while the results also support further interdisciplinary work within the One Health approach, emphasizing collaboration between veterinary, medical, and environmental sectors to improve zoonosis prevention and control.

Keywords: helminths, OneHealth, distribution, climate change, zoonoses

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P068. Species specific disparity in incidental pulmonary silicates depositions in mammals at Barcelona Zoo

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Pulmonary silicate-laden macrophages (SLMs) accumulation is an emerging marker of environmental particulate inhalation in animals, often occurring incidentally without clinical silicosis. Following findings in an asymptomatic banded mongoose (*Mungos mungo*), this study evaluated SLMs prevalence across species with varying ground-level exposure at Barcelona Zoo.
This retrospective study (2010–2024) reviewed lung samples from 19 animals dying from unrelated causes. Species were selected based on their environmental interaction: digging, including banded mongooses (n=8) and meerkats (*Suricata suricatta*, n=5); and non-digging from the same sector, including Rothschild's giraffes (*Giraffa camelopardalis rothschildi*, n=3) and lions (*Panthera leo bleyenberghi*, n=3). SLMs were graded (0–3) following Walker *et al.* (2023) and confirmed via Ziehl-Neelsen (ZN) staining. Spearman correlation was performed in R v.4.4.3 ($p < 0.05$) to evaluate the age-SLMs relationship in mongooses.
Giraffes and lions were negative (Grade 0). Mongooses were the most affected (100% positive): Grade 1 (n=1), Grade 2 (n=2), and Grade 3 (n=5). No significant age-related correlation (Spearman's rho=0.35; p=0.38) was found. Meerkats were predominantly negative, with only one Grade 1 case. Ziehl-Neelsen staining confirmed acid-fast crystalline material in all positive cases.
Absence in lions and giraffes suggests shared sectors are not primary risk factors. The disparity between meerkats and mongooses, despite their similar ecology, highlights the potential role of species-specific factors or unidentified environmental sources. In mongooses, the 100% prevalence and lack of age-related differences in SLMs grading could suggest a uniform and early exposure, aligning with previous reports. Given the limited sample size and lack of soil characterization, these findings provide a baseline; expanding the case series and integrating mineralogical analysis will be essential to clarify the origin and drivers of these accumulations.

Keywords: non-fibrotic pneumoconiosis, herpestidae, lung, environmental exposure

P069. Antimicrobial resistance in wild animals in captivity (*ex situ*): a scoping review

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Wild animals are thought to play a role in the emergence, maintenance, and dissemination of antimicrobial resistance (AMR). To date, most research on this topic has focused on free-ranging wild animals, while captive wild animals – often in closer contact with humans – likely experience different exposure pathways to AMR depending on their setting. Currently, no comprehensive evidence synthesis exists on AMR in captive wild animals. To address this gap, a scoping review was conducted to answer the question "What is the current evidence of AMR in wild animals in captivity (*ex situ*)?".
A protocol was published a priori in accordance with PRISMA and JBI guidance. A comprehensive search strategy was applied across eight electronic databases (BIOSIS Citation Index, CAB Abstracts, LILACS, Medline, ProQuest Dissertations & Theses Global, SciELO Citation Index, SciELO.org, and Scopus), as well as specialised repositories such as the Peregrine Fund Research Library Catalog and the National Wildlife Rehabilitators' Association Wildlife Rehabilitation Bulletin. Retrieved records were imported into the Rayyan web-based tool for deduplication. Study inclusion is being conducted in two stages (title and abstract screening followed by full-text screening), and data charting and synthesis are underway. Studies were included for full-text screening if they met the following criteria: (a) title and abstract available; (b) abstract in English or Spanish; (c) published before July 1st, 2025; (d) primary research article; and (e) title and abstract indicated that AMR microorganisms were isolated from biological samples collected from wild animals in temporary or permanent captivity (e.g., zoos, aquariums, rehabilitation centres) worldwide. Review articles that appeared relevant based on their title and abstract were subjected to backward and forward snowballing.
The title and abstract of 2,673 records were independently screened by two reviewers. Of these, 938 studies met the inclusion criteria and are currently undergoing full-text screening by two independent reviewers. Data from the final set of included studies will be extracted to compile: (a) general study information, (b) terminology referring to captive wild animals, their settings, and AMR, (c) characteristics of the animals and settings studied, (d) AMR microorganisms isolated and their resistance profiles, and (e) methodologies employed. The poster presented at this conference will summarize the results of the review.
This review will provide a foundation for more consistent terminology in future AMR studies, highlight existing knowledge gaps, and inform further research on AMR in captive wild animals.

Keywords: scoping review, antimicrobial resistance, AMR, wild animals, captivity

Funding source: This review is being funded by a University of Bristol Postgraduate Research Scholarship.

P070. The great 'trait-off': Host traits and infection patterns at the wildlife–livestock interface

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Gastrointestinal parasites (e.g. nematodes and coccidia) pose significant concerns due to their association with production losses in livestock and potential negative effects on species abundance in wildlife. These effects are particularly pronounced in regions with increasing livestock–wildlife interactions. This study aimed to evaluate the prevalence and infection intensity of gastrointestinal parasites in co-grazing host species across different interface areas in the Maasai Mara ecosystem in Kenya. We collected 974 fresh faecal samples from 14 sympatric wild and domestic herbivore species (>10 kg) across mixed (livestock-wildlife) and single-species type (livestock or wildlife dominated) land use areas. Parasite prevalence and infection intensity were estimated by quantifying nematode eggs and coccidia oocysts in each sample using the Mini-FLOTAC technique. We investigated the effects of host evolutionary history (phylogeny) and host traits (proportion of dietary grass, body mass, sex, and species type [wildlife vs. livestock]) on parasite infection patterns across land-use (mixed vs. single-occupancy) types. Although parasite prevalence and intensity varied among host species, inclusion of phylogeny did not improve model performance, suggesting limited phylogenetic signal in nematode or coccidia infection patterns. Among the ecological traits examined, host body mass was the only consistent predictor, with smaller host species showing higher prevalence and infection intensity across parasite groups. Other host traits were only weakly or inconsistently associated with parasite infection patterns, with effects varying between nematodes and coccidia. A possible explanation for the observed effect of body mass across all parasite groups is variation in immune function, as larger, longerlived species typically exhibit more developed, antibody-mediated immune responses and higher immune investment. These enhanced immune capabilities may allow larger hosts to more effectively control parasite infections, thereby reducing both prevalence and infection intensity. Overall, these findings highlight the dominant role of host body mass in in shaping parasite infection patterns at the wildlife–livestock interface.

Keywords: wildlife-livestock, interface, parasite, gastro-intestinal

P071. Influence of geographical location on embryotoxic potential of *Vipera ammodytes* snake venom originating from different regions of the Balkan peninsula

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Vipera ammodytes, commonly known as horned viper or long-nosed viper is one of the most recognised and widely distributed venomous snake species in the Balkan peninsula. Owing to its high adaptability and potent venom, this member of family *Viperidae* is responsible for the majority of human envenomation cases among all vipers inhabiting this region of Southern Europe.
In our study we collected samples of *V. ammodytes* venom from three geographically distinct localities: Skadar in Montenegro, Saint Helena in Romania and Biser region in Bulgaria. We subsequently compared venom toxicity through Chicken Embryotoxicity Screening Test (CHEST) and assessed the mortality rate by calculating the lethal dose (LD_{50}), determining the toxicity of each venom sample. Furthermore, we evaluated changes in overall embryo weight, as well as in the liver and heart weights, as these organs are among the first to respond to exposure to toxic substances. Following data analysis and comparison, the highest toxicity was observed in venom obtained from *V. ammodytes* specimens collected at the Skadar locality, which showed the lowest LD_{50} value of 3.9 µg/egg. Venom from the Biser region demonstrated intermediate toxicity, with an LD_{50} value of 4.1 µg/egg, whereas the Saint Helena samples exhibited the weakest embryotoxicity, reflected by the highest LD_{50} value of 6.9 µg/egg.
These differences could suggest that despite belonging to the same species, *Vipera ammodytes* populations may exhibit geographically driven venom variation as an adaptive response to environmental factors such as altitude, precipitation pattern and temperature fluctuation. Such factors may directly influence venom composition while also shaping local prey availability and ecological interactions. Consequently, these adaptations may lead to significant alterations in venom biochemical composition, which may introduce new challenge for the pharmaceutical industry in the field of effective antivenoms development. To further evaluate the significance of our findings we recommend additional proteomic analyses together with validation studies focused on antivenom efficacy.

Keywords: *Vipera ammodytes*, embryotoxicity, Balkan peninsula

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P072. An open-source thermal camera platform to monitor wildlife: a pilot study in thermoregulatory behaviour of European adders (*Vipera berus*)

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Infrared thermography measures emitted radiation and therefore provides a passive, non-invasive method to detect and monitor animals independently of visible light conditions. However, thermal cameras have historically been expensive and primarily available as handheld devices, limiting opportunities for automation and long-term deployment. Here, we present a low-cost, modular sensing platform built around a Raspberry Pi single-board computer and equipped with a thermal camera core. We provide an open-source library to record radiometric thermal footage, while protection of the camera unit is achieved through modular 3D-printed enclosures. To demonstrate automated long-term operation, we recorded thermoregulatory behaviour of European adders (*Vipera berus*) in the Mendip Hills, UK, with potential applications for non-invasive health and disease monitoring.

Adders were monitored while basking on corrugated roofing sheets. The black bitumen surface, placed near vegetation, warms more rapidly than the surrounding environment, providing an attractive basking site during morning hours. The sheet was used as a thermal reference, with its temperature recorded via a contactless infrared sensor for calibration and time-synchronised with thermal frames. In parallel, RGB footage was acquired using a visible-light camera on the platform to facilitate species and sex identification (e.g. distinguishing adders from grass snakes).

The platform successfully recorded continuous thermal and RGB footage over several weeks under field conditions, supported by exchangeable USB power banks and battery swaps every few days. The system reliably captured radiometric data suitable for subsequent quantitative thermal analysis.

This pilot demonstrates a low-cost, open-source sensing platform capable of automated, long-term thermal monitoring in the field. The modular design enables flexible configuration, including independent control of sensor activity, data formats (including raw radiometric output), and on-board encryption. The system provides a scalable tool for passive wildlife monitoring, with potential applications in behavioural ecology and non-invasive assessment of health and disease-related processes.

Keywords: infrared thermography, European adder, Raspberry Pi, thermoregulation

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P073. Copper deficiency in wild ruminants in Vojvodina (Republic of Serbia)

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Copper is an essential trace mineral required for the proper function of multiple body systems. Its deficiency can lead to a range of clinical disorders. Copper deficiency was diagnosed in herds of European bison (*Bison bonasus*) and mouflon (*Ovis gmelini musimon*). In both cases, animals were fed primarily on natural vegetation within enclosures, with hay and grain supplementation during dry periods and winter. No additional mineral supplementation was provided.
A group of five European bison was kept together with 44 red deer (*Cervus elaphus*) in a 150-ha enclosure consisting of forest and a smaller pasture area. A flock of 200 mouflon was maintained in a separate 200-ha enclosure composed of forest, shrubs, and meadows.
In one male European bison, intermittent diarrhea was observed in spring, progressively worsening over time. Other animals showed emaciation, lethargy, and soft to watery feces. Despite antiparasitic treatment and dietary adjustments, the condition did not improve, and the male died. Laboratory analyses were negative for parasites, bovine coronavirus (BCoV), and paratuberculosis (serology). Liver copper concentration was 14.73 mg/kg DM, markedly below the physiological threshold (34 mg/kg DM).
In mouflon, chronic diarrhea and weight loss were observed during winter, primarily in older animals, along with sudden deaths across age groups. Necropsy of two animals indicated enterotoxemia, confirmed by isolation of *Clostridium perfringens*. An older animal with chronic diarrhea showed abomasitis and parasitic findings (low cecal, higher pulmonary nematode burden). Serology analyses for paratuberculosis were negative. Liver copper levels in three animals (20.13, 4.33, and 5.4 mg/kg DM) were significantly below critical thresholds (50 mg/kg,).
These findings are consistent with clinically manifested copper deficiency in wild ruminants. Given the reported prevalence of low hepatic copper levels in such populations, copper deficiency should be considered an important differential diagnosis in health disorders of wild ruminants, particularly in enclosed systems without mineral supplementation.

Keywords: copper deficiency, wild ruminants, Vojvodina

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P074. Welfare of game animals in fenced hunting grounds and breeding facilities

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Housing wild animals in fenced areas carries several risks that can compromise their welfare. Disruption of natural migration patterns limits access to natural food sources, while higher population density increases susceptibility to infectious and parasitic diseases. Wild animals kept in enclosed areas are thus placed in a situation similar to that of domestic animals—they become largely dependent on human care, while still retaining their instincts and behaviors. For this reason, sustainable management requires careful consideration of all factors affecting their health and welfare. Although game animals in fenced areas are not exposed to predators, which positively contributes to their welfare, the fence itself can pose a risk of injury or even death. One of the most important factors affecting welfare is nutrition, especially in wild ruminants, which largely depend on natural forage available within the habitat. Problems arise when the amount of available natural food decreases due to an increased number of animals, as well as when plant diversity declines and non-palatable species become dominant. This results in reduced food intake and the occurrence of malnutrition. Supplementary feeding is most commonly carried out during winter months and periods of drought, but if not properly planned, it can also lead to additional imbalances. The number and distribution of feeding sites also play a significant role in maintaining welfare. An insufficient number of feeding points, or their inaccessibility to certain groups, can result in unequal food intake, where dominant individuals consume more, while younger or weaker animals remain deprived. Furthermore, an inadequate distribution of feeding sites, which leads to the concentration of a large number of animals in one place, can increase the risk of pathogen transmission and thus threaten the health of the entire population. Lameness and excessive hoof growth in deer are often consequences of laminitis caused by excessive intake of concentrated, grain-based feed. Furthermore, in breeding facilities, the human–animal relationship plays a crucial role in ensuring animal welfare. Working with animals requires adequate conditions in terms of infrastructure, as well as well-trained personnel with a responsible approach. Handling procedures should minimize stress as much as possible, and in certain situations may require sedation or full anesthesia to ensure the safety of both humans and animals. Keeping wild animals in fenced areas requires careful management of habitat, nutrition, health risks, and human interaction to ensure their long-term welfare and sustainability.

Keywords: welfare, hunting game, management, human-animal relationship

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P075. The emergence and spread of fibropapillomatosis in red deer (*Cervus elaphus*) in Norway

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Papillomaviruses (PVs) are genetically diverse DNA viruses that cause benign proliferative lesions in a wide range of vertebrate hosts. In cervids, PV-associated fibropapillomatosis has been reported sporadically across Europe, but information on temporal and spatial spread within naïve populations remains limited. Fibropapillomatosis was first diagnosed in Norwegian red deer in 2019, and this study describes the emergence and subsequent spread within the Norwegian red deer population.

Data were obtained through the Norwegian wildlife health surveillance programme (ViltHOP), coordinated by the Norwegian Veterinary Institute. Cases were reported passively by hunters, municipal wildlife managers, the Norwegian Food Safety Authority and members of the public, with varying levels of metadata. Diagnoses were based on gross pathological examination of submitted carcasses or organs, or macroscopic assessment of photographs and case descriptions. Information on geographic distribution and timing of cases was collated for the period 2019-2025.

The first cases of fibropapillomatosis in red deer were identified in 2019 from two municipalities on the Norwegian west coast. In the following years, a rapid increase in reported cases was observed, with progressive geographic spread both northwards and southwards along the coast. By 2025, cases had been reported from a substantial number of municipalities in western Norway. Most reports occurred during the hunting season (September–December). Lesions were most frequently located on the inner thighs and inguinal region, but were also observed on the neck, abdomen, head and genital region. Lesions ranged from small solitary nodules to extensive multifocal lesions, occasionally with secondary ulceration and inflammation. Hunters in several areas reported an apparent high prevalence of affected animals in local populations.

Following its first detection in 2019, fibropapillomatosis has spread rapidly within the Norwegian red deer population, resembling patterns observed in cervid populations elsewhere in Europe; however, the route of introduction remains unknown, and the nearest regions with documented fibropapillomatosis are geographically distant. Increased awareness among hunters may have contributed to higher reporting rates; however, the clear temporal and spatial expansion suggest true spread within a previously naïve population. Continued surveillance is essential to monitor disease dynamics, assess potential population-level effects, and improve understanding of transmission and risk factors.

Keywords: fibropapillomatosis; papillomavirus; red deer; wildlife health surveillance; Norway

P076. Circulation of Domestic Dog Viruses in Wild Carnivores: Evidence from a Large-Scale Croatian Monitoring Program

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The substantial increase in wild canid populations in urban and peri-urban areas has highlighted the risk of interspecies transmission of infectious diseases. Wild canids, such as foxes and jackals, can serve as both hosts and vectors for common domestic canine viruses, facilitating the persistence of these viruses in the environment and enabling re-infection of pets or other wildlife. In this study, brain tissue samples from apparently healthy wild canids were screened for viruses that most commonly occur in dogs.
Brain specimens from 890 wild canids (red fox, golden jackal, grey wolf) and mustelids were analysed using polymerase chain reaction (PCR) followed by partial Sanger sequencing to detect the presence of canine distemper virus (CDV), canine circovirus (CanineCV), and carnivore protoparvovirus-1 (CPPV-1) genome sequences. These samples were systematically collected across Croatia from December 2023 to March 2025 as part of a nationwide oral vaccination campaign against rabies.
The CanineCV genome was most frequently detected (5.03%), followed by CPPV-1 (3.47%) and CDV (3.13%). Instances of coinfection were also documented. Genomic sequences were additionally identified in six mustelids. Sequence and phylogenetic analyses showed that: 1) wild canids in Croatia are more likely to be infected with feline parvovirus than with canine parvovirus; 2) circovirus sequences clustered with those from domestic dogs; and 3) CDV sequences showed identity with other CDVs from wild canids identified in neighbouring countries.
The genomic sequences of viruses commonly associated with significant infectious diseases in domestic dogs have been detected in the brain tissue of healthy wild canids. CPPV-1 and CDV identified in foxes, jackals, and wolves do not exhibit a direct genetic correlation with those derived from domestic canids, rather, these sequences appear to originate from wild canid lineages. Circoviruses found in foxes, jackals and wolf are related to dog circoviruses and may represent a potential risk to domestic dog populations. The genomic material identified may originate from asymptomatic infections or be residual from previous infections. These findings confirm that apparently healthy wild canids can serve as reservoirs of "domestic" pathogens, facilitating their presence within the ecosystem and the potential re-infection of domestic dogs or other wildlife, thereby complicating the efficacy of disease management strategies. Ongoing molecular surveillance of both wild and domestic carnivorous species is essential for identifying potential future host switches.

Keywords: wild canids, brain tissue, Canine CV, canine distemper virus, carnivore protiparvovirus-1

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P077. Is captivity associated with different microbiomes in two species of raptors?

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Every year, hundreds of injured, sick and orphaned raptors are admitted to wildlife rehabilitation centers. Antimicrobials and probiotic treatments are commonly used in raptor rehabilitation but may disrupt the gut microbiome, potentially affecting health and post-release survival. However, not much is known about what a healthy gut microbiome should look like or how captivity and treatments may modify it. The goal of this study was to evaluate if captivity and treatment influence the gut microbiome of raptors.

In this cross-sectional study, cloacal samples were collected between 2021-2022 from two raptor species, Red tailed hawks, RTHA (*Buteo Jamaicensis*) and Northern saw-whet owls, NSWO (*Aegolius acadicus*). Samples were collected from injured birds admitted to The Raptor Center (TRC) at the University of Minnesota (MN, U.S.) and the same two species were sampled from the banding station Hawk Ridge, HR (MN, U.S.). In TRC birds, samples were collected at the time of admission (timepoint A) and before release/euthanasia/transfer (timepoint B), while samples from HR were collected once during banding. DNA was extracted from all samples, and then the V4 hypervariable region from the 16SrRNA gene was sequenced to characterize bacteria. Alpha and beta diversity metrics were calculated, and Wilcoxon rank test and PERMANOVA were calculated to compare microbiomes in the groups.

Microbiomes were significantly different in birds from TRC and HR. Regarding alpha diversity within each bird, HR had significantly higher Pielou's evenness compared to TRC (P=0.03), although no significant differences were found in the number of bacterial species (richness p=0.12). In TRC-RTHA, higher richness was found in time A (mean: 195.3, SD: 96.5) over time B (mean:122, SD: 62.45), where the diversity between location was also significantly different (PERMANOVA: R2: 0.063, P<0.001). No significant association was found between antimicrobial use and microbiome in either captive bird species.

This study suggests that captivity is associated with different microbiome patterns. Considering that rehabilitated birds are intended to be released into the wild, this study is relevant for wildlife health and biodiversity.

Keywords: raptor, microbiome, antimicrobial, captivity

P078. Advanced Methods for the Analysis of Pheasant Semen Quality

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Advanced analytical methods enable precise evaluation of semen quality in avian species. Parameters such as sperm concentration and motility, acrosomal membrane integrity, DNA fragmentation and morphology strongly influence fertility and hatching success. Successful restocking programs depend, among other factors, on adequate reproductive capacity of captive-reared males. Limited information is available on semen quality and reproductive capacity in pheasants, despite their importance for restocking programs and maintenance of wild populations.

This study evaluated semen quality in pheasant roosters from a flock with reduced reproductive performance. Four 55-week-old males were analyzed before and after a period of sexual abstinence. Semen samples were collected from the vas deferens and seminiferous ducts following euthanasia and pathomorphological examination.

Pathomorphological findings showed good body condition and no pathological changes in internal organs. Testes were well developed but exhibited reduced vascularization, suggesting decreased functional capacity. Semen quality was assessed using CASA analysis, flow cytometry, and cytomorphological evaluation.

Results demonstrated preserved spermatogenesis but poor semen quality overall. Semen volume was low (2–50 µl), motility was reduced (total 26.35%, progressive 6.17%), and sperm concentration was low (333.059 million). Samples collected after sexual abstinence showed increased semen volume and slightly improved motility. Flow cytometry revealed generally preserved membrane and acrosome integrity, except in one individual with severe acrosomal damage (81.64%). Chromatin damage was higher before abstinence, while lower post-abstinence values (23.12 ± 12.47%; class II) indicated partial improvement. Cytomorphological analysis identified a high proportion of sperm with tails bent over the head (average 24%).

Feed analysis detected elevated concentrations of mycotoxins, suggesting a major role in impaired semen quality and reduced reproductive performance. The findings indicate that mycotoxin contamination of feed significantly decreased reproductive efficiency in the flock. Mycotoxins can represent a significant issue in the process of spermatogenesis, with their adverse effects being particularly pronounced during mitotic and meiotic processes, where they may cause inhibition of these processes, oxidative stress, DNA damage, and apoptosis.

These results emphasize the importance of advanced semen quality assessment methods together with strict feed quality control for monitoring reproductive performance and fertility in captive pheasant populations intended for restocking. Early detection of abnormalities in semen and mycotoxin contamination of feed, allows timely corrective measures and improvement of reproductive efficiency and overall production performance. Such research is particularly important because farm-reared pheasants are routinely released into natural habitats, where impaired male fertility may influence the reproductive success and genetic contribution to wild populations.

Keywords: CASA, flow cytometry, cytomorphology, mycotoxins, acrosome, DNA fragmentation

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P079. Novel Description of Cartilage and Bone at the Aortic Base of Free-Ranging Eurasian Lynx (*Lynx lynx*) from Switzerland

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Systematic postmortem examination of free-ranging Swiss Eurasian lynx (*Lynx lynx*) led to the incidental discovery of cartilage and bone at the aortic base by histopathology. Such tissues, present in a few species, are termed heterotopic cartilage and bone, and when located in the cardiac skeleton, are referred to as *cartilago* and *ossa cordis*, respectively. They are hypothesised to occur in areas exposed to mechanical stress and may contribute towards structural support of the heart. They have also been reported in association with cardiac pathologies. In Eurasian lynx, these structures have recently been reported in association with subaortic stenosis. Here, we present histopathological features of chondral and osseous tissue observed in lynx hearts to explore potential links between these structures and cardiac pathologies in a species of conservation concern.

We retrospectively assessed the presence of chondral and osseous tissue in lynx carcasses submitted to our institution for postmortem examination over a 16-month period (09.2024–12.2025). Appearance and location of chondral and osseous tissue were assessed on a H&E-stained longitudinal section through the interventricular septum at the level of the right coronary cusp of the aortic valve. In addition, concurrent cardiac pathologies were documented.

When present, a single focus of well-differentiated chondral or osseous tissue was consistently located within the connective tissue at the aortic base, in proximity to the *annulus aortae*. The morphological spectrum ranged from mature hyaline cartilage and calcified cartilage to well-differentiated lamellar bone, occasionally containing fatty or haematopoietic marrow. Overall, out of 51 cases, chondral and osseous tissue were observed in 20 lynx across all age groups and both sexes (prevalence: 39.2%). In 19 of 20 cases, additional cardiac lesions were present, including myocardial fibrosis, arteriosclerosis, inflammation, and one case of subaortic stenosis.

A considerable proportion of Swiss lynx exhibit cartilage and bone in their heart. Determining whether these structures represent *cartilago* and *ossa cordis* requires further analysis of their precise location. Their occurrence may be physiological, as described in other species. However, their simultaneous occurrence with other cardiac pathologies suggests a potential pathological process in their development. Further investigations could focus on whether other Eurasian lynx populations show similar findings in the cardiac skeleton, which would help clarify their relevance to cardiac health in Swiss lynx, an important aspect of the species' conservation.

Keywords: *Cartilago cordis*, *ossa cordis*, cardiac health, wild felids, wildlife health surveillance

P080. Analgesia and Wildlife Immobilisations – a promising start in the Eurasian lynx

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Foot-snares installed at prey are an efficient, selective, and safe capture method for immobilising free-ranging Eurasian lynx. In contrast to télédart systems, they can be safely applied in mountainous terrain while maintaining a high selectivity in comparison to box traps. However, the thus immobilised lynx retains a certain range of motion in the trap and can exert considerable force on the caught limb. This results in muscular and other soft tissue damages, likely culminating in inflammatory reactions and pain. To mitigate these negative impacts, we implemented the application of meloxicam - a non-steroidal anti-inflammatory drug (NSAID) - into the capture protocol. We hypothesise that lynx receiving meloxicam will experience less pain post-capture and consequently move more. Here we present the first data comparing movement speed of lynx that received meloxicam to lynx that did not receive any NSAIDs.
We captured 11 female free-ranging Eurasian lynx in foot snares within the framework of research projects in the Swiss Alps and Midlands between 2021 and 2026. All animals underwent general anaesthesia and were equipped with a GPS collar. Three animals were captured twice, resulting in a total of 14 capture events. Starting in 2023, lynx received a subcutaneous injection of 0.2 mg/kg meloxicam (n=6 capture events). We compared the median movement speed (meters/hour) within the first 48 hours after the antagonisation of the anaesthesia.
Lynx that received meloxicam during the immobilisation showed a higher mean of median movement speed (n=6, mean=143 m/h) during the first 48 hours post-capture compared to lynx that did not receive meloxicam (n=8, mean=74 m/h). This increase in the covered distance per hour was particularly pronounced 24-48 hours post-capture – the period corresponding to the night following the capture.
Our results suggest that the administration of a single dose of meloxicam reduces inflammatory pain to such an extent that it has a noticeable effect on the movement behaviour of lynx. Considering the low sample size as well as individual variations, such as age, reproductive status and characteristics of the home range we consider the marked increase in movement speed highly promising. These findings indicate that even small refinements in immobilisation protocols could result in measurable improvements of animal welfare in wildlife immobilisation procedures.

Keywords: refinement, animal welfare, capture methods, meloxicam, *Lynx lynx*

P081. Smarter disease risk analysis for better conservation translocation decisions

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Conservation translocations, including population reinforcements, reintroductions and conservation introductions, aim to restore wildlife populations and ecosystems. However, they pose multiple risks, including disease risks to wildlife, domestic animals, humans, and the translocated individuals themselves. Disease risk analysis (DRA; also called health risk analysis) is used to characterise and manage these risks. Existing DRA approaches are typically qualitative, time-consuming and often siloed from other aspects of translocation planning. The DRA process is frequently constrained by limited data and high uncertainty, and it remains challenging to translate qualitative risk estimates into transparent, comparable and actionable management decisions. Here, we present a set of methodological tools designed to expedite DRA for conservation translocation and to strengthen its scientific rigour and utility for decision making.

DRA comprises the key steps of hazard identification and risk assessment and sits within a broader framework encompassing disease risk management and post-release health surveillance. It is intended to inform decision making across the translocation lifecycle. Over the last decade, we have developed novel methodological approaches for different stages of the process and applied them in DRAs for multiple conservation translocations.

To expedite the DRA process, for hazard identification we propose aggregating infectious hazards across defined transmission pathways associated with translocation, termed 'infectious hazard pathways'. To reduce reliance on single-expert opinion and strengthen the scientific rigour of DRA, we introduce a novel semi-quantitative approach to risk assessment based on formal expert elicitation. To address the common separation between risk assessment and management, we integrate evaluation of alternative management options within the DRA process.

The aggregation of infectious hazards across infectious hazard pathways enables scalable and context-adaptable DRAs. The semi-quantitative, elicitation-based approach to risk assessment captures variation in expert judgement, highlights agreement and disagreement, and communicates uncertainty transparently. Integrating evaluation of alternative management options within the DRA process allows direct comparison of estimated risks across disease risk management strategies and translocation scenarios. To streamline repeat DRAs, we advocate the development of taxon-specific reference lists of hazards and management measures. Together, these approaches represent practical advances in DRA for conservation translocation, with broader applicability to other wildlife disease risk contexts.

Keywords: Disease risk analysis, health risk analysis, wildlife, conservation translocation, reintroduction

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P082. Radiographic Prevalence of Metabolic Bone Disease in a Population of South-West England European Hedgehogs (Erinaceus europaeus) and Associated Risk Factors

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European hedgehog (*Erinaceus europaeus*) populations are declining, and nutritional imbalances are increasingly recognised as threats. Metabolic bone diseases (MBD) are disorders of bone density caused by disrupted calcium–phosphorus (CaP) homeostasis. This study investigates the radiographic prevalence of MBD in 122 hedgehogs from South-West England and examines associations with dental disease, region, age and sex supported by histopathology and urinalysis. Radiographs were graded for MBD severity and selected cases underwent histopathological confirmation; dental disease was scored independently. Urine samples were analysed to identify disproportionate calcium and phosphorus excretions. Radiographic evidence of MBD was present in 61.3% of hedgehogs, with 11.6% classified as severe. Typical findings included diffuse osteopenia, cortical thinning and pathological fractures. Histology confirmed lesions were consistent with osteoporosis, osteomalacia and rickets. Dental disease was common with grade 2 being most frequent (34.1%). MBD severity correlated significantly with dental disease severity (ρ = 0.22, p = 0.0146). Regional differences were observed; severe cases were limited to Somerset and Gloucestershire. No significant associations were identified between MBD grade and age or sex. Urinalysis revealed high inter-individual variability; in the healthy subgroup, juveniles had higher Ca:Cr and P:Cr ratios than adults (p = 0.042 and p = 0.028), whereas no significant age-related differences were detected within MBD cases. The high prevalence and statistical correlation of MBD and dental disease suggests nutritional imbalances as a potential driver of skeletal pathologies. Reassessing dietary requirements and developing appropriate guidelines for wildlife rescue centres and the public are essential to steer conservation strategies and improve welfare.

Keywords: European hedgehog, *Erinaceus europaeus,* metabolic bone disease, dental disease, X-rays.

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Competing interests: The author declares no relevant financial or non-financial interests to disclose.
Ethical Approval: This study uses deceased hedgehogs donated from wildlife centres for post-mortem evaluation. Ethical approval number: UIN-25-037 (expiry date: 02/04/2028).

P083. Comparative histological characterization of the epidermis in Portuguese wildlife

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The skin plays essential roles in protection, thermoregulation, and interaction with the environment. Histological characterization of skin in wild species provides important information on structural variation with potential application in veterinary dermatopathology. This study aimed to describe and compare the epidermal layers of selected species of Portuguese wild fauna, highlighting their diagnostic relevance and association with species-specific adaptations.
Skin samples were collected from the dorsal region of five wild species: wild boar (*Sus scrofa*), European badger (*Meles meles*), Eurasian otter (*Lutra lutra*), roe deer (*Capreolus capreolus*), and ladder snake (*Rhinechis scalaris*) at the UTAD Wildlife Rehabilitation Centre. Samples were fixed in 10% buffered formalin, routinely processed, embedded in paraffin, sectioned at 4 µm, and stained with hematoxylin and eosin. Histological slides were digitized, and the thickness of the total epidermis, viable epidermis, and stratum corneum was assessed morphometrically.
Marked interspecies variation was observed across all epidermal layers. The ladder snake exhibited the lowest values for total epidermis (145.24 ± 27.8 µm), viable epidermis (108.93 ± 29.7 µm), and stratum corneum (36.31 µm). The roe deer presented 1,296.07 ± 203.6 µm, 1,232.71 ± 204.8 µm, and 63.36 µm, respectively. The wild boar showed 1,884.38 ± 385.4 µm, 1,812.25 ± 379.6 µm, and 72.13 µm. The otter presented 2,035.23 ± 200.3 µm, 1,933.42 ± 233.0 µm, and 101.81 µm, respectively, while the badger exhibited the highest values: 2,124.77 ± 531.7 µm, 2,009.84 ± 544.6 µm, and 114.93 µm. The stratum corneum represented 25.0% of total epidermal thickness in the ladder snake, compared with only 3.8–5.4% in mammals. The stratum spinosum ranged from 2–3 layers in the ladder snake to 5–7 layers in the badger, while the stratum granulosum was absent or poorly differentiated in the ladder snake and comprised 1–3 layers in mammals. The ladder snake also showed a distinctive lamellar, coiled stratum corneum consistent with reptilian ecdysis, contrasting with the compact orthokeratotic cornification seen in all mammalian species.
These findings provide baseline histological data on the epidermal structure of five Portuguese wild fauna species, contributing to the understanding of species-specific skin adaptations and their potential applications in wildlife dermatopathology. Future studies including more species and anatomical regions will help establish validated reference patterns.

Keywords: skin; epidermis, histology; wild fauna; comparative morphology.

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Session 5

Avian influenza, African swine fever & potential pandemics in wildlife

Oral Presentations

Environmental Risk Mapping of African Swine Fever in Wild Boar Using MCDA with Exploratory Fly-Based Surveillance

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African swine fever (ASF) is an internationally spreading, viral pig disease with a high case fatality ratio and a massive socioeconomic impact. The disease is particularly challenging to control if it occurs in the native wild boar population, where the disease can persist and facilitate further spread, threatening agricultural pig production and trade. Identifying high-risk areas and accurately delineating outbreak zones are critical for targeted and resource-efficient control strategies.
A previous systematic review (Bergmann et al., 2022, https://doi.org/10.3390/v14102107) identified environmental risk factors for ASF occurrence, which were integrated into a spatial multi-criteria decision analysis (MCDA) model to map environmental risk in eastern Germany. Building on this work, we conducted an updated systematic literature review to capture newly reported environmental risk factors associated with the ongoing global spread of ASF. From 1414 deduplicated records, 201 were selected for full-text analysis, revealing additional evidence that further strengthened existing risk factors, and which were used to refine the MCDA model. The updated model integrates current evidence to generate risk maps that support the identification of high-risk areas in both disease-free and affected regions, thereby informing risk-based surveillance and control planning.
In parallel, we explore the potential of fly-based environmental surveillance as a complementary tool for outbreak delineation. Flies trapped in Europe regularly contain wild boar DNA through contact with boar excrement and carcasses. Flies have previously also proven useful for mapping the spatial extent of environmentally tenacious pathogens (e.g., sylvatic anthrax; *Bacillus cereus* biovar *anthracis;* Jahan et al., 2023, https://doi.org/10.1002/edn3.401). Guided by the updated risk maps, flies are being collected in and around an active ASF outbreak, including near infected carcasses, to assess the detectability of ASFV and the feasibility of this approach for spatially resolving outbreak extent.
This combined approach links evidence-based risk mapping with targeted field surveillance. While MCDA-derived risk maps support proactive identification of high-risk areas, fly-based surveillance may offer a novel, non-invasive method to complement conventional field data for early and spatially explicit outbreak delineation.

Keywords: African Swine Fever, Wild Boar, Risk Factors, Risk Mapping, Fly-Based Environmental Surveillance

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Integrating Hunting with Strategies for African Swine Fever Control in Wild Boar: Lessons from Europe

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African swine fever (ASF) remains one of the most challenging transboundary animal diseases affecting both domestic pigs and wild boar populations worldwide. The persistence of the African swine fever virus (ASFV) in the environment and within wild boar populations complicates control efforts, particularly in Europe where wildlife plays a critical epidemiological role. Hunting is frequently proposed as a key tool for managing wild boar populations and limiting disease spread; however, its effectiveness remains controversial and highly context dependent. This study provides a comparative analysis of ASF control strategies implemented across European countries, focusing on the role of hunting within integrated disease management frameworks. Drawing on published scientific evidence and operational experiences, the analysis examines key interventions including surveillance systems, carcass search and removal, fencing, zoning, and population reduction measures. The findings highlight that successful ASF eradication is consistently associated with early detection of the disease at a limited spatial scale, followed by rapid implementation of coordinated control measures. In these contexts, hunting activities were initially suspended within infected areas to prevent disturbance-induced dispersal of wild boar. This was combined with the rapid establishment of physical barriers and intensive enhanced passive surveillance based on systematic carcass detection and removal. Only after effective spatial containment was achieved, hunting was reintroduced in a highly regulated manner as a targeted depopulation tool under strict biosecurity supervision. In contrast, where measures were delayed or poorly coordinated, hunting alone did not prevent continued spread. In these cases, hunting alone did not prevent virus persistence and, in some situations, may have contributed to disease spread through increased animal movement and human-mediated transmission. Overall, the study demonstrates that hunting is neither inherently beneficial nor detrimental for ASF control. Its epidemiological impact depends on timing, coordination, and integration within a structured and veterinary-led control strategy. Effective ASF management requires a combination of wildlife population management, surveillance, biosecurity, and strong governance, with hunters acting as operational partners within a coordinated system rather than independent actors. These findings provide practical insights for designing adaptive and evidence-based ASF control policies, emphasizing the need to move beyond simplistic approaches and toward integrated, context-specific strategies for wildlife disease management.

Keywords: African Swine Fever Virus (ASFV); epidemiology; hunting; wild boar

Genetic evolution of a panzootic pathogen – African swine fever virus complete genome sequencing in Germany

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Over the past two decades, African swine fever virus (ASFV) has emerged as a panzootic pathogen affecting wild and domestic suids with significant ecological and socio-economic impacts. Following the introduction of genotype II into Europe in 2007, the virus spread across Eastern Europe and reached Germany in September 2020. Subsequent outbreaks occurred in wild boar and domestic pigs, particularly in federal states bordering Poland, with occasional introductions into previously unaffected areas. In this study, sample sets collected from 2020 to 2026 were sequenced to monitor the evolutionary history of ASFV in Germany and to implement a meaningful molecular epidemiology based on viral complete genomes.

Complementary short-read Illumina and long-read nanopore sequencing methods were implemented for complete genome sequencing from a broad spectrum of sample matrices. Obtained complete genome sequences were screened for genetic markers and classified in lineages and variants according to characteristic mutational patterns. Phylogenetic analyses were conducted to reconstruct the genetic relationship between German variants and published ASFV complete genomes.

Between 2020 and 2026, over 50 complete genomes from eight federal states were generated and analysed. Sequences obtained from East Germany showed characteristic mutations that were previously described for Polish ASFV variants. With the continued circulation in East German wild boar populations from 2020-2024, the ASFV genome underwent a steady genetic diversification resulting in five distinct lineages represented by characteristic mutation patterns. While case numbers significantly declined in East Germany in 2024 and 2025, two independent introductions into wild boar founded new ASFV outbreak cluster in West Germany. Phylogenetic analyses of sequences from both ASFV incursions revealed a high genetic relationship with sequences from Italy and South East European countries.

The ongoing genetic monitoring of German ASFV outbreaks presents a crucial complementation for in-depth epidemiological investigations. Due to the high resolution of complete genome datasets, the spread and evolution of distinct virus lineages and variants was revealed, and new introductions were traced back to potential sources within and across Germany.

Keywords: African Swine Fever Virus, Next-Generation Sequencing, Molecular Epidemiology, Complete Genomes

Re-emergence of African Swine Fever in Spain: early spread dynamics and control in wild boar

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African swine fever (ASF) re-emerged in Spain in wild boar after more than 30 years of absence, in a densely populated area near Barcelona. This study quantifies the early spatiotemporal dynamics of the outbreak and summarizes key control measures implemented during the initial response.
Measures included enhanced passive surveillance based on systematic carcass search with trained dogs, rapid carcass removal, targeted population reduction, and installation of movement barriers. Surveillance data between November 2025–March 2026 were analysed using reconstructed mortality timings for carcasses and epidemic front analyses to assess early spread of the outbreak.
ASF virus (genotype II) was first confirmed in two wild boars found dead the 25th and 26th of November 2025. Initial emergency zoning defined a 20 km infected area with a 6 km high-risk zone. Subsequent regionalisation (restricted zone I and II) was applied to support risk-based containment. By March 2026, 243 wild boar cases tested PCR-positive out of 2437 cases analysed. Positivity was strongly associated with passive surveillance streams (96.3 % enhanced passive vs 3.7% active surveillance). Cases were spatially restricted to two sectors within the managed area. Reconstructions of the timeline indicated that virus circulation likely began around early September 2025. Median detection delay on wild boar carcases was 4 days (up to 82 days). Spatial spread remained limited, probably because of the physical barriers applied. The outbreak front reached ~12 km from the inferred origin over 204 days (based on estimated t_0), with a mean radial spread of 0.066 km/day (~1.98 km/month). However, spread was non-linear, with a significant increase in speed after late December. Directional analyses showed marked anisotropy, with faster expansion towards the southern sector.
ASF circulation preceded detection by several weeks, underscoring the importance of robust passive surveillance systems for early detection. Rapid implementation of carcass search, containment measures, adaptive zoning, and wild boar density management is critical for effective ASF control. This outbreak also highlights the potential role of urban wild boar in facilitating long-distance spread of ASF.

Keywords: African swine fever, wild boar, epidemiology, surveillance, emerging infectious diseases

African swine fever in Lombardy: strategies for the management of the disease in wild boars

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African swine fever virus (ASFV) was introduced in Lombardy (northern Italy) in 2023. The study analyzes the strategy adopted for the management of the wild boar (Sus scrofa) population in different affected areas of the region, through four years of continuous surveillance (2022–2026).
Camera trapping and the application of the Random Encounter Model (REM) were used to investigate population dynamics obtaining quantitative estimates of the density and evaluate the effectiveness of the control measures adopted. The necessary effort used in different years and in different phases of disease expansion was also evaluated both for culling purposes and for the active search for carcasses. This study was conducted in three ASF-affected areas: Oltrepo Pavese, Parco del Ticino e a part of the CEV Zone falling within the province of Lodi.
The results showed a significant reduction in wild boar (Dt1=6.73±2.56 ind/km^2) population density following the introduction of the virus, with a progressive downward trend up to minimum values of 0.6 individuals/km^2. The integration of the REM estimates with the data on felling (n = 2,054, of which 1,940 ≥ 6 months) made it possible to quantify the effectiveness of the felling activities, estimated on average at 12.25%, with marked variability between the different monitoring periods. The analysis of the population structure showed a constant predominance of the adult class and fluctuations in the youth component, with signs of demographic resilience even in the presence of the disease and management pressure. The effort required to search for and remove carcasses is closely related to the density of the population, but also to the type of main habitat present in the study area.
The study demonstrates how, in a disease control strategy, knowledge of the ecological characteristics of the affected populations is fundamental for disease eradication in complex epidemiological contexts. The results provide useful indications for optimizing surveillance and containment of the affected species, in order to limit the spread of the disease.

Keywords: African swine fever, Wild boar, Camera trapping, Population dynamics.

Relevance of wildlife rescue centres in the epidemiological surveillance of high pathogenicity avian influenza in France

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Outbreaks of high pathogenicity avian influenza (HPAI) in wild bird populations were historically rarely associated with high mortality. Recent epidemiological changes (e.g. panzootic, host range, seasonality, lethality rates) drive wildlife rescue centres (WRCs) to question their involvement in HPAI surveillance. French WRCs admit each year approximately 150 000 distressed live wild animals. Here we aim to explore the exposition of bird populations admitted in WRCs to avian influenza viruses (AIV) subtype H5 in in order to identify the most relevant strategy for HPAI surveillance in WRCs, in respect to pre-existing cost-effective, mortality-based surveillance programmes.
We recruited five voluntary French WRCs which collected oropharyngeal and cloacal swabs on admitted wild birds following pre-determined inclusion criteria between June 2024 and March 2025. Swabs were tested for subtype H5 AIV and positive samples were submitted for sequencing in order to determine the pathotype. Results were analysed in regard to surveillance data provided by the French mortality-based surveillance programme to identify complementarities.
Over the study period, 3422 swabs were collected from 1754 birds (107 species), of which 24 showed positivity for AIV subtype H5. Most of the positive birds belonged to the *Laridae* family (19/24). Positivity was not systematically associated with HPAI compatible clinical signs. Analysis of the spatio-temporal detections suggest that, in some situations, WRCs could be able to contribute to the early detection of viral circulation.
WRCs could be a useful complement to traditional wild bird surveillance programmes for HPAI. Specific aims (such as description of non-lethal circulation, early detection, etc.) and cost-effective strategies need to be discussed to shape a novel, WRC-led HPAI surveillance scheme.

Keywords: wildlife rescue centre, surveillance, HPAI, early detection

Funding source: OFB and ENVT PhD grant.

Identifying undersurveilled wild bird species associated with highly pathogenic avian influenza outbreaks using large-scale citizen science data

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Highly pathogenic avian influenza (HPAI) represents an increasing threat to wildlife, livestock, and public health, yet transmission dynamics within wild bird communities remain insufficiently understood. Since 2021, its epidemiology in wild birds has shifted in ways that challenge long-standing assumptions. Infections have expanded to taxa not previously considered important hosts, including larids and crane species, and across a broader geographic range. These changes have been accompanied by unprecedented mortality events and a breakdown of established seasonal patterns, with outbreaks becoming increasingly difficult to predict. Together, these changes call into question surveillance frameworks built around a narrow set of historically implicated species. We identify undersurveilled species that share ecological niche space with known HPAI reservoir taxa and may represent overlooked links in interspecific transmission networks.

We analyse eBird, a large-scale citizen science dataset comprising over 100 million wild bird observations across the Western Palearctic, to characterise ecological niches of nearly 1,000 species, including many that fall outside conventional surveillance programmes. We integrate weekly species occurrence records with high-resolution environmental and life-history covariates, including land cover, vegetation indices, climate variables, topography, and traits drawn from the BIRDBASE database. Using a bayesian multivariate niche framework, we estimate species-specific niches and quantify pairwise niche overlap within ecologically defined species clusters.

Our results reveal substantial niche overlap between known host species and numerous co-occurring, often overlooked species whose ecological and behavioural traits associations place them in repeated contact with high-risk environments. Many of these species are underrepresented in surveillance data, limiting our ability to assess their role in HPAI dynamics.

These findings highlight the value of large-scale citizen science bird occurrence data as a complementary source of ecological information to guide targeted HPAI surveillance, providing a spatially and ecologically explicit basis for prioritising species for epidemiological monitoring.

Keywords: highly pathogenic avian influenza, wildlife, citizen data, Europe

Exposure to diverse avian influenza viruses in sympatric UK seabirds

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H5N1 clade 2.3.4.4b high pathogenicity avian influenza virus (HPAIV) has caused substantial global mortality across domestic and wild avian species, with a shift in viral ecology and unusual expansion in affected host range. Viral reassortment of HPAIV with co-circulating low pathogenicity AIV (LPAIV) subtypes facilitated extensive viral spread among previously unaffected seabird species, with unprecedented mass mortality. Further, the wide-ranging migratory and foraging movements of seabirds have been implicated in both local, and inter-continental, dissemination of HPAIV. Understanding the epidemiology of circulating AIV subtypes is vital in predicting the ongoing risk of viral reassortment, persistence and transmission of AIV within global seabird populations.

We assessed for evidence of LP and HPAIV in apparently healthy individuals of 15 breeding seabird species from populations across the UK. We tested birds for active AIV infection via rRT-PCR and for previous exposure to AIV via ELISA for antibodies (Abs) against the nucleoprotein (NP) of Influenza A virus, highly conserved among all AIV subtypes, and for Abs specifically against H5 AIV. We then used a multiplex, Luminex-based assay to identify antibody subtypes in a subset of individuals (n=113).

Seropositivity for NP Abs ranged from 0–100% across species with species differences in prevalence and dominant subtypes persisting across years. Abs to diverse circulating subtypes were detected (n=15 HxNx subtypes), with the highest subtype diversity observed in auks. Exposure to multiple subtypes was noted in 5 individuals. Prevalence levels of active virus are currently being analysed.

Evidence of diverse circulating subtypes, and the exposure of individuals to multiple subtypes, reveals ongoing potential for viral reassortment and spread of subtypes with novel characteristics. These results highlight the importance of serological testing in apparently healthy migratory species, providing crucial information regarding the potential occurrence, transmission and reassortment of AIV subtypes across populations, and highlighting potential species of importance for ongoing serological monitoring.

Keywords: avian influenza; seabirds; antibodies; subtype diversity; exposure

Session 5

Avian influenza, African swine fever & potential pandemics in wildlife

Poster Presentations

P084. African Swine Fever Virus Transmission Dynamics and Population Impact in an Enclosed Wild Boar Hunting ground: A Serbian Case Study

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African swine fever (ASF) represents one of the most important viral diseases of wild boars with strong influence in hunting management. In Serbia, ASF virus was detected for the first time in the wild boar population in 2020 and since then the virus has been confirmed in more than 90 hunting grounds. The aim of the work was to present the transmission dynamics of ASF virus in the fenced hunting ground located in Vojvodina region.
The studied hunting ground is a lowland-type hunting area, with a total fenced area of 2,281.00 ha. The epidemiological investigation was conducted in the 2023-2026 period i.e.in two consecutive hunting seasons. After the first detection of ASF the epidemiological data included the analysis of wild boar population positive samples structure according to the age and sex. The samples for laboratory diagnostic included the long bones or/and blood swabs. The data collected in the frame of passive surveillance were systematically presented through the more than three years period and analysed according to the season.
After the first detection of ASF virus in the hunting ground during the 2023- 2024 hunting season, a total of 84 wild boar carcasses were found, of which 95% tested ASF positive (molecular diagnostics, real-time PCR). In the first year, the highest number of positive results was detected in the period from September to November. During the next 2025–2026 hunting season, only a total of 9 wild boar carcasses were found, all of which tested ASF positive. With regard to age category in the 2023–2024 hunting season, adult categories older than 3 years predominated (58.75%). In terms of sex, ASF-positive wild boars were more frequently males (61.25%) compared to females (38.75%). In contrast, in the 2025–2026 hunting season, the virus was predominantly detected in samples originating from sub-adult (growing) individuals (88.9%), while in terms of sex, females predominated (66.7%) among ASF-positive cases.
The obtained results indicate that, after its introduction into a fenced hunting ground, the virus exhibits a characteristic target population dynamic, with the highest mortality in the first year occurring among adults. The second hunting season showed a lower mortality rate, predominantly affecting younger categories. The source of infection remains an open question. Considering the large number of ASF outbreaks in the domestic pig population in villages surrounding the hunting ground, the anthropogenic factor cannot be excluded.

Keywords: wild boars, ASF, enclosed hunting ground, Serbia

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P085. Characterisation of wild boar carcass decomposition in a temperate ecoregion: environmental drivers and implications for African swine fever surveillance

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African swine fever (ASF) remains a critical threat to the European swine industry and wild boar populations. Carcasses of infected animals contribute significantly to virus persistence, making the understanding of decomposition dynamics crucial for effective surveillance and control of ASF. This study aimed to (i) characterise seasonal patterns of wild boar carcass decomposition and (ii) develop predictive models linking decomposition rates to environmental factors.
The study was conducted in the Regional Park of the Euganean Hills (PRCE), with two sites selected based on pedoclimatic suitability for the placement of wild boar carcasses. Four seasonal trials were carried out, each lasting at least 60 days, using three wild boar carcasses per site. Ambient temperature and relative humidity were continuously recorded at 30-minute intervals. Carcass decomposition was assessed through field inspections using the Total Body Score (TBS), divided into four stages: fresh (1–3), early decomposition (4–13), advanced decomposition (14–25), and skeletonization (26–35). Seasonal decomposition patterns and relationships with environmental variables were modelled using an Information-Theoretic approach (IT-AICc) combined with Generalized Additive Models (GAMs).
Decomposition varied with season, progressing slowest in winter and fastest in summer, with spring and autumn showing intermediate rates. Considerable variability characterised the early post-mortem interval, indicating an influence of microclimatic conditions, particularly precipitation rate and short-term thermal fluctuations. After 25–30 days, carcasses generally reached advanced decomposition and skeletonization. The IT-AICc models identified accumulated degree days (ADD), mean humidity, and daily temperature range as key predictors. GAM analyses revealed non-linear relationships and potential interactions among variables, suggesting the effect of additional biotic constraints, likely related to entomofauna, on carcass degradation.
The study provides a detailed characterisation of wild boar carcass decomposition in a temperate ecoregion, identifying environmental determinants of decay. These findings inform ASF surveillance and epidemiological assessments, offering a transferable framework for predictive modelling in comparable ecological settings to support context-specific ASF management.

Keywords: ASF, wild boar, surveillance, decomposition

Funding source & Acknowledgement: This work was supported by the Ministry of Health, Italy (RC IZSVe 06/2022).

P086. Biosecurity Measures in Wild Boar Hunting Grounds in the Vojvodina Region: From Theory to Practice

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The practical implementation of biosecurity measures has made substantial progress over the past decade in the domestic pig sector. However, when it comes to biosecurity measures in wild boar hunting grounds, major challenges are encountered in bridging the gap between theoretical concepts and what is feasible under practical field conditions.
In the present study, environmental and regional risk factors were considered from an epidemiological perspective in ten wild boar hunting grounds located in the Vojvodina region. According to location and habitat characteristics of the hunting grounds, the possibilities for the practical implementation of both external and internal biosecurity measures under field conditions were descriptively analyzed.
With respect to external biosecurity, the critical risk factors identified in the majority of hunting grounds include the immediate presence of rivers, as well as proximity to main transport routes. The domestic pig population can be viewed at two risk levels, but the most important is the free-range domestic pig population located in nearby forests. The second is the immediate proximity of villages and rural households with domestic pigs surrounding the hunting grounds. Within internal biosecurity, the critical risk factors identified include the possibility of entry by unauthorized persons (illegal hunting, collection of mushrooms, berries, wood by local residents). An additional risk is the safe disposal of inedible offal following the wild boar hunting. A critical environmental factor is the availability of sources of running potable water, which is essential for carcass processing after hunting and for the hygiene measures in general. In all hunting grounds, the entry of transport vehicles (equipment, feed delivery), as well as hunters entry, is strictly controlled. Additionally, in the cases of introduction of new wild boars, quarantine measures are strictly implemented in accordance with Serbian legal regulations.
The practical implementation of biosecurity measures in wild boar hunting grounds is not straightforward under field conditions. Numerous factors related to the local environment and geographical characteristics of the area cannot be realistically controlled. A particular challenge is posed by human activities and settlements, which have dynamically changed over time and are increasingly encroaching upon hunting grounds. The key biosecurity risks identified in our study are human–wild boar interactions, as well as the potential interface between wild boars and the domestic pig population.

Keywords: biosecurity measures, wild boars, hunting grounds, Vojvodina

Funding source & Acknowledgement: This work was funded by Ministry of Science, Technological Development and Innovation of Republic of Serbia by the Contract of implementation and funding of research work of NIV-NS in 2026, Contract No: 451-03-33/2026-03/200031.

P087. Emergency response protocols for preventing the transmission of Highly Pathogenic Avian Influenza as a Tool for the Conservation of Threatened Species

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The emergence of the H5N1 strain of Highly Pathogenic Avian Influenza (HPAI), specifically Clade 2.3.4.4b, has fundamentally shifted the conservation landscape for European avifauna. This strain is has resulted in rapid disease transmission and unprecedented mass mortality events in wild bird populations, particularly among colonially breeding species closely associated with waterbodies (which can serve as viral reservoirs). As part of a European Commission-funded contract to identify and implement conservation measures for Birds Directive Annex II species in non-secure conservation status, we outline an emergency HPAI response protocol to be triggered in the case of suspected HPAI infections at colonies to mitigate outbreaks, with specific reference to Black-headed Gull (*Chroicocephalus ridibundus*) and Mew Gull (*Larus canus*). Protocols should include surveillance (establishing passive and active surveillance at critical colony sites to monitor for sick or dead birds), access restriction (closing colony sites to the public and suspending nearby high-stress activities, such as hunting or recreation, to prevent human-mediated transmission and bird dispersal), biosecurity (enforcing strict disinfection of equipment and clothing for essential personnel) and carcass management (evaluating the removal of carcasses on a site-by-site basis to reduce viral load while weighing the risks of entry-induced disturbance). These actions should be integrated into a "One Health" approach, recognizing that the health of wild bird populations is indistinguishably linked to broader environmental and public health issues. To ensure accountability, Member States are expected to implement this measure and report progress through annual questionnaires as part of this EU-wide process. This measure illustrates how targeted disease management should be undertaken to support the recovery and long-term conservation of threatened European bird species.

Keywords: HPAI, avian influenza, policy, conservation

P088. Exposure to avian influenza virus across distinct populations of Barnacle Geese (*Branta leucopsis*) in the UK

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Re-emergence of high pathogenicity avian influenza virus (HPAIV) has caused devastating mortality of wild birds on an unprecedented global scale. Understanding the epidemiology of HPAIV and co-circulating low pathogenicity (LP) AIVs in previously unaffected migratory avian species is vital in predicting ongoing viral persistence, transmission and risk across migratory routes. Barnacle Geese (*Branta leucopsis*) are long-distance migrants with distinct flyway populations. Largely unaffected in previous outbreaks of HPAIV, Barnacle Geese suffered unusual mass mortality following recent re-emergence of H5N1 clade 2.3.4.4b HPAIV in Europe. With flyway routes to the Arctic, these birds now form a key species of interest regarding potential inter-continental transmission, yet epidemiological evidence of AIV, and of factors dictating variation in infection across their flyway populations, remains limited.

We assessed for evidence of LP and HPAIV in five distinct populations of Barnacle Geese in the UK in 2024 and 2025: two migratory populations with distinct long-distance flyway routes, and three naturalised populations with more limited movement, noting a degree of mixing between two of the five populations. Apparently healthy birds were tested for active AIV infection via rRT-PCR, and for previous exposure to AIV via ELISA, testing for antibodies (Abs) against the nucleoprotein (NP) of Influenza A virus, highly conserved among all AIV subtypes, and for Abs specifically against H5 AIV. We then used a multiplex, Luminex-based assay to identify Ab subtypes in a small subset of individuals (n=11).

Seropositivity for NP Abs ranged from 48-92.3% across populations, with a range of 28-58.6% for H5 specific Abs. Significant differences in both H5 and NP Ab levels were detected between one migratory and one naturalised population. Diverse circulating subtypes were also detected, with Abs to at least five AIV subtypes (HxNx), and exposure of one individual to both H5N1 and H9N2. To date, no active virus has been detected but analysis is ongoing.

These results highlight the importance and complexity of serological testing in apparently healthy migratory species, providing crucial information regarding potential persistence, transmission and reassortment of AIV subtypes across distinct geographical routes and populations, and of survival and recovery post AIV infection. This understanding is vital in predicting the ongoing potential for viral reassortment and rapid geographical spread of novel subtypes with potentially dangerous characteristics.

Keywords: avian influenza virus; migration; flyways; wildfowl; antibodies

P089. Multiple Introductions of Highly Pathogenic Avian Influenza Viruses into the High Arctic: Svalbard and Jan Mayen, 2022–2025

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Since autumn 2020, highly pathogenic avian influenza viruses (HPAIVs) of H5Nx subtypes belonging to clade 2.3.4.4b have caused substantial mortality in wild and domestic birds globally, with increasing spillover to mammals. The objective of this study was to describe the occurrence and genomic characteristics of HPAIVs in the High Arctic.

Svalbard is an Arctic archipelago located between the productive Greenland and Barents Seas. Passive surveillance for avian influenza in the Svalbard archipelago and on the island of Jan Mayen was conducted between 1 January 2022 to 31 August 2025, while active surveillance was conducted on Svalbard in 2021 and 2022. In total, 325 wild birds and 17 mammals were tested for avian influenza during the study period.

Of these, 23 birds of six species and six mammals of two species tested positive for HPAIVs of H5Nx subtypes belonging to clade 2.3.4.4b, comprising four distinct genotypes: EA-2020-C (H5N1), EA-2021-AB (H5N1), EA-2021-I (H5N5), and EA-2022-BB (H5N1). Multiple seabird species were affected (2022 and 2023), with sporadic spillover to walrus (2023) and Arctic foxes (2025). Phylogenetic analyses showed several independent virus introductions rather than local persistence, with links to both mainland Norway and transatlantic/circumpolar lineages.

Our findings demonstrate high genetic diversity and repeated introductions of HPAIVs into Svalbard and Jan Mayen. The co-occurrence of distinct genotypes in dense seabird colonies suggests that Arctic breeding areas may function as hubs for viral mixing and long-distance dissemination. These findings highlight the need for continued surveillance in remote Arctic ecosystems.

Keywords: Genetic diversity, H5N1, H5N5, surveillance, wildlife

P090. Avian influenza in minks: rapid mammalian adaptation after spillover and evidence of exposure in wild populations

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The ongoing panzootic of H5N1 clade 2.3.4.4b high pathogenicity avian influenza virus (HPAIV) is increasingly affecting mammalian hosts, raising concerns about viral adaptation and zoonotic risk. American mink (*Neogale vison*) has emerged as a key species at the wildlife–domestic interface, highlighted by recent outbreaks linked to infected seabirds. Here, we combined experimental infections with ongoing field surveillance to investigate the role of mink in H5N1 ecology and adaptation. Using controlled infections, we challenged minks with an avian-origin H5N1 (H5N1/gull). Minks developed subclinical infection with limited viral shedding; however, viral RNA was detected in the brain of 2/4 animals, where a key mammalian adaptation mutation (PB2 T271A) emerged de novo. This highlights the capacity of avian-origin viruses to rapidly acquire adaptive mutations despite minimal systemic infection. Notably, all experimentally infected minks seroconverted, with robust anti-nucleoprotein (NP) antibody responses, confirming efficient infection even in subclinical cases. To complement these experimental findings, we leveraged the ongoing American mink eradication program in Catalonia (Spain) to assess exposure in invasive wild populations. Preliminary serological results indicate a low but consistent seroprevalence (~1–2%) against H5 viruses, including NP seropositivity, suggesting repeated natural exposure of wild minks to avian influenza viruses in the environment. Together, our results demonstrate that while H5N1 spillover from birds to minks may often result in mild or undetected infections, it can still drive rapid viral adaptation in the mammalian host. Combined with evidence of ongoing exposure in wild invasive populations, this reinforces the role of minks as potential intermediate hosts and highlights the need for integrated surveillance at the wildlife–livestock interface.

Keywords: Mammalian adaptation, RNA virus, active surveillance, host-pathogen

P091. High Pathogenicity Avian Influenza H5N1 (Clade 2.3.4.4b) Associated with a Mass Mortality Event in Eurasian Cranes (*Grus grus*) in Germany

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High pathogenicity avian influenza virus (HPAIV) H5N1 (clade 2.3.4.4b) has established enzootic status in European wild bird populations, yet frequently causing mass die-offs. In autumn 2025, increased mortality was reported in Eurasian cranes (*Grus grus*) in north-east Germany and soon observed in several other regions. This study aimed to identify the causative agent of this mass mortality event and characterized associated pathological and virological findings.
Post-mortem investigations were performed on Eurasian crane carcasses collected through passive wildlife disease surveillance. Initially, tissue samples and swabs were screened in generic RT-qPCRs targeting influenza A virus RNA, followed by sub- and pathotype-specific tests. Positive samples were subjected to whole-genome sequencing to determine the HPAIV genotype and perform phylogenetic analysis. Histopathological and immunohistochemical examinations characterized lesion patterns and tissue distribution of viral antigen.
Between October and mid-November 2025, more than 18,000 dead cranes had been reported in Germany. HPAIV H5N1 (clade 2.3.4.4b) was consistently detected in examined cranes, identified as genotype EA-2024-DI.2.1. Associated lesions were consistent with an acute systemic infection and fatal outcome, characterized by severe pancreatic necrosis, widespread viral antigen distribution—most prominently within the central nervous system—and only minimal inflammatory response, indicative of rapid disease progression. Phylogenetic analyses showed that crane-derived viruses formed a closely related cluster, very similar to viruses detected in other wild birds and poultry in Europe during the same period. Mortality clusters and rapid spread likely reflected efficient transmission at communal roosting and feeding sites.
The estimated mortality rate of ~10% in the Western European flyway-subpopulation of Eurasian cranes classifies the scenario as yet another HPAIV-driven mass die-off; the full population impact, however, remains to be studied. There remain critical knowledge gaps in our understanding of HPAIV H5 epidemiology in wild and/or domestic birds, which need clarification to disentangle their potential roles as amplifying hosts or spreaders of the pathogen, or as victims of HPAI.

Keywords: Avian Influenza, HPAIV H5N1, animal disease, mass mortality, cranes

P092. Evaluating exposure of vultures in Spain to H5N8 and H5N1 high pathogenicity avian influenza virus (2010–2024)

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Since 2020 High pathogenicity H5N1 and H5NX avian influenza viruses (AIVs) are causing an unprecedented panzootic among wildlife characterised by loss of seasonality, expansion to new geographic areas and an increased host spectrum including avian scavengers. Outbreaks have been observed in griffon (*Gyps fulvus*) and bearded vultures (*Gypaetus barbatus*) but not in cinereous (*Aegypius monachus*) and Egyptian vultures (*Neophron percnopterus*). We use subtype specific serology to investigate species exposure prior to and during outbreaks.

A total of 305 griffon vulture sera collected between 2010 and 2023 across Spain, 301 nestling cinereous vulture samples collected between 2010 and 2017 in central Spain and 181 Egyptian vulture sera collected between 2021 and 2024, were screened for antibodies against AIV by generic competitive ELISA, followed by a specific ELISA for H5 AIV in positive samples. All H5-positive sera were analysed by seroneutralisation against H5N8 (IDCDC-RG71A-A/Astrakhan/3212/2020) and H5N1 (IDCDC-RG78A (A/American wigeon/South Carolina/22-000345-001/2021)) viruses.

In total 25.25% (77/305) griffon vulture sera tested positive in the generic ELISA, and 5.57% (17/305) were confirmed as positive for H5 AIV. Seroneutralisation assays revealed activity exclusively against H5N8 AIV in 2.62% (8/305) of the sera and against H5N1 AIV in 1% (3/305) of the samples. All sera that demonstrated seroneutralisation against H5N1 also neutralized H5N8 with higher titres. In Egyptian vultures, 2.21% (4/181) of the individuals tested positive in the generic ELISA, although none were confirmed as positive for H5. Similarly, 2 out of 301 (0.7%) cinereous vulture nestlings tested positive in general ELISA but negative for H5. Seropositivity against H5 AIV was recorded only in 2022 and 2023, thus closely associated with the documented AIV outbreaks in griffon vultures.

The studied vulture species are exposed to avian influenza viruses and griffon but not Egyptian vultures to H5 avian influenza viruses during 2022/23 in Spain despite often close contact at feeding events. No conclusion on cinereous vultures is possible with respect to H5 avian influenza due to lack of samples during outbreak years. The stronger response to H5N8 and patterns of possible cross-seroneutralisation suggest the existence of partially shared immunity between subtypes, which could influence the susceptibility and epidemiological role of these birds. Our findings highlight the value of these species as sentinels and provide relevant information for the surveillance and understanding of avian influenza ecology.

Keywords: Avian influenza; Vultures; Serology; H5N1/H5N8; Spain

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P093. Wild boar carcass decomposition and post-mortem interval estimation: a systematic review and quantitative synthesis of decomposition dynamics and forensic entomological evidence

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Wild boar (*Sus scrofa*) carcasses play an important epidemiological role in the persistence and transmission of African swine fever virus. Estimating the post-mortem interval (PMI) of detected carcasses may therefore contribute to reconstructing infection timelines and supporting surveillance and carcass-removal strategies. However, decomposition is strongly influenced by environmental conditions, and evidence specifically derived from wild boar remains fragmented.
A systematic review was conducted according to PRISMA guidelines. PubMed, Scopus, Web of Science and Google Scholar were searched without restrictions on publication date, geographical area or language. Studies investigating wild boar carcass decomposition, PMI estimation and/or associated entomological succession were eligible. Data on study design, carcass number, decomposition stage, PMI, total body score (TBS), accumulated degree-days (ADD), environmental conditions and entomological succession were extracted. Where sufficiently comparable data were available, decomposition stages were harmonised into five ordinal categories (fresh, early, active, advanced and skeletonisation), and stage-specific PMI trajectories were quantitatively compared across studies.
Evidence remained limited and heterogeneous, but quantitative decomposition data were available from five independent studies representing approximately 120 wild boar carcasses, including longitudinal experiments comprising up to 73 carcasses and 601 repeated observations. Decomposition stage was consistently associated with PMI, although stage-specific timing differed markedly among environments. In temperate/Mediterranean studies, advanced decomposition generally occurred approximately 10–30 days post-mortem, while skeletonisation commonly began between approximately 30 and 60 days, but substantially longer persistence was observed under cold, shaded or waterlogged conditions. Conversely, under tropical conditions, active decay was reached by approximately day 3 and advanced decay/incipient skeletonisation by day 4, indicating an approximately one-order-of-magnitude difference in calendar time between climatic extremes. In a large European longitudinal experiment, decomposition stage was the strongest linear predictor of PMI and the final predictive model achieved $R^2 = 0.80$ in validation. In an independent Mediterranean experiment, TBS was strongly associated with thermal accumulation (Spearman $\rho = 0.923$; $n = 173$; $p < 0.01$); advanced decomposition occurred at 3–11 days in summer versus 25–46 days in winter, and skeletonisation was observed from 5 versus 39 days, respectively. Preliminary cross-study synthesis suggested that adjustment for thermal accumulation reduced, but did not eliminate, between-study variability, indicating residual effects of season, microhabitat and carcass characteristics. Entomological succession showed a complementary temporal pattern, with Diptera predominating during early decomposition and Coleoptera becoming increasingly informative during advanced decay and skeletonisation.
Decomposition stage provides substantial information for wild-boar PMI estimation, but fixed stage-to-calendar-time relationships are not transferable across climatic settings. Combining standardised decomposition scoring with thermal accumulation and entomological succession may provide a more robust framework for estimating PMI in carcasses detected during ASF surveillance.

Keywords: African swine fever, wild boar, carcass decomposition, post-mortem interval, accumulated degree-days, forensic entomology

Session 6

Food safety of game meat, AMR and Ecotoxicology, pollutants and wildlife health

Oral Presentations

Antimicrobial resistance at the wildlife–environment interface: a planetary health perspective

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Planetary health recognizes that human health and well-being are fundamentally dependent on the integrity of natural systems, highlighting the interconnectedness of human, animal, and environmental health, particularly in the context of antimicrobial resistance (AMR). Increasingly recognized as a critical planetary health threat, AMR is extending beyond clinical and agricultural settings into natural ecosystems. The objective of this study was to evaluate the role of veterinary antimicrobial use in shaping environmental AMR dynamics and its implications for wildlife within a planetary health framework.

A narrative review of peer-reviewed literature was conducted, integrating pharmacological, ecological, and environmental perspectives on antimicrobial use, environmental dissemination, and resistance emergence across wildlife populations.

The reviewed literature indicates that veterinary antimicrobial use is a major driver of environmental contamination, leading to the presence of antimicrobial residues and resistant bacteria in soil, water, and sediments. Identified exposure pathways include manure application, wastewater discharge, and runoff, enabling interactions between environmental, domestic, and wildlife-associated microbial communities. Environmental bacteria can acquire and exchange resistance genes through horizontal gene transfer, facilitating the persistence and spread of resistance traits. These determinants disseminate across ecological interfaces via multiple transmission pathways, including environmental exposure, the food chain, and interactions among domestic animals, wildlife, and humans. Aquatic environments, particularly those impacted by wastewater, represent critical reservoirs enabling transfer of resistant bacteria to terrestrial wildlife. The persistence of antimicrobial compounds in environmental matrices contributes to prolonged selective pressure and maintenance of resistance. Peridomestic wildlife species, especially small mammals in urban and agricultural settings, have been identified as carriers of clinically relevant multidrug-resistant bacteria, highlighting their role as indicators and conduits of AMR dissemination.

Antimicrobial resistance should be recognized as a planetary health challenge requiring integrative and transdisciplinary approaches. Incorporating wildlife into AMR surveillance and strengthening the role of veterinary pharmacology in environmental risk assessment are essential for mitigating resistance spread and protecting ecosystem and public health.

Keywords: antimicrobial resistance, antimicrobials, environmental contamination, planetary health, wildlife

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White-tailed eagles (*Haliaeetus albicilla*) as a reservoir of resistant and virulent *Escherichia coli* strains in the protected "Gornje Podunavlje" biosphere reserve

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Monitoring the resistance of indicator bacteria such as *Escherichia coli* (E. coli) in wild animals and birds provides evidence that they can serve as ecological reservoirs of bacterial resistance. In this study, the focus was on the isolation and identification of commensal *E. coli* in one of the largest populations of the white-tailed eagle (*Haliaeetus albicilla*) nesting in the Gornje Podunavlje nature reserve in the Republic of Serbia. Gornje Podunavlje is part of the UNESCO protected biosphere reserve known as the "European Amazon" since 2017.

The study included almost the entire nesting population in the reserve (20 out of 21 active nests). After incubation in peptone water, samples were plated on MacConkey agar and identified by PCR targeting the *E. coli*-specific *gadA/B* gene, while other isolates were identified by MALDI-TOF mass spectrometry. Detection of resistance and virulence genes, as well as RAPD and replicon type analyses, was performed by PCR, and sequencing was conducted commercially.

From the 20 collected fecal samples, bacteria were isolated from 18 samples, with one bacterial species identified in each. *E. coli* was isolated from 11 fecal samples, *Citrobacter freundii* from three samples, *Raoultella planticola* from two, *Pantoea agglomerans* from one, and *Klebsiella oxytoca* from one sample. One multidrug-resistant *E. coli* isolate showed a high level of resistance to fluoroquinolones, caused by mutations in topoisomerase genes (*gyrA*, *parC*, and *parE*). This *E. coli* isolate carried the resistance genes *sul1* and *tetB*, as well as the virulence gene *iutA*. Analysis of genetic diversity using the RAPD method combined with phylogenetic typing, revealed significant heterogeneity among the 11 *E. coli* isolates. A total of five replicon types were detected (IncFIB, IncFIA, IncFIC, IncY, and IncI1), with most isolates carrying multiple replicons, suggesting a strong potential for horizontal transfer of resistance and virulence genes.

The presence of at least two virulence genes, along with a multi-replicon status in three *E. coli* isolates, indicates the potential to cause extraintestinal infections and to disseminate pathogenic genetic traits within bacterial populations. Detection of resistance to synthetic antibiotics in isolates from white-tailed eagles indicates an indirect human impact as a source of antibiotic contamination, as well as the presence of resistant bacteria in the food chains of wild animals. The occurrence of *E. coli* resistance to fluoroquinolones in wildlife populations is concerning, as these antibiotics are often used as first-choice treatments for bacterial infections in humans and domestic animals.

Keywords: white-tailed eagles, environmental pollution, fluoroquinolones, resistance, virulence

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Genomic characterization and clonal relationship of Multidrug-Resistant *Staphylococcus pseudintermedius* isolated from surgical wounds in rescued wild carnivores

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Staphylococcus pseudintermedius is a major opportunistic pathogen in veterinary medicine. In wildlife rescue centers, animals undergoing orthopedic surgery for trauma are at high risk of post-operative infections. This study aimed to characterize the genomic profiles and antimicrobial susceptibility of isolates from surgical wounds of wild carnivores to evaluate the risk of multidrug-resistant (MDR) strain circulation in clinical wildlife settings.

Five *S. pseudintermedius* isolates were collected from orthopedic wounds of wild carnivores (Wolf, *Canis lupus*; Fox, *Vulpes vulpes*) rescued from three Northern Italian provinces and treated in 2025 in the same hospital. Whole Genome Sequencing (WGS) was performed on the Illumina MiSeq platform. Bioinformatic analysis included MLST 2.0, ResFinder 4.0 for resistance genes (ARGs), and SNP-based phylogenetics (CSI Phylogeny). Phenotypic resistance was determined by broth microdilution, assessing Minimum Inhibitory Concentrations (MIC) for 18 antimicrobial agents.

WGS identified two Sequence Types: ST496 (n=4) and ST85 (n=1). SNP typing revealed high genetic relatedness among ST496 isolates (maximum distance of 16 SNPs), suggesting a clonal relationship. Most isolates showed high MIC values for beta-lactams (Penicillin >16 µg/ml; Oxacillin >8 µg/ml; Amoxicillin/Clavulanate up to >32 µg/ml), fluoroquinolones (Enrofloxacin >4 µg/ml), macrolides (Erythromycin >8 µg/ml), and tetracyclines (Tetracycline >16 µg/ml), aminoglycosides (Kanamycin >16 µg/ml) and SXT (>4 µg/ml). WGS identified several ARGs, including *mecA, blaZ, aac(6')-aph(2''), erm(B)*, and *dfrG* consistently matching the observed phenotypes.

The study confirms the presence of Methicillin-Resistant *S. pseudintermedius* (MRSP) with broad MDR profiles in hospitalized wildlife. The close genetic proximity (ST496) indicates potential nosocomial transmission or a common environmental source within the recovery facilities. These findings highlight a significant conservation and public health concern, emphasizing the need for rigorous biosecurity and antimicrobial stewardship in wildlife clinical settings to prevent the environmental spread of resistant pathogens.

Keywords: MRSP, MIC, WGS, SNP typing, Orthopaedic surgery

Commercial brown bear (*Ursus arctos*) meat products are highly contaminated with lead (Pb) from hunting ammunition

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Lead (Pb) ammunition is widely used for hunting and Pb residues are a health risk for humans consuming meat from game harvested with Pb-based ammunition. A maximum level (ML) for Pb in meat from domestic animals exists (> 100 µg Pb/kg wet weight) in the European Union (EU) whereas no ML for game meat has been set. This study investigated the presence of Pb in brown bear (*Ursus arctos*) meat products purchased in three EU countries.

We assessed lead (Pb) contamination from ammunition in 59 consumer packages (44 vacuum-packed and 15 canned) of hunted brown bear from six manufacturers in Sweden, Finland and Estonia. Medical X-ray imaging was used on the 44 vacuum-packed products to detect radiodense objects ≥ 0.1 mm, assumed to be Pb fragments. Synchrotron X-ray imaging was then used on four products with radiodense objects to determine if they were Pb. Inductively-coupled plasma mass spectrometry (ICP-MS) was used on 54 products (39 vaccum-packed and 15 canned) to determine the Pb concentration and isotopic composition.

Medical X-ray imaging showed that 15 (34%) of the samples contained 1–3 radiodense objects ≥ 0.1 mm. All radiodense objects observed in the medical X-ray images of four products were confirmed to be Pb by synchrotron X-ray imaging. ICP-MS showed that 32 (59%) of the samples contained > 100 µg Pb/kg wet weight. The Pb isotopic compositions were similar to those of Pb-based rifle hunting bullets from European manufacturers.

Several types of commercial brown bear meat products on the market in Sweden, Finland and Estonia were highly contaminated with Pb from spent ammunition. Although no ML of Pb has been set for game meat in the EU, we strongly advise against consumption of bear meat products exceeding the ML for meat from domestic animals.

Keywords: Consumer safety, food safety, One Health, public health, toxicology

GPS tracking reveals emerging NSAID-induced mortality in a critically endangered Griffon vulture (*Gyps fulvus*) population

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The increasing use of veterinary non-steroidal anti-inflammatory drugs (NSAIDs) poses a growing threat to scavenging birds. While NSAID-induced vulture population collapses are well documented in Asia, their impact in the Eastern Mediterranean remains poorly understood. The Griffon vulture (*Gyps fulvus*) population in Israel is critically endangered, with poisoning identified as a major mortality factor. This study quantifies the contribution of NSAIDs to mortality and evaluates the role of GPS-tracking in detecting poisoning events.

Between 2019-2024, we compiled mortality and morbidity data from 103 free-ranging Griffon vultures (89 dead, 14 injured), 70 of which were GPS-tagged. Causes of death were determined by necropsy, toxicological analysis (LC-MS/MS of liver samples), and GPS/accelerometer data. Movement data from GPS-tagged individuals recognised NSAID-exposure events and estimated time-to-death and post-ingestion movement distances. Logistic regression models assessed factors influencing the detection of NSAID-related mortality.

Cause of death was confirmed in 65 individuals and suspected in 9. NSAID poisoning accounted for 21 cases (28.4%), making it the second leading cause of mortality after pesticide poisoning (31 cases; 41.9%). NSAID-related deaths were detected mostly from 2021 onwards. Diclofenac and flunixin were the primary compounds identified; these are the first described cases of diclofenac poisonings in vultures in the Middle East. Liver analyses detected NSAIDs in multiple individuals, with diclofenac concentrations ranging from 4-44 ppb (10 positive cases, median 16.5 ppb) and flunixin from 15–2554 ppb (6 positive cases, median 713.5 ppb). Visceral gout was present in most confirmed cases. GPS data identified 9 poisoning events involving at least 21 vultures (15 confirmed, 6 suspected). Among GPS-tagged individuals, median time from ingestion to death was ~72 hours (range 23–134 h), with vultures travelling a median of 41 km (net displacement) and 134 km total distance before death. Model selection showed that GPS-related variables (presence of transmitter and number of active devices) were the strongest predictors of detecting NSAID poisoning, highlighting detection bias linked to monitoring effort.

NSAID poisoning is a major and increasing mortality factor in this population since 2021. GPS tracking significantly enhances the detection of poisoning events and reveals substantial spatial displacement between exposure and death, complicating carcass-based surveillance. These findings highlight the urgent need for stricter regulation of veterinary NSAIDs, improved carcass management, improved awareness among veterinarians and cattle breeders, promoting the use of non-toxic alternatives, and continued high-resolution monitoring to mitigate this preventable threat.

Key words: Wildlife toxicology, Vultures, Conservation medicine, GPS-tracking, NSAID (Non-steroidal anti-inflammatory drug) poisoning

Persistent Risk of Lead Exposure in Captive Scavengers: Evidence from Two Andean Condors

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Lead exposure continues to pose a serious health concern for obligate scavengers such as the Andean condor (*Vultur gryphus*), including individuals maintained under human care. This report presents two cases of acute lead intoxication in captive condors from a zoological collection, associated with the ingestion of contaminated meat originating from hunted game. Both birds developed vague and nonspecific clinical signs, including lethargy, reduced feed intake, decreased activity, and gastrointestinal abnormalities. A comprehensive diagnostic approach was applied, encompassing hematology, serum biochemistry, blood lead quantification, and radiographic imaging. Initial findings revealed significantly elevated blood lead concentrations in both individuals, while imaging identified numerous metallic densities within the gastrointestinal tract, consistent with ingested lead fragments. In one condor, repeated blood lead measurements during treatment documented a gradual decline, although low-level exposure persisted for a prolonged period. Chelation therapy using disodium ethylenediaminetetraacetic acid (Na_2EDTA), together with supportive care, led to steady clinical recovery in both cases. Sequential radiographic evaluations confirmed the eventual disappearance of metallic material from the digestive system, followed by stabilization of the animals' condition. These cases demonstrate that lead intoxication remains a relevant risk even in controlled captive environments and underline the importance of combining imaging techniques with toxicological testing for accurate diagnosis. The findings also highlight limitations of current feeding practices and reinforce the need for stricter control of food sources, as well as continued efforts to reduce environmental availability of lead, particularly from ammunition.

Keywords: poisoning, hematology, radiography, therapy, *Vultur gryphus*

Acknowledgement: The study was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contract number 451-03-34/2026-03/200143).

GreenBait – Progress Toward Environmentally Safer Rodenticides

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The global control of rodent pests relies heavily on second-generation anticoagulant rodenticides (SGARs). However, their widespread use and environmental persistence have led to documented adverse effects on non-target wildlife, including mammalian predators, scavengers, and raptors. Previous studies from Norway have demonstrated the presence of several SGARs in species such as foxes and owls. The GreenBait project aims to develop improved chemical analytical methods to enhance understanding of individual anticoagulant compounds and the occurrence of their isomeric forms. In parallel, antibodies are under development and these will be used to develop immunological antibody-based tools, including ELISA methods and rapid screening tests to enable faster and simpler detection in cases of suspected poisoning. Planned activities include investigations of anticoagulant transport through soil and *in vitro* studies of the metabolism of different compounds in wild animals. Overall, the project emphasizes improved monitoring and the development of solutions that support the use of anticoagulant rodenticides with reduced environmental impact. Through the generation of new insights and knowledge, GreenBait aims to evaluate and rank candidate rodenticides that possess well-characterized toxic properties while lacking the high environmental persistence of current products.

Randomly selected scavengers and predators, such as foxes, lynxes and wolverines, from several areas of Norway were collected, and then extracted and analysed by LC-MS for a series of SGARs. Statistical analyses of the full dataset, combined with assessments of health and welfare risks to non-target species, will be performed.

Multiple anticoagulant rodenticides were detected in several animals, with individuals showing exposure to more than one compound. Certain rodenticides appeared more frequently in one species than the other, although overlap in exposure patterns was observed. Several commonly used SGARs were prevalent in several species, while some compounds were detected only sporadically or appeared to be species-specific.

Various levels of SGARs can be found in non-target wildlife, most likely because of biomagnification due to the species' dietary preferences. To counter the problem of persistent rodenticides, sustainable solutions like degradable rodenticides need to be introduced in rodent-infested areas. GreenBait aims to identify and evaluate candidate rodenticides with such properties.

Keywords: rodenticides, anticoagulants, predators, biomagnification, sustainability, SGARs

Funding source or Acknowledgement: Funded by the Norwegian Research Council (NFR); Other partners in the project are Norwegian Institute for Bioeconomy Research (NIBIO), Norwegian Agricultural Advisory Service (NLR), AniCura, Landcare Research's Toxicology Laboratory in New Zealand.

Session 6

Food safety of game meat, AMR and Ecotoxicology, pollutants and wildlife health

Poster Presentations

P094. Why is large game meat consumption low in Serbia? Insight into production and consumers behaviour

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Game meat represents relatively small, yet not insignificant, segment of the meat sector in Serbia. In 2021, total production of meat from domestic animals reached 578,000 tons, while large game meat accounted for only 800.08 tons (1.4%). Within this category, wild boar clearly predominates (528.11 tons), followed by roe deer (193.92 tons), and red deer (68.02 tons), whereas fallow deer, chamois, and mouflon contribute only marginally. When compared to other European countries, Serbia can be considered a minor producer. In Serbia, game meat is most often obtained directly through hunting and is primarily consumed within hunters' households. Its presence in the formal market is limited, being available only in selected restaurants and some retail outlets. This pattern is consistent with observations from other Eastern European countries. Consumption habits are strongly influenced by demographic factors, with higher intake reported among men, rural populations, and adults. While certain food safety concerns exists-particularly regarding *Trichinella spp*.-game meat is generally perceived as a natural and environmentally friendly food. At the same time, its specific taste and aroma remain an important factor shaping consumer preferences, contributing both to its appeal and its limited acceptance. Despite these generally positive perceptions, the overall consumption of large game meat in Serbia remains low. The estimated annual intake is 0.120 kg per capita, increasing slightly to 0.176 kg in Vojvodina region. This corresponds to only 0.3-0.4% of total meat consumption, which averages 45.9 kg per capita in Serbia. In comparison with other European countries, where consumption typically ranges from 0.1 to 1.0 kg per capita, Serbia is positioned at the lower end. However, markedly higher consumption levels are observed among hunting families, where intake can reach several kilograms per year. Taken together, the low levels of production and consumption suggest that there is room for further development of this sector. Factors such as the relatively lower price of wild boar meat compared to pork, and venison compared to beef, may represent an opportunity for increased market uptake. Improving products availability, strengthening consumer awareness, and addressing existing food safety concerns could contribute to a broader acceptance of game meat and its greater inclusion in the regular diet.

Keywords: hunters, market, consumers, attitude

P095. Heavy metals in wild boar (*Sus scrofa* L.) liver: regional differences and One Health implications

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In this study, for the first time, the concentrations of heavy metals (lead, cadmium, mercury, and arsenic) were analyzed in liver samples of wild boars (*Sus scrofa*) from two locations (Laktaši, Republic of Srpska, and the Kolubara District, Republic of Serbia), to determine heavy metal levels and assess the potential risk to human health. Unlike many organic pollutants, heavy metals are not subject to degradation but instead accumulate in soil, water and biota, making them a long-term risk to ecosystems and human health.

Using inductively coupled plasma mass spectrometry (ICP-MS), a total of 60 liver samples from wild boars (30 from each region), aged up to 6 years, were analyzed. The samples were collected during the hunting season in 2024.

The results indicate statistically significantly higher concentrations of arsenic, cadmium, and mercury in samples collected in the Republic of Srpska ($p < 0.001$). No significant differences were observed in lead concentrations between the studied regions. According to EU Regulation (EU) 2023/915, levels exceeding the maximum permitted concentrations of heavy metals in food of animal origin were identified in 25 samples (84% from the Republic of Srpska), with mercury most frequently exceeding the maximum limits (30%), followed by lead (6.7%) and cadmium (5%). Based on the legislation of the Republic of Serbia, deviations were considerably less frequent and were detected in 5% of samples, specifically for Cd and Hg. Correlation analysis revealed a significant interrelationship among the majority of analyzed metals, suggesting a possible common source or similar pathways of intake and accumulation within the organism.

The obtained results highlight the importance of continuous monitoring of wild boars as reliable bioindicators of environmental contamination, as well as the need for a regular assessment of the game meat safety for human consumption. The observed regional differences in heavy metal concentrations, together with the frequent exceedances of maximum permissible levels (particularly for mercury), further emphasize the importance of analyzing their spatial distribution and identifying potentially high-risk areas. This approach may serve as a foundation for developing recommendations and guidelines for animal and human health risk assessment, as well as improving monitoring systems for public health protection.

Keywords: heavy metals, wild boar (*Sus scrofa*), liver, bioaccumulation, One Health

Acknowledgement: The study was supported by the Ministry of Science, Technological Development and Innovation of the Republic of Serbia (Contracts number: 451-03-34/2026-03/200143 and 451-03-33/2026-03/200031).

P096. Occurrence of *Trichinella* spp. larvae in wild boar meat in the Srem and South Bačka districts (Republic of Serbia) during the period 2021-2025

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Wild boar meat represents a significant source of Trichinella spp. infection in humans, underscoring the necessity of mandatory inspection and systematic control measures to ensure food safety and protect public health. The aim of this study was to determine the prevalence of *Trichinella* spp. in wild boar meat originating from hunting associations in the Srem and South Bačka districts (Republic of Serbia) during the period 2021-2025.

Testing of wild boar diaphragm samples were performed using the artificial digestion method according to SRPS EN ISO 18743:2016. A total of 866 wild board diaphragm samples collected from multiple hunting associations across the two districts were analysed over a five-year period for the presence of *Trichinella* spp.

Positive findings were detected in four (1.6%) samples in 2021 and one (0.3%) sample in 2022, while no positive samples were recorded in 2023, 2024, and 2025. Overall, five (0.6%) samples tested positive for *Trichinella* spp. during the study period. The results indicate a low prevalence of *Trichinella* spp., with a decreasing trend observed in recent years, suggesting an improvement in control measures and surveillance practices.

These findings emphasize the importance of systematic inspection of wild boar meat as a key measure in the prevention of *Trichinella* spp. transmission to humans. Strict implementation of mandatory testing within hunting associations is essential to ensure compliance with regulations and to reduce the risk of infection. Continuous surveillance and adherence to control measures represent fundamental components in safeguarding food safety and protecting public health.

Keywords: artificial digestion, public health, wildlife, food safety

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P097. Microbiological risks related to feedgrounds for deer in agricultural landscape

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The white-tailed deer (*Odocoileus virginianus*) is an abundant game species in the southern part of Finland. Deer are commonly fed during winter with variable food items (hay, apples, root vegetables) and shot in the autumn from a lookout next to a feeding place. Generous feeding of the increasing white-tailed deer population has raised concerns about the risks the feedgrounds may pose on animal and human health. Our objective was to study the spread of pathogens and antimicrobial resistance factors in feedgrounds in agricultural landscape using faecal samples and food samples collected in feeding sites. Faecal samples of white-tailed deer, and food samples, were collected as fresh as possible three times per winter feeding season from 26 feeding sites in southwest Finland. Both faecal and food samples were screened for *Listeria* spp. and *Salmonella* using enrichment culture methods. Faecal samples were also screened with selective media for enteropathogenic *Yersinia* spp., *Campylobacter* spp., *Candida auris,* and clinically significant antimicrobial-resistant bacteria (MRSA, ESBL producing bacteria, CPE, and VRE). Antimicrobial resistance (AMR) factors in composite faecal samples were screened with a custom high-throughput qPCR (HT-qPCR) array (Resistomap, Helsinki, Finland) targeting 144 genes, using a reindeer faecal sample as a control.
Bacterial cultures revealed *Yersinia enterolitica, Y. pseudotuberculosis* and *Listeria monocytogenes* both in faecal samples and food samples. AMR bacteria were not found in selective cultures. HT-qPCR detected class A–D carbapenemase genes in all composite feedground samples but not the reindeer sample. Phenicol, β-lactam, quinolone, and aminoglycoside AMR factors were more numerous in feedground samples but not completely absent in the reindeer sample. Tetracycline and macrolide-lincosamide-streptogramin B (MLSB) AMR factors were ubiquitous in all samples. Vancomycin resistance genes *vanA* and *vanB* were also found in all samples, including the control.
Feedgrounds commonly harbour potentially pathogenic bacteria such as *Yersinia* spp. and *Listeria monocytogenes*. Deer visiting feeding sites can spread multiple AMR factors in their faeces. Microbiological risks should not be overlooked when feeding game animals close to in agricultural environment.

Keywords: deer, feeding, bacterial pathogens, antimicrobial resistance factors

Funding source: Ministry of Agriculture and Forestry of Finland/ MAKERA Funding

P098. Wildlife–poultry interfaces as hotspots of antimicrobial resistance transmission: insights from integrated eco-epidemiological surveillance

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The intensification of poultry production and the popularity of systems with outdoor access have increased ecological interfaces where wildlife, poultry, and humans interact, facilitating the transmission of pathogens and antimicrobial resistance (AMR). This study aimed to characterise pathogen circulation and AMR dynamics at the wildlife–poultry interface in south-central Spain in comparison to wetlands using an eco-epidemiological approach.
Surveillance was conducted across poultry production systems (indoor and outdoor layer farms, gamebird farms) and in wetlands in the same area. Samples were collected from wild birds (n = 914), rodents (n = 141), insects (n = 63), environmental matrices (n = 27), and poultry manure and dust composite samples (n = 45). Molecular and microbiological analyses were performed to detect avian influenza virus (AIV), avian orthoavulavirus 1 (AOAV-1), avian coronaviruses (ACoV), flaviviruses, *Escherichia coli*, *Salmonella* spp., and to obtain phenotypic antimicrobial resistance profiles of *E. coli* isolates.
Viral detections in wild birds were limited (AIV: 1 out of 108; 0.9%, ACoV: 1 out of 261; 0.4%). However, flavivirus seroprevalence, including West Nile virus (WNV), was significantly higher among wetland-associated birds (23 out of 101; 19.8%) than among farm-associated birds (2%). In contrast, *E. coli* was ubiquitous across all compartments, with higher prevalence in poultry faeces and environmental samples than in wild birds. Notably, multidrug-resistant (MDR) *E. coli* was significantly more prevalent in wild birds associated with outdoor layer farms than in other environments. Rodents and insects carried resistant *E. coli* and vaccine-derived coronavirus RNA, suggesting a potential role as mechanical vectors at the interface.
Our findings indicate limited circulation of avian viruses but reveal substantial ecological connectivity for enteric bacteria and AMR at the wildlife–poultry interface, particularly in outdoor systems in the continental Mediterranean. The results highlight the importance of integrated, interface-focused surveillance frameworks to understand transmission pathways better, mitigate pathogen spillover risks, and inform targeted biosecurity measures addressing the environmental dimension of AMR dissemination.

Keywords: Wild bird–poultry interface; antimicrobial resistance; *Escherichia coli*; rodents; insects

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P099. Milk Microbiota, Quality, and Antimicrobial Resistance in Free-Ranging Mares at the Wildlife-Livestock Interface: A Case Report from the Kučaj Mountains

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Free-ranging horses maintained under extensive, low-intervention conditions represent an understudied wildlife-livestock interface, raising important public health questions. Despite minimal or absent antimicrobial exposure, these populations may harbour bacteria with clinically relevant resistance traits, while data on milk hygiene and the occurrence of such bacteria in these systems remain scarce. This case report aimed to investigate the microbiological profile of milk and udder skin, alongside milk quality, in two free-ranging mares from the Southern Kučaj Mountains (Serbia).

Two lactating mares (Haflinger, 8 years; Arabian, 6 years), kept under extensive management conditions at approximately 1000 m above sea level, were sampled in August 2025. Animals were maintained in large enclosures during summer and ranged freely in forested areas during winter, with minimal handling and no documented antimicrobial or routine veterinary treatments. Udder skin swabs were collected prior to aseptic milk sampling. Samples were transported under cold chain conditions and analyzed using standard microbiological methods. Identification and antimicrobial susceptibility testing were performed using an automated biochemical system (Automic-i600 system, Autobio, China). Milk chemical composition, somatic cell count, and total bacterial count were determined using FTIR and flow cytometry. Due to limited sample volume, milk quality analysis was performed in the Haflinger mare only.

In the Haflinger mare, *Aerococcus viridans* was isolated from both udder skin and milk. The isolate from milk showed resistance to ceftriaxone, while skin isolates exhibited resistance to penicillin and ceftriaxone. In the Arabian mare, *Streptococcus equi* subsp. *zooepidemicus* was isolated from milk, displaying multidrug resistance to penicillin, ampicillin, oxacillin, cefoxitin, erythromycin, clindamycin, and vancomycin. Udder skin samples yielded *Staphylococcus haemolyticus* with resistance to penicillin and ampicillin. The chemical composition of milk in the Haflinger mare was consistent with values reported in the literature for mare's milk, including low fat and protein content and high lactose proportion, with low somatic cell and bacterial counts.

These results emphasize that although milk quality parameters were within expected ranges, the safety of raw mare's milk cannot be assured without microbiological evaluation. The detection of opportunistic and zoonotic bacteria in milk and on the udder of free-ranging mares highlights the ecological dimension of antimicrobial resistance. The identification of multidrug-resistant *Streptococcus equi* subsp. *zooepidemicus*, alongside *Aerococcus viridans* and *Staphylococcus haemolyticus*, suggests that such populations may act as reservoirs of antimicrobial resistance independent of direct antimicrobial pressure. These findings support the need for targeted microbiological monitoring in extensive management systems.

Keywords: mare's milk, free-ranging horses, antimicrobial resistance, raw milk safety, milk microbiota

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P100. Prevalence of antimicrobial resistance in commensal *Escherichia coli* isolated from wild carnivores in the Republic of Serbia

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Wild carnivores occupy the top of the food chain and represent important bioindicators of environmental conditions, as well as potential reservoirs of bacteria carrying antimicrobial resistance determinants. Their feeding habits and interactions with different components of the ecosystem enable the accumulation of microorganisms from natural and anthropogenic sources, making them a suitable model for monitoring the distribution of antimicrobial resistance under natural conditions. The aim of this study was to investigate the prevalence of antimicrobial resistance in commensal *E. coli* isolated from wild carnivores.

Rectal swabs were collected from carcasses of wild carnivores submitted from different regions of Serbia to the Scientific Veterinary Institute "Novi Sad" during 2025, in order to determine the cause of death. A total of 45 rectal swab samples were examined, originating from 25 golden jackals (*Canis aureus*), 8 red foxes (*Vulpes vulpes*), 6 wolves (*Canis lupus*), 3 martens (*Martes spp.*), 2 wildcats (*Felis silvestris*), and 1 weasel (*Mustela nivalis*). Isolation of commensal *E. coli* was performed using standard microbiological methods, including buffered peptone water (BPW) and Tryptone Bile X-glucuronide agar (TBX), while identification was carried out using an automated biochemical system (AUTOBIO I-600). Antimicrobial susceptibility testing was performed using the disk diffusion method in accordance with the guidelines of the European Committee on Antimicrobial Susceptibility Testing (EUCAST).

Commensal *E. coli* was isolated from all 45 rectal swabs. Resistance was observed in 48.9% of isolates, multidrug resistance in 15.6%, while 35.5% of isolates were fully susceptible. The highest frequency of resistance was recorded for macrolides with 17 isolates and tetracyclines with 12 isolates, while resistance to fluoroquinolones and third- and fourth-generation cephalosporins was low and detected in 7 isolates. Isolates originating from golden jackals and red foxes showed higher levels of resistance and the presence of multidrug resistance, whereas isolates from wolves exhibited lower levels of resistance without detection of multidrug-resistant strains. In other wild carnivore species, resistance was sporadic. Resistance to antibiotics of clinical importance in human medicine was detected in 2 isolates, specifically to amikacin.

The results of this study indicate that antimicrobial resistance in wild carnivore populations cannot be considered an isolated phenomenon, but rather a result of complex ecological interactions and horizontal gene transfer within a unified epidemiological system encompassing the environment, domestic animals, and wildlife. In this context, the obtained results contribute significantly to the understanding of antimicrobial resistance distribution in wild carnivore populations and confirm their role as bioindicators of environmental antimicrobial burden.

Keywords: wild carnivores, *Escherichia coli*, antimicrobial resistance, wildlife ecology, bioindicators

Funding source & Acknowledgement: This work was funded by Ministry of Science, Technological Development and Innovation of Republic of Serbia by the Contract of implementation and funding of research work of NIV-NS in 2026, Contract No: 451-03-33/2026-03/200031.

P101. Trace element monitoring in blood samples of carrion crows (*Corvus corone*) in northern Germany

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Carrion crows (*Corvus corone*) are widespread in Europe and, as omnivores that eat carrion and waste, are heavily affected by environmental contamination. The aim of this study was to determine the concentration of various trace elements with toxic potential in the blood of this species.
Lithium-heparin whole blood samples were taken as part of health screenings from crows, predominantly young birds, which were brought to a rescue center in northern Germany for various reasons between May and August 2025. The elements arsenic (As), cadmium (Cd), chromium (Cr), copper (Cu), lead (Pb), mercury (Hg), thallium (Tl), and zinc (Zn) were measured retrospectively from frozen samples using inductively coupled plasma mass spectrometry (NexION 1100 ICP-MS) in January 2026.
The results revealed the following mean values ± standard deviations: As 5.76±5.06 µg/L, Cd 0.30±0.30 µg/L, Cr 0.27±0.32 µg/L, Cu 0.39±0.17 µg/L, Pb 34.24±28.01 µg/L, Hg 11.69±12.38 µg/L, Tl 0.10±0.08 µg/L and Zn 2.18±0.63 µg/L.
The study detected elevated Pb levels in the blood of the animals, but As and Hg were also found. This shows that heavy metals play a role as environmental contaminants in crows. However, further investigations are necessary to evaluate clinical impacts of these contaminants as well as factors like age and location on the blood concentration of these trace elements.

Keywords: blood monitoring, crows, environmental pollution, heavy metals, lead

P102. Exposure of Wild Birds of Prey to Potentially Toxic Elements in Slovenia

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We investigated exposure to certain potentially toxic chemical elements in selected dead wild birds of prey, found in Slovenia between 2018 and 2022. A total of 33 common buzzards (*Buteo buteo*), 13 common kestrels (*Falco tinnunculus*), 8 Eurasian sparrowhawks (*Accipiter nisus*), 7 tawny owls (*Strix aluco*), 6 long-eared owls (*Asio otus*), 5 Ural owls (*Strix uralensis*), 4 Eurasian eagle owls (*Bubo bubo*) and 1 Eurasian scops owl (*Otus scops*) were included in the study. In all birds pathoanatomical examination was performed and samples of the liver, kidneys, skeletal muscle, and feathers were collected for determination of the concentrations of potentially toxic chemical elements like lead (Pb), cadmium (Cd), chromium (Cr), arsenic (As), zinc (Zn) and copper (Cu) in the organs using inductively Coupled Plasma Mass Spectrometry (ICP-MS).
In the study, in 56 % of tested birds the concentration of at least one potentially toxic chemical element was elevated. A total of 49 % tested birds had elevated concentrations of As, 36 % had elevated levels of Cd, 9 % had elevated levels of Pb, and in 6 % of birds elevated levels of Zn were detected. Elevated levels of Cr and Cu were not detected in any of the tested birds. Elevated levels of As were most frequently found in the feathers, and occasionally in other samples. Elevated levels of Cd were also most often found in the feather samples, less frequently in the kidneys, and occasionally in the liver and muscles. Pb levels were most frequently elevated in the feathers, and in one case in the liver and kidney sample. Zn levels were more often elevated in the liver and muscles, and less frequently in feathers and kidneys. In partial migrants like common buzzard, common kestrel and Eurasian sparrowhawk detection of toxic chemical elements were more common. All owls except the Eurasian scop's owl are non-migratory and results of our study showed lower exposure to toxic chemical elements in these species.

Keywords: wild birds of prey, potentially toxic elements, coupled plasma mass spectrometry, organs, feathers

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P103. Poisoning of Eastern Imperial Eagles (*Aquila heliaca*) caused by lead intoxication and illegal pesticide use

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The eastern imperial eagle (*Aquila heliaca*) is a critically endangered and the rarest bird of prey in Serbia, which is successfully recovering from the brink of extinction, with about 30 breeding pairs recorded at the beginning of 2026, mostly in the northern Banat. As a national symbol, this bird is subject to intense protection. In the period from 2020 to 2025, we had two cases of death, where intoxication was suspected.

The first case occurred in 2021: An adult male imperial eagle died soon after being placed in a rehabilitation center at the "Palić" Zoo. The bird was found in an emaciated state in the area of the Apatin municipality. The cadaver was submitted for necropsy to determine the cause of death. Virological (Avian Influenza, West Nile and Paramyxovirus), bacteriological and toxicological examinations were carried out on intestine and internal organs samples. The bird was in poor condition. The pathological examination revealed a fibrinous epicarditis, pericarditis and multifocal subserosal haemorrhages in ileum. *Escherichia coli* and *Clostridium perfringens* were isolated from the tissues. *Paramyxovirus* was detected by RT-PCR. A high lead concentration (50.96 mg/kg in the liver, 13.50 mg/kg in the kidney tissue) was detected by inductively coupled plasma mass spectrometry. The results show that the bird was exposed to toxic doses of lead. These likely had a negative effect on the immune status and consequently increased the susceptibility infections.

The second case was recorded in 2024.: A juvenile eastern imperial eagle was found dead in the area of village Mol, Ada municipality. It was suspected that it was secondary poisoning because the carcasses of a gray magpie and a gray crow were found nearby. The necropsy showed that the corpse was over two weeks old and the internal organs were affected by the putrefactive process and were eaten by insect larvae. Parts of muscle, fat tissue and small intestines, as well as parts of hair and feathers were found in the eagle's esophagus, crop and gizzard. The tested viruses (Avian Influenza and Paramyxovirus) were not identified. Toxicological analysis of the contents of the crop and a liver tissue sample, using liquid chromatography with a PDA detector, proved the presence of carbofuran.

thoroughly forensic examinations including toxicology are essential to monitor wildlife fatalities, especially cases with suspected poisoning to identify culprits and hot spots in the area of illegal persecution to finally eliminate highly toxic substances from the environment.

Keywords: *Aquila heliaca*, intoxication, lead, carbofuran

P104. Iatrogenic pyridoxine intoxication in four Eurasian griffon vultures (*Gyps fulvus*) at a wildlife rehabilitation center in France

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Four juvenile male Eurasian griffon vultures (*Gyps fulvus*), weighing between 5.37 and 6.45 kg, were found alive in southwestern France between August 26 and 29, 2025. All individuals were admitted to a wildlife rehabilitation center. Following a complete physical examination, they were force-fed and received an intramuscular injection of 2.5 ml of a vitamin complex containing thiamine (vitamin B1) and pyridoxine (vitamin B6) (Corébral, Vetoquinol France, 37 rue de la Victoire, 75009 PARIS), corresponding to a total of 111.5 mg (17.3–20.8 mg/kg) of thiamine and 51.4 mg (8.0–9.6 mg/kg) of pyridoxine. All birds died or were euthanized due to rapid clinical deterioration within 48 hours of admission. Post-mortem radiographic examination did not reveal any metallic foreign body. Necropsy findings included the presence of digestive material in the oral cavity (3/4), urate crystal deposits on the walls of the air sacs (3/4), renal enlargement (3/4) and pallor (2/4), and/or multicentric congestion (4/4). The liver, kidneys, crop, and stomach from two individuals were submitted for standard histopathological examination. Histological examination revealed acute diffuse hepatic degeneration and necrosis with congestion, as well as acute multifocal tubular renal necrosis. The lesion pattern is consistent with vitamin B6 intoxication, which is considered the most likely cause of this mortality event, although alternative etiologic hypotheses are not excluded. This case series highlights the potential for iatrogenic pyridoxine toxicity and raises concerns regarding the safety of parenteral vitamin supplementation in raptors.

Keywords: Eurasian griffon vulture, *Gyps fulvus*, intoxication, pyridoxine, vitamin B6

P105. Monitoring of per- and polyfluoroalkyl substances (PFAS) in German wolves (*Canis lupus*)

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Per- and polyfluoroalkyl substances (PFAS) are a group of organic chemicals of solely anthropogenic origin. Due to several desirable properties, they are used in many industrial and commercial applications. Because of their persistent nature, PFAS are also known as 'forever chemicals' and once they enter the environment they can accumulate in wildlife, especially in scavenger and predator species. The detection of PFAS and their impact on wildlife as well as the detection of emerging emission sites still challenges researchers and government agencies.
The presented study aimed to measure the PFAS burden in liver samples (n=150) of adult wolves (*Canis lupus*) from four German federal states (Brandenburg, Saxony, Saxony-Anhalt and Lower Saxony) covering a time span of ten years (2013 to 2023) representing years of return and establishment of the species to growth of the population in these areas. To achieve this, a target method for the quantification of 30 PFAS via ultra-high-performance liquid chromatography coupled to high-resolution mass spectrometry (UHPLC-HRMS) was used.
PFAS levels above the limit of quantification (LOQ; LOQs between 0.05 and 10 µg/kg) were found in all liver samples. Total PFAS concentrations ranged from 2.1 to 363 µg/kg wet weight. The predominant substance was perfluorooctane sulfonic acid (PFOS) representing between 7% and 100% of the samples' total PFAS burden, followed by medium-chain to long-chain perfluoroalkyl carboxylic acids (PFCAs from C7 to C13) and perfluoroalkyl sulfonic acids (PFSAs; C6, C7 and C10). Besides PFCAs and PFSAs, two additional PFAS (ADONA and 6:2 fluorotelomer sulfonic acid (6:2 FTS)) were detected in some samples.
Over the course of ten years, no statistically relevant change in PFAS concentrations (assessed for PFOS, perfluorooctanoic acid (PFOA) and the sum of all PFAS) was observed. Furthermore, there was no difference in PFAS concentration between female and male wolves. A spatial comparison on the federal-state level showed large deviations within the four surveyed German states, but a closer look showed individual PFAS hotspots close to possible emission centers such as industrial parks and mining areas. Therefore, the results of this study show that the PFAS burden of adult wolves' liver might be indicative of the position of emerging and existing emission centers.

Keywords: anthropogenic pollutants, apex predator, ecotoxicology, temporal trends

P106. Honey bees and bee products as monitors of toxic elements environmental contamination

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The honey bee (*Apis mellifera L.*) is a vital insect, a fundamental component of ecosystem stability and human survival. Due to their complete dependence on flowering plants and the collection of materials such as nectar, pollen, and propolis over vast areas, honey bees act as highly sensitive bioindicators of environmental quality. Toxic and potentially toxic elements affect the health, survival, and behavior of honey bees. On the other hand, they affect the safety and quality of bee products. High-risk elements are lead, arsenic, and cadmium. These elements are non-essential and can be toxic even in trace levels. Lead, as one of the most widespread contaminants, enters the biosphere through industrial emissions and fossil fuel combustion, accumulating in bee organs and negatively affecting their immune system, appetitive learning, and long-term memory. Arsenic, originating from diverse agrochemicals, functions as a protoplasmic poison, causing tissue disintegration and high mortality of foragers and nurse bees. Cadmium, introduced into the food chain through phosphate fertilizers and industrial activities, significantly reduces bees' immunocompetence. The micronutrient metals (zinc, copper, iron, selenium, chromium, etc.) are essential, but if they are outside their biological range, they can have potentially harmful effects. These elements can contribute to neurodegeneration. Copper reduces the learning and memory performance of bees. Aluminum can impair bees' cognitive processes, altering their sugar perception and hindering floral decision-making. Selenium in high concentrations leads to population decline due to direct toxicity and reduced responsiveness to food resources. In addition, the combined effects of co-exposure to different elements can also occur. The transfer of these contaminants occurs through the soil-plant-bee-human chain, with plants accumulating toxins from the soil and atmosphere. Although worker bees partially mitigate contamination during the honey-processing phase, final products remain vulnerable to chemical residues. The type of plant, the mobility and bioavailability of toxic elements affect transfer from soil to flowers or other parts of the plants visited by foraging bees. Beyond environmental factors, improper harvesting, extraction, and storage procedures further contribute to honey contamination. Given that current regulations primarily limit lead content, a more comprehensive monitoring of the environment and bee health, as well as monitoring of honey safety, is imperative to prevent future ecological and food safety risks.

Keywords: honey bee, honey, toxic elements

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P107. Evaluation of Potentially Toxic Elements in Donkey Milk from Banat and Balkan Donkey Breeds in the Zasavica Nature Reserve

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Donkey milk is increasingly valued due to its nutritional properties and hypoallergenic potential, making it suitable for sensitive consumer groups. However, the presence of potentially toxic elements, such as arsenic (As), cadmium (Cd), mercury (Hg), and lead (Pb), may pose risks to food safety and public health. These elements can enter milk through environmental contamination, feed, water, or improper handling. Compared with cow, goat, and sheep milk, limited data are available on the occurrence of potentially toxic elements in donkey milk. The aim of this study was to evaluate the presence of selected potentially toxic elemets (As, Cd, Hg, and Pb) in donkey milk from autochthonous Banat and Balkan donkey breeds.

Milk samples were collected monthly over a one-year period from the Zasavica Nature Reserve, where approximately 300 lactating donkeys are raised under extensive farming conditions. Donkeys graze on pasture for nine months per year and are fed mainly corn and triticale during winter. A total of 36 composite milk samples were analyzed. Concentrations of As, Cd, Hg and Pb were determined using inductively coupled plasma mass spectrometry (ICP-MS) (Agilent ICP-MS 7700, Agilent Technologies).

The results showed that most milk samples contained low concentrations of potentially toxic elements. As ranged from <LOD to 0.004 mg/kg. Pb ranged from <LOD to 0.041 mg/kg. Hg ranged from <LOD to 0.007 mg/kg, while Cd ranged from <LOD to 0.006 mg/kg. However, in two samples collected during the spring period, Pb concentrations exceeded the prescribed regulatory limits. These findings suggest that seasonal factors and environmental exposure may influence the presence of contaminants in donkey milk.

The growing consumption of donkey milk in Europe highlights the importance of monitoring chemical contaminants to ensure food safety. Although the detected levels of most elements were low, the presence of elevated Pb concentrations in some samples indicates the need for continuous monitoring of environmental contamination sources. Future studies should focus on broader sampling strategies, risk assessment, and the development of preventive measures to ensure the safety and sustainability of donkey milk production.

Keywords: donkey milk, autochthonous donkey breeds, heavy metals, food safety, environmental contamination

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P108. Spatial variability of heavy metals in the Danube and bioaccumulation in crayfish (*Faxonius limosus*)

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Faxonius limosus, an invasive crayfish species, poses a threat to Danube biodiversity but also has potential for valorization through its meat and exoskeletons. This study aimed to determine heavy metal concentrations in crayfish meat and assess water and sediment quality at collection sites, to evaluate the relationship between environmental metal levels and bioaccumulation. Analyses were conducted following current regulations for contaminant levels in food and environmental matrices.

Crayfish, surface water, and sediment samples were collected from four sites along the Danube River in Serbia (Apatin, Bogojevo, Begeč, and Sremski Karlovci). Metal concentrations were analyzed using inductively coupled plasma mass spectrometry (ICP-MS, 7700 Series).

The mean concentrations of Cd (0.017 mg/kg), Hg (0.190 mg/kg), and Pb (0.033 mg/kg) in crayfish meat were below the maximum permissible levels established by the Regulation on Maximum Contaminant Levels in Food (Official Gazette of RS, Nos. 73/2024, 90/2024, 47/2025, 61/2025, and 103/2025), confirming its safety for human consumption. Metal concentrations in water varied as follows: Cr (0.05–0.16 µg/L); Mn (5.82–12.06 µg/L); Fe (73.9–125 µg/L); Zn (<0.01–0.92 µg/L); As (1.14–1.63 µg/L); Cu (0.28–5.67 µg/L), with the highest values recorded at Begeč (Cr, Zn, Cu), Sremski Karlovci (Mn, Fe), and Apatin (As). All measured concentrations in water were within the threshold values specified in the Regulation on Limit Values of Pollutants in Surface and Ground Waters and Sediments (Official Gazette of RS, No. 50/2012), indicating good surface water quality. Sediments showed higher metal accumulation: Cr (4.12–13.7 mg/kg); Cd (1.55–2.68 mg/kg); Hg (0.09–0.12 mg/kg); Zn (42.35–142 mg/kg); As (5.26–14.3 mg/kg); Cu (4.65–33.8 mg/kg); Pb (15.9–35.8 mg/kg); Ni (7.33–11.4 mg/kg), with the highest values observed at Bogojevo (Cr, As, Hg), Apatin (Cu), and Begeč (Cd, Zn, Pb, Ni). Metal accumulation in sediment highlights the need for continuous monitoring, especially at sites with elevated concentrations, in accordance with regulatory limits.

Trends indicate that, although sediments accumulate higher concentrations of metals compared to surface water, metal levels in the tissue of *Faxonius limosus* remain below the maximum permitted values, reflecting low bioaccumulation of Cd, Hg, and Pb. *Faxonius limosus*, despite being invasive, may represent a potential resource for human consumption and industrial valorization, while sediments remain a key indicator of metal loading in the ecosystem and an essential parameter for continuous ecological monitoring.

Keywords: faxonius limosus, invasive species, heavy metals, sediment, water

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P109. Neural tube defects in seals

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Neural tube defects (NTDs) are malformations that arise when the brain or spinal cord fail to close properly during early embryonic development. Severe defects are incompatible with life, resulting in abortion or death shortly after birth. The description of such congenital defects is still poor in veterinary medicine and even more limited in wildlife. Here we present two rare cases in free-ranging seals: holoprosencephaly (HPE) in a grey seal (*Halichoerus grypus*) and anencephaly-exencephaly in a harbor seal (*Phoca vitulina*).

Both fetuses were discovered during routine health monitoring: one during necropsy of a stranded grey seal (found 2026-03-01, Skåne, Baltic Sea) and the other from a legally hunted harbor seal (taken 2018-01-27, Västra Götaland, Skagerrak). The grey seal's cause of death is under investigation (influenza A and morbillivirus excluded) while the harbor seal was otherwise healthy.

The grey seal fetus (♀, 4,1kg and 56cm) was near term but markedly small. It presented with severe craniofacial malformations of HPE characterized by a single eye located in the facial midline (cyclopia) with a proboscis located above the eye. The nose and mouth were rudimentary. CT, MRI, and subsequent dissection confirmed alobar HPE—the most severe form—and a closed craniofacial skeleton with a non-functional eye. The harbor seal fetus (♀, 821g, 29.5cm) was in the second trimester and lacked dorsal cranial structures (40×45mm) with exposed neural tissue, consistent with anencephaly-exencephaly.

NTDs such as HPE and anencephaly-exencephaly are etiologically heterogeneous conditions. They typically occur sporadically due to genetic abnormalities (chromosomal defects, gene mutations), environmental influences such as teratogenic toxins and toxicants or nutritional imbalances. Infectious agents and chronic maternal diseases are less common causes. Multifactorial origins are possible. These defects are rare and identifying their causes is challenging due to survival bias, delayed detection, and diverse potential etiologies. Nevertheless, developmental defects warrant comprehensive long-term surveillance, particularly in the recovering Baltic grey seal population, previously affected by high exposure to persistent organic pollutants. A conjoint health and disease surveillance program of marine mammals, run by SVA and NRM enables detection of health trends and emerging threats to the marine mammal populations in Sweden.

Keywords: embryological defects, holoprosencephaly, cyclopia, anencephaly

Funding source & Acknowledgement: Sweden's health and disease surveillance program for marine mammals is funded by the Swedish Agency for Marine and Water Management as part of Sweden's environmental monitoring

P110. Methodological approaches for assessing microplastic impacts on wildlife: challenges and future directions

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Microplastic (MP) pollution is increasingly recognized as a threat to wildlife, yet current evidence is shaped strongly by the methods used to detect, quantify, and interpret exposure. This review evaluates methodological approaches used to assess MP impacts on wildlife, with particular focus on sampled matrices, extraction procedures, analytical identification, biological endpoints, and the extent to which studies distinguish exposure from actual adverse effects.
This study is based on a review of 21 articles (2018-2025) focusing on MP exposure and effects in wildlife. The focus was placed on sample matrices, extraction and digestion procedures, as well as particle identification techniques. Potential health effects were assessed by considering polymer type, particle morphology, and their possible impacts on physiological and metabolic processes in wildlife species.
The reviewed studies showed substantial methodological diversity regarding sample matrices and analytical techniques used for identification of MPs. Each study generally focused on a specific sample matrix which provided valuable but partial insight into MP exposure. Fecal and gastrointestinal studies usually underestimate exposure because of potential translocation of said particles in tissues. On the other hand, tissue-based studies are often demanding and results can lead to false negative results because of the small sample size. Analytical approaches in identifying MPs were also diverse. Visual identification is practical but prone to misclassification. Spectroscopic methods improve polymer confirmation, but are time-consuming and limited by particle size. HPLC-UV and pyrolysis-GC/MS techniques on the other hand lose information on particle number, shape and morphology. It should be noted, that health effects of MPs are frequently discussed but less consistently measured, with most studies providing stronger evidence of exposure than of direct adverse effects.
Current methodologies are more consistent in demonstrating MP exposure than in proving biological harm. Future research should be directed on standardization of extraction and analytical techniques but also on the developing of methods that will assess adverse outcomes of MPs on health and welfare of wildlife.

Keywords: Microplastics, Wildlife, Detection, Challenges

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Session 7

One Health Initiatives: integrated surveillance of zoonotic pathogens in wildlife & future pandemic preparedness

Oral Presentations

Invited lecture

One Health initiatives: perceptions and facts on the linkage between wildlife and human health

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The health of humans, animals and ecosystems is intricately linked, a One health approach is needed to sustainably balance and optimize health. The perception of disease risks posed by wildlife oftentimes does not reflect scientific evidence. Ten aspects will be discussed:

1. Healthy ecosystems provide multiple benefits (ecosystem services) and well-being to humans. Wildlife is an integral part of ecosystems, and its health should be protected.
2. Human exposure to wildlife in unnatural ways, such as through the wildlife trade and encroachment of nature, risks the emergence of diseases.
3. Wildlife is often seen as the culprit for the spillover and emergence of diseases in humans and livestock; however this is primarily the result of anthropogenic drivers. Livestock contributes relatively more to zoonotic spillovers than wildlife.
4. Wild animals are often designated as reservoirs of infections without sufficient epidemiological evidence.
5. Wildlife health surveillance needs to be strengthened. Early warning relies on early detection, which is most effectively achieved through passive surveillance. Active and passive wildlife health surveillance are complementary and can be advantageously combined with environmental and human health surveillance. Such surveillance data are needed to identify risks, limit spillover and spread, and are therefore essential for prevention.
6. Wildlife impacts livestock health, however many high-impact diseases actually originate from spillover events from livestock to wildlife. Growing livestock populations increase contact with wildlife and reduce their natural habitats.
7. Sustainable and appropriate wildlife management is needed to prevent and control diseases. Culling wildlife may be necessary as part of control and eradication strategies, but caution must be exercised because it can be unethical, unsustainable, shrink biodiversity and may not solve the problem.
8. Pathogens continuously evolve. Surveillance should include genomic sequencing to detect changes in their host range and pathogenicity, as well as to predict changes in epidemiology.
9. Invasive Alien Species (IAS) can cause severe biodiversity loss and are a growing threat to the sustainability and health of ecosystems. Furthermore, they may introduce new diseases and increase the impact of existing zoonoses.
10. Key elements for the science-based management of wildlife health include data sharing, collaborating, networking, and openness in reporting. Wild animals know no political boundaries, and neither should we when it comes to the protection of biodiversity and wildlife health.

Education and the communication of scientific facts are essential to understanding the importance of preserving healthy wildlife populations.

Keywords: wildlife health, surveillance, One Health

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Contrasting effects of anthropogenic environmental changes on zoonotic disease risk from small mammals

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Anthropogenic environmental changes affect wildlife communities and consequently affect the zoonotic disease risk. Though some underlying mechanisms are fairly straightforward, e.g. changed abundance or host communities, these alone do not explain infection patterns seen and we still lack a good insight on other relevant factors and their interplay. For example, when and how often dilution or amplification effects occur and what mechanisms underly these phenomena is poorly understood. Here, I present results from three studies performed in our group that investigate zoonotic pathogens in small mammal communities in three different ecological settings.
The following studies are discussed:
1) Urban greening: gradients of greenness in urban environments and the effects on zoonotic pathogens in small mammals;
2) Comparison of land use types: zoonotic pathogens in small mammal communities in grids containing mixed forest, urban areas and farmland;
3) Forest restoration: small mammal communities and their zoonotic pathogens along a gradient of regenerated forest compared to pristine forest.
In all studies, small mammals, i.e. varying species of rodents and insectivores, were collected and multiple zoonotic pathogens were tested for, e.g. tick-borne pathogens, leptospira and orthohantaviruses.
Overall, in all three studies, for the majority of the tested pathogens there was no association detected between anthropogenic changes of the environment and the prevalence of zoonotic pathogens. For the few pathogens for which associations were detected, different patterns were detected in the three ecological settings. For example, the tick-borne pathogen *Borrelia* spp. in rats increased in prevalence when urban areas were greener. Similarly, the infection prevalence of *Borrelia* spp. in small mammals was higher in mixed forests, compared to urban areas and farmland. However, in the third study on forest restoration, the small mammals from pristine and more regenerated forest plots harboured lower infection rates with *Borrelia burgdorferi* s.l. compared to the less regenerated forest plots.
These studies underline that the associations between pathogen prevalence and human affected environments are complicated and ecosystem-dependent and suggest that transmission mode of the pathogen is also an important factor. There will likely be no one-size-fits-all principle, but having a better understanding of these associations in various ecological contexts can help mitigate zoonotic disease risk.

Keywords: eco-epidemiology, zoonoses, anthropogenic drivers, public health

Advancing wildlife-borne pathogen surveillance by determining mammal species' vulnerability to land use change

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Anthropogenic land use changes (LUC) may alter the risk of wildlife-borne pathogens for human and animal health through effects on e.g. local species assemblage composition (i.e. which wildlife species are present and at what abundances) and host quality (i.e. contribution of a host to parasite fitness). This study aims to identify geographical areas and species of increased interest for wildlife-borne pathogen surveillance based on expected shifts in pathogen transmission dynamics in wild terrestrial mammals under historical LUC and two future LUC scenarios for the Netherlands.

A trait-based vulnerability assessment (TVA) framework with three dimensions (exposure, sensitivity and adaptive capacity) was used to assess 59 terrestrial mammal species native to the Netherlands. For historical LUC (2007-2008 until 2021) and two future LUC scenarios (2020 until 2050), the cumulative habitat suitability change across species' ranges was calculated and corrected for variability in species-specific observation data. Relevant biological traits were selected and sensitivity and adaptive capacity scores were assigned based on species' trait values. Mammals scoring high for both exposure and sensitivity were classified as highly vulnerable or potentially adaptive depending on their adaptive capacity scoring.

In all three LUC analyses, nearly all species classified as highly vulnerable or potentially adaptive were species of the order *Chiroptera*. Potential hotspots for wildlife-borne pathogen surveillance were identified based on: (1) the spatial distribution of species classified as highly vulnerable or potentially adaptive and (2) the spatial distribution of habitat suitability changes (frequency and magnitude) across species.

TVA's are commonly performed to inform conservation actions based on species' estimated relative extinction risk due to a stressor of interest. Here, we used a TVA to pro-actively inform wildlife disease surveillance efforts in order to cost-effectively minimize risks for human and animal health.

Keywords: wildlife, surveillance, vulnerability, habitat suitability

High-risk activities for the zoonotic spillover of pathogens in the legal wildlife trade

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Increasing trends in zoonotic spillover events are of major public health concern globally, with wildlife trade identified as one of the sources of these events. The global trade in wild animals and their products is extremely complex and varied, operating across differing scales, geographic regions and taxa. It can provide numerous opportunities for interactions and conditions which could lead to disease outbreaks, however there is a lack of clarity around which activities within the trade chain pose the greatest risk for a zoonotic spillover event. Therefore, the aims of this study were: a) to gain an understanding about the activities throughout the legal wildlife trade pathway that may pose the highest risk for zoonotic spillover events; and b) to develop insights into prevention measures which could be applied to those high-risk events.

We conducted a survey and semi-structured interviews, targeting experts in the field of wildlife trade and zoonoses. A total of 23 experts responded to the survey and three participants were interviewed. In the survey, experts were asked to rank various risk factors across events in the legal wildlife trade chain that could influence the likelihood of a spillover event. Follow-up interviews were conducted online with the first portion of the interview focussing on the survey and spillover risk factors and the second half gathering opinions on possible preventive measures. Summary statistics were calculated for the survey data and thematic analysis was conducted on the interview transcripts.

From the survey, sale of live animals was the event across the wildlife trade pathway which received the highest risk score. Within this event, unsanitary environment followed by human-animal contact were the factors considered of highest risk for zoonotic spillover. Other relevant factors were species mixing and animal stress. In the follow-up interviews, experts expressed that preventing spillovers from happening at these junctures was critical, suggesting measures such as improved biosecurity, education and regulations. Experts acknowledged that almost all events in the trade chain carried a high risk of spillover and emphasised the interconnectedness of the factors and the relationship with animal welfare.

This preliminary work helps to identify critical control points where zoonotic spillover is most likely to occur across the legal wildlife trade supply chain. This information can help prioritise further research in this field with the ultimate goal of informing policies for pandemic prevention.

Keywords: wildlife trade, zoonoses, spillover, disease

When Science Sings: International One Health Collaboration Communicating Wildlife-Associated Disease Risks Through Music

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Emerging infectious diseases originating from wildlife reservoirs pose a persistent threat to both animal and human health. Communicating these risks effectively remains challenging, particularly in settings where ecological complexity, cultural diversity, and varying health literacy intersect.
Within the framework of the Global Health Protection Programme (GHPP), the COPE (Community-based One Health Participatory Empowerment) project focused on One Health interventions for Lassa fever in Nigeria. As a complementary activity at the margins of the project, a participatory music video was developed during a binational workshop at the Island of Riems, bringing together researchers from Nigeria and Germany alongside professional musicians and producers.
The narrative emphasizes pathogen emergence at the wildlife–livestock–human interface, illustrating how viruses can cross species barriers and spread across regions without regard for borders. It highlights the role of wildlife as reservoirs of zoonotic agents and underscores the importance of early detection, cross-sectoral surveillance, nature protection and coordinated global responses to mitigate spillover risks and prevent future pandemics.
Unusually, the scientists themselves became part of the message: contributing to songwriting, performance, and storytelling. This participatory process fostered ownership, credibility, and interdisciplinary exchange beyond conventional communication formats. The video complements a quasi-experimental study assessing participatory versus traditional risk communication strategies in Lassafever combat in Southeast Nigeria. As part of the EWDA presentation, the performance music video will be shown in full, providing a unique opportunity for attendees to experience the integration of scientific content and creative expression.
By blending art and science, this project challenges how we communicate wildlife-associated disease risks. It demonstrates that creative, interdisciplinary approaches can enhance understanding, trust, and engagement across sectors and audiences. In a world where pathogens travel faster than information is trusted, innovative communication may be as critical as surveillance itself.

Keywords: One Health, Music, Video, Participatory, Science message, story telling

Funding source or Acknowledgement Global Health Protection Program of the German Ministry of Health, NEOH project: Nigeria Engaging One Health

The OneBAT project: One Health approach to understand, predict and prevent viral emergencies from bats

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Bats are associated with a large variety of viruses, including ones phylogenetically related with human emerging pathogens. While these evidences nominate bats as possible reservoirs for Pathogen X, we are still far from understanding triggers of emergence going beyond viral detection. In Europe, the migratory bat *Miniopterus schreibersii* hosts lyssaviruses, filoviruses and coronaviruses, providing a unique opportunity to optimize resources and efforts for fieldwork and diagnostic while providing relevant data on three priority viruses with zoonotic potential. In line with the "One Health" concept, the project OneBAT, financed under the umbrella of Horizon EU, adopts a cross-disciplinary integrated approach to study key steps favuring the spillover of viruses associated with *M. schreibersii*.
We mapped the distribution of *M. schreibersii* and addressed its possible interface with humans and domestic animals. We harmonized field activities within 14 roosts in five EU countries and developed, standardized and harmonized a novel diagnostic platform to obtain comparable data on virus prevalence and investigate seasonality, shedding pattern and phylogeny. We employed pit-TAGs to define bat movements, survival and longitudinal virological data upon recapture.
We confirmed the association of *M. schreibersii* with karst. However, we also described peculiar roosting sites in Italy located within urban settlements and confirmed the presence of an interface where the spillover might occur. We confirmed the co-circulation of the filovirus LLOV, distinct species of lyssaviruses (WCBV and LLEBV) and coronaviruses (MiCoV-1, HKU8, HKU7) across the distribution range of their host. Molecular detection of CoVs allowed confirming phylogenetic similarity of EU strains with no geographical clustering. On this matter, capture-recapture showed movements of animals between study sites, also across countries. We found shedding of CoVs in individual samples of saliva and faeces and in air samples collected within roosts. We described consistent seasonal trends of prevalence/sero-prevalence, supporting yearly peaks of transmission where likelihood for spillover is highest.
OneBAT provides a full assessment of priority viruses widely circulating in *M. schreibersii*, including spillover interfaces, peaks of transmission and routes for exposure. In order to achieve these scientific goals, OneBAT developed tools that could be exploited by the research community, including field protocols and technologies, laboratory methods, reagents and sequences.

Keywords: OneHealth, bats, spillover

Integrating Ecological–Diagnostic Surveillance in Bats: A Comparative One Health Case Study in Italy and Spain

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Although wildlife surveillance is a key component of the One Health (OH) approach, European initiatives often remain fragmented. Ecological monitoring and veterinary diagnostics tend to operate in separate compartments, rarely establishing interdisciplinary connections, limiting the ability to characterise pathogen circulation in the context of host ecology. Bats serve as a primary model for integration due to their ecological importance and their role as reservoirs for several zoonotic pathogens. Within the European Partnership Animal Health & Welfare (EUP AH&W), the Wildlife Network aims to identify gaps in surveillance programs and harmonise monitoring systems. In this regard, IZSLER (Italy) and IREC-ENETWILD (Spain), which have extensive experience in bat monitoring, started a comparative analysis of their respective surveillance architectures, evaluating the complementarities between the Italian veterinary-led diagnostic network and the Spanish ecology-focused framework and identifying potential areas for integration.

The study compared two operational models between 2020 and 2025. The IZSLER approach was based on passive surveillance in Northern Italy (1,320 individuals belonging to 23 species). This approach focused on high-resolution laboratory diagnostics, including necropsy, cell cultures and molecular characterization of viral strains. The IREC-ENETWILD framework used a structured field-sampling (2,337 bats, 27 species) design across multiple Spanish regions. This framework combined population monitoring with active screening for pathogens in various biological matrices and ectoparasites to understand host-pathogen interactions in relation to the ecological context.

The Italian passive surveillance model proved highly effective for detecting unusual mortality events. This diagnostic workflow enabled the identification of previously undescribed or unexpected viral agents including Vaprio ledantevirus and Hypsugopoxvirus, as well as emerging viruses with a zoonotic potential such as Issyk-kul virus, MERS and SARS-related Coronaviruses and Orthoreoviruses. The Spanish ecological surveillance model provided complementary insights into host population dynamics and subclinical infections, often missed by passive systems. These preliminary results show that the two surveillance systems could complement each other, and integrating their data streams allows diagnostic finding to be interpreted within their ecological context.

Our findings suggest that ecological monitoring and veterinary diagnostics generate different yet highly complementary information. Whereas the diagnostic approach offers rapid response and high-resolution pathogen data, the ecological framework provides the necessary context for evidence-based risk assessment. This study may serve as a scalable model for European wildlife surveillance promoting integrated workflows between ecologists and veterinarians, improving early warning and preparedness for emerging zoonotic threats.

Keywords: integrated surveillance, wildlife, bats,

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Surveillance of emerging viral pathogens in insectivorous bats in Ukraine

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Due to their unique biology, bats serve as hosts for a wide range of emerging zoonotic pathogens and may play a role in the maintenance and transmission of infectious agents to other vertebrates, including humans. Surveillance of bat pathogens is essential for predicting and preparing for future outbreaks and pandemics. The main objective of this study was to assess the role of bats as natural reservoirs of pathogens relevant to human and animal health in Ukraine.
Biological material from bats was collected in different regions of Ukraine according to standard methods. Reverse transcription PCR and real-time RT-PCR were used for detection of the RdRp gene (coronavirus), PB1 gene (orthomyxovirus), and L gene (paramyxovirus).
In total, during 2022–2025, 1125 bats were captured in natural habitats and 474 bats were collected in urban areas representing 20 species across 10 regions of Ukraine (Poltava, Kharkiv, Kyiv, Khmelnytskyi, Odesa, Zhytomyr, Ternopil, Cherkasy, Rivne, and Lviv oblasts). In urban areas, approximately 4.3–69.2% of insectivorous bats tested positive for coronaviruses (CoV): *Nyctalus noctule* (4.3–7.9%), *Eptesicus serotinus* (12.9–50%), *Pipistrellus kuhlii* (20–100%). In natural habitats, 2.7–100% of insectivorous bats were positive for CoV: *N. noctule* (14.6–25.7%), *E. serotinus* (36.2–50.0%), *M. nattereri* (20.0%), *M. daubentonii* (38.9–41.7%), *R. hipposideros* (3.8–28.6%), *M. blythii* (25.0%), *M. dasycneme* (50.0%), *N. leisleri* (20.0%), *P. nathusii* (9.1%), *P. pygmaeus* (60.0%). PCR results showed fluctuations in the prevalence of paramyxoviruses in urban and natural areas across different regions (0.52–33.3%). No positive samples for orthomyxoviruses were detected in any of the examined species.
The first large-scale, systematic surveillance of viral pathogens in bats across Ukraine was conducted and covered 11 regions and 20 bat species, yielding the first evidence of coronavirus and paramyxovirus circulation in bat populations in Ukraine, while no orthomyxoviruses were detected. Detection of viral pathogens of importance to human and animal health highlighting the potential risk of spillover from wildlife reservoirs to domestic animals and humans. Continued surveillance in Ukraine remains critically important. As infectious diseases do not recognize borders, surveillance efforts in Ukraine are regionally important and beneficial for Europe.

Keywords: emergent viral pathogen, bat, surveillance, Ukraine

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Tracking Avian Influenza Virus in the environment: A longitudinal study across Scotland

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Early warning systems for timely detection of Avian Influenza Virus (AIV) strains are essential due to the rapid mutation and adaptation of viral subtypes. Yet, detection of AIV in wild birds heavily relies on opportunistic carcass sampling, a system that leaves substantial gaps in our understanding of the distribution, evolution, and spread of this pathogen. Environmental monitoring can complement carcass-based surveillance but is not currently integrated into the official United Kingdom framework for early detection and preparedness for AIV. Questions remain regarding its implementation, performance, and contribution to the epidemiology of AIV.

In collaboration with a large network of Scottish wildlife organizations, this project aimed to develop and test field protocols for the collection of sediment, water, and faecal samples from high-risk locations where wild bird species, primarily of the orders Anseriformes (ducks, geese, swans) and Charadriiformes (gulls, terns), congregate at high densities throughout the year. Samples were screened using nested PCR targeting Segment 7 (matrix gene) developed at the Roslin Institute, followed by Sanger sequencing to confirm positives. Whole-genome sequencing was performed using Oxford Nanopore Technologies (ONT).

Since 2024, 3,356 environmental samples have been collected from 20 sites in Scotland (80.4% faecal, 17.0% sediment, and 2.5% water). AIV has been confirmed in 50 samples, corresponding to a 1.5% detection rate. Increased detection of AIV in environmental samples coincides with periods of high detection in carcasses. However, unique environmental detections have also occurred in remote locations where carcass collection is logistically unfeasible or not detected through official monitoring. ONT sequencing achieved heterogeneous recovery of viral segments across sample types. Phylodynamic analyses show that environmental sequences cluster well with the most recent circulating AIV reassortants, strengthening the outputs of these models.

Longitudinal environmental sampling supports the recovery of partial viral sequences and is a non-invasive, field-friendly approach with potential as an early warning tool for monitoring AIV in wild bird populations. The combined field and laboratory workflows generated valuable data for disease mapping, risk assessment, and epidemiological modelling within a One Health framework, but sustained implementation will depend on strong partnerships, particularly in sites with logistical constraints.

Keywords: Avian Influenza Virus, Environmental monitoring, Seabirds, Waterfowl, Nanopore sequencing.

Beyond dogs: multilocus microsatellite typing (MLMT) reveals wildlife as putative reservoirs of *Leishmania infantum* in northeaster Italy

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In the Emilia Romagna Region (RER) different *Leishmania infantum* strains circulate in sand-flies (SF) and vertebrate hosts, including dogs in which the parasite causes canine leishmaniasis (CanL). In humans, *L. infantum* is responsible for both visceral (VL) and tegumentary leishmaniasis (TL). The role of dogs as the main reservoir in this area has been questioned, as *L. infantum* is also widespread in wildlife hosts, with a preferential tropism for skin tissues. The aim of this study was to investigate the genetic variation of Leishmania in wild animal samples to integrate previous data from human, canine and sand-fly strains, to better understand the parasite epidemiology in RER. A total of 40 *L. infantum* DNA samples obtained from wild mammal carcasses (26 roe-deers; 8 foxes; 5 hares; 1 wolf), collected in RER during 2021-2024, were analysed. Samples were genotyped by multilocus microsatellite typing (MLMT) using 15 polymorphic loci. Genetic relationships among parasites were inferred through a MLMT-based tree using the BEASTvntr package implemented in the BEAST2. 2.4.3, including an integrated dataset of 133 known strains: 25 VL, 44 TL, 52 CanL, 12 from SF, and 4 selected WHO reference strains: 3 representatives of *L. infantum* zymodemes MON-1, MON-72, MON-24, and 1 *L. donovani* strain. The MLMT-based tree revealed three major clades. Clade A grouped all the 52 CanL strains, the *L. infantum* reference strains MON-1 and MON-72, 2 TL human samples and only 1 sample from a fox. Thirty-nine samples from wild animals were distributed between the other two clades: 21 samples clustered in clade B, which comprised all (n=25) VL-associated strains, a subset (n=9) of TL strains, and 11 SF samples. The remaining 19 wild animal samples were comprised in clade C, which included 35 TL-associated strains and showed close correlation with the *L. infantum* MON-24 reference strain. The *L. donovani* reference strain formed a distinct long branch. The topology of the MLMT-based tree was consistent with previously described population structure in RER. The uniform distribution of *Leishmania* samples from wild animals in clade B and C, associated with the majority of human VL and TL respectively, provides strong evidence for the role of different wild mammal species in the epidemiology of *L. infantum* in RER. Further studies are needed to assess whether wildlife species act as maintenance hosts and to demonstrate their infectivity to sand flies, thereby confirming their role as a source of infection for humans.

Keywords: Leishmania infantum; wild animals; MLMT; reservoir

Wild Boars as Sentinels and Victims of Viral Diseases in Croatia

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Wild boar (*Sus scrofa*) is a key wildlife species in Croatia with an important role in the epidemiology of viral diseases, functioning simultaneously as reservoirs, sentinels, and susceptible hosts by which they directly influence disease management strategies, food safety considerations, and veterinary public health planning. Their rapid population growth, ecological adaptability, and increasing interface with domestic animals and humans necessitate continuous and structured surveillance. This study synthesizes two decades of surveillance data to clarify their role in the maintenance, emergence, and transmission of viral pathogens.

Over a 20-year period, wild boars in Croatia were systematically investigated through passive and active surveillance for major viral pathogens, including classical swine fever (CSF), African swine fever (ASF), Aujeszky's disease (AD), porcine circovirus type 2 (PCV2), porcine reproductive and respiratory syndrome (PRRS), rotaviruses (RV) and hepatitis E (HE) viruses. Surveillance was expanded to include less commonly studied viruses such as causes of tick-borne encephalitis (TBE), porcine sapelo- and teschoviruses, porcine lymphotropic herpesvirus (PLHV), and swine influenza A (SI) to better characterize their sentinel and reservoir potential.

The emergence of ASF in 2023 in both domestic pigs and wild boars represents a pivotal epidemiological event, demonstrating the central role of wild boar populations in virus persistence and spread. Environmental stability of the virus and carcass-mediated transmission significantly prolong circulation and hinder eradication. Wild boars were also confirmed as hosts of PCV2, PRRS and AD viruses, posing sustained risks to domestic pigs and, in the case of AD, to carnivores. The persistence of hepatitis E highlights ongoing zoonotic risk associated with game meat handling and consumption. Detection of TBE, PLHV RV and SI further identifies wild boars as reservoirs of zoonotic agents and potential drivers of viral evolution. Notably, the absence of CSF and sapelo-/teschovirus infections, was confirmed throughout the study period.

This study provides evidence of multi-pathogen circulation within wild boar, proving their role in viral disease ecology in Croatia, acting as both amplifiers and early indicators of infection. Therefore, integrating wildlife surveillance into a One Health framework is essential for timely risk assessment and response. Future risks will increasingly depend on ecological change, hunting practices, and cross-border animal movements, all of which demand coordinated regional monitoring and rapid information exchange. Sustained, coordinated monitoring linking veterinary, ecological, and public health sectors, is critical for improving early warning systems and mitigating the impact of emerging and transboundary diseases.

Keywords: wild boar, sentinels, viral diseases, zoonoses, Croatia.

Session 7

One Health Initiatives: integrated surveillance of zoonotic pathogens in wildlife & future pandemic preparedness

Poster Presentations

P111. Towards improved wildlife disease surveillance in Europe

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The European Partnership Animal Health and Welfare project "A European network for terrestrial and aquatic mammals and birds" aims at enabling, supporting and promoting wildlife disease surveillance (WDS) in Europe, a key instrument for the early detection, notification and management of wildlife diseases. The assessment of WDS needs is a first step towards improvement of existing systems.
An inventory of WDS systems for 33 European countries was conducted through a Survey sent to Central Veterinary Authorities (CVA) and Universities and Institutions (U&I) and a grey literature review. It also included mapping and assessment of needs, difficulties and limitations that hamper efficient WDS in Europe.
Greška! Nije pronađen izvor reference. The main limitations for U&I were the low number of animals investigated, economic constraints and limited ability to extrapolate results to the wildlife population level. In passive surveillance, captive wild animals and invasive alien species were seldom included and there was a strong focus on wild boar and birds. Other taxa were investigated in low numbers, especially small-bodied animals and marine mammals and there was high variation in number of carcasses investigated annually among countries. Logistic and operational challenges included the detection and/or observation of carcasses or sick animals and carcass transport to diagnostic laboratories. Laboratory capacity may be insufficient for large-scale epidemic events. Active surveillance focused primarily on a narrow range of high-priority pathogens from regulatory and economic perspectives. Diagnostic capacity was heterogenous across Europe.
Surveillance systems must be purpose-built. Important requirements for their successful implementation include: 1) continuity, i.e. regular investigation and monitoring of pathogens and diseases over time; 2) sufficient and representative geographical coverage across different epidemiological scenarios (e.g., varying degrees of wildlife-domestic interfaces, including natural, agricultural, peri-urban systems), as well as across host species and number of individuals; 3) timely communication of results to end-users and stakeholders to inform decision-making and action. Ideally, all of Europe should progress towards a level of passive WDS sufficient to enable the rapid detection and characterisation of emerging infections in wildlife, complemented by the active surveillance of priority pathogens. Active surveillance should not be limited to pathogens regulated by legislation or those with the highest economic impact, but should also include those that have severe effects on wildlife health and threaten biodiversity conservation.

Keywords: wildlife disease surveillance, Europe, implementation limitations, economic constraints, wildlife conservation

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P112. Wildlife disease surveillance systems in Europe: an integrated assessment based on a multi-country survey and grey literature review

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Wildlife plays a key role in the epidemiology of infectious diseases at the animal-environment-human interface. However, surveillance systems across Europe remain heterogeneous and poorly characterised. Within the European Partnership for Animal Health and Welfare (EUPAH&W) project, one of the key objectives is to map and analyse national wildlife disease surveillance systems (WDS).
WDS in Europe were described using a questionnaire and a grey literature review (GLR) as complementary data sources. The questionnaire was distributed to 317 professionals from European Central Veterinary Authorities (CVAs), regional services, and universities and research institutions (U&I). The GLR examined government reports, institutional summaries, surveillance plans, websites and publicly available datasets. Information on surveillance structure, targeted species, diagnostics, and data management and sharing were collected. Active surveillance data was collected for 19 wildlife diseases occurring in Europe, not previously covered by other projects and relevant to domestic animals. Results were analysed by surveillance type and institutional category. The survey and GLR captured wildlife disease surveillance systems in 32 European countries. Passive surveillance is present in all countries but varies in scope. Wild birds and wild boar are the most frequently monitored taxa, reported by 25 and 22 countries respectively, while rodents, bats, and amphibians are less covered. Diagnostic approaches differ: authorities rely primarily on necropsy and molecular methods, whereas U&I apply a broader range of techniques, including parasitology and bacteriology. Active surveillance targets a narrow set of priority pathogens, with African swine fever, Trichinellosis, and mammalian tuberculosis being the most consistently monitored by authorities. U&I cover a broader range of pathogens and under-represented taxa. Synanthropic and captive wildlife remain poorly covered. Economic constraints represent the most critical barrier to surveillance overall. Antimicrobial resistance monitoring is conducted systematically by some authorities but remains occasional in research settings.
Wildlife disease surveillance exists across all countries studied, but capacity and scope largely vary. Some degree of passive surveillance is widely established, yet taxonomic coverage prioritises wild birds and wild boar over other epidemiologically relevant species. Diagnostic approaches differ between authorities and U&I, with the latter applying a broader range of methods. Active surveillance encompasses a broad set of pathogens; however, its geographical distribution is often scattered or limited to a few countries, and sampling intensity varies. Strengthening taxonomic coverage, diagnostic capacity, and open data interoperability would enhance early detection capabilities and support a more integrated One Health approach across Europe.

Keywords: Active surveillance; EUPAH&W; Europe; One Health; passive surveillance; wildlife disease surveillance

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P113. Balancing Animal Welfare, Health Risks and Food Safety in Agroforestry Systems: A One Health Perspective from Serbia

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Agroforestry systems involving livestock are increasingly recognized for their potential to enhance animal welfare, environmental sustainability, and farm resilience. At the same time, these systems create complex interfaces between domestic animals, wildlife, and the environment, raising important challenges within the One Health framework.

This study presents field-based observations and contextual analysis of traditional agroforestry practices in Serbia, including extensive forest grazing systems (horses, sheep, goats, geese) and small-scale poultry integration in orchards and gardens. These systems enable animals to express natural behaviours, benefit from improved microclimatic conditions, and experience reduced stress compared to intensive production systems.

However, increased environmental exposure also introduces specific risks. These include predation, limited health monitoring, and closer contact with wildlife reservoirs and environmental pathogens. Such conditions may contribute to the emergence and spread of infectious agents, including antimicrobial-resistant bacteria. Field observations and routine sampling indicate potential contamination risks in animal-derived products (milk, eggs) and at the level of animal skin, with implications for food safety and processing.

The findings highlight that improved animal welfare does not automatically result in improved health status or product safety. Instead, agroforestry systems require adaptive and knowledge-based management approaches that balance natural living conditions with biosecurity, disease prevention, and hygiene control.

This work frames agroforestry systems as dynamic One Health environments, where animal welfare, ecosystem interactions, and public health are closely interconnected. It underlines the need for integrated monitoring, targeted training, and context-specific management practices to ensure that welfare benefits are not offset by increased health and safety risks.

Keywords: silvopastoral systems, livestock–wildlife interface, animal welfare, biosecurity, veterinary public health

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P114. Tracking avian influenza in the wild: environmental surveillance at waterfowl aggregation sites

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Avian influenza viruses (AIVs) are widely distributed among waterfowl populations and include both low pathogenicity (LPAIV) and high pathogenicity (HPAIV) strains. Since the emergence of the Goose/Guangdong (Gs/Gd) lineage, H5Nx HPAIVs belonging to clade 2.3.4.4b have caused extensive mortality in wild birds and poultry, along with increasing spillover events in mammals, including humans.
Although LPAIVs generally induce little or no clinical disease in wild birds, they play a central role in AIV ecology. By maintaining a large and diverse genetic reservoir, they create opportunities for reassortment events that drive the diversification of Gs/Gd HPAIVs. In addition, certain H5 and H7 LPAIV subtypes can directly evolve into HPAIVs following the acquisition of a polybasic cleavage site.
Comprehensive surveillance across both wild and domestic compartments is therefore essential to capture viral diversity, monitor evolutionary dynamics, and anticipate the emergence of novel HPAIV genotypes.
In this context, the PREZODE ZOO-FLU project aims to develop innovative environmental surveillance strategies at the wildlife–domestic interface. This approach integrates the analysis of environmental matrices from both compartments to characterize viral circulation and gene flow.
On the wildlife side, environmental samples—including surface water, sediments, feathers, and feces—were collected from multiple water bodies hosting aggregations of wild waterfowl in southwestern France. These samples were analysed to detect and sequence circulating AIVs.
Between September 2025 and March 2026, seven sites were sampled every two weeks, resulting in the collection of 57 water and sediment samples, 142 fecal samples, and 36 feather sets. All samples were screened for AIV matrix gene as well as H5 and H7 hemagglutinin genes. Concurrent bird surveys were also conducted.
AIV RNA was detected at all seven sites and in all four environmental matrices. Notably, one site showed repeated positivity in water samples over time. More than half of the positive detections corresponded to H5/H7 subtypes, with Ct values ranging from 28 to 37. Although analyses are ongoing, these results support the relevance of environmental sampling as a complementary tool for monitoring AIV circulation.

Keywords: Avian influenza, waterfowl, environment, water, France

P115. Proof of concept: Evaluating the Feasibility of Non-Invasive Wheat-Supplemented Water Bins for Longitudinal Screening of Pathogens in Wild Mammals in Riems Island, Germany

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Wildlife often plays a crucial role in the epidemiology of zoonotic diseases, serving as a reservoir or a means of pathogen transmission to humans and domestic animals. Collecting wildlife samples can be challenging and often involves invasive methods, which can cause discomfort for both animals and humans. This study aimed to evaluate the feasibility of non-invasive pathogen screening using wheat-supplemented water bins in wild mammals from two locations, combined with wildlife activity monitoring using wildlife cameras.

Water samples and swab samples were collected from wheat-supplemented bins for bacterial and viral pathogen screening at two locations twice a week over a 5-month period. In addition, an existing swab sample batch was included in the study for retrospective analysis of Antimicrobial Resistance (AMR) bacteria. For bacterial pathogens, we first screened for antimicrobial-resistant bacteria using selective culturing. Further, we analysed promising isolates for their antimicrobial susceptibility profile, followed by molecular characterization applying Whole Genome Sequencing (WGS). For viral pathogens, water samples were concentrated using Polyethene Glycol (PEG) and then screened for pan-Betacoronaviruses using conventional RT-PCR, followed by confirmation by Sanger sequencing. A wildlife camera was also installed to record wildlife activity around the water bins.

Through wildlife cameras, we observed seven mammal species, such as brown rats, raccoons, European badgers, otters, red foxes, martens, and roe deer, at the sample sites. A total of 95 swabs were collected from the water bins. Eight isolates were identified as *Acinetobacter baumannii*, *Enterococcus casseliflavus/gallinarum* and *Bacillus cereus*. Resistance gene analysis using ResFinder revealed *blaZ_12* in Bacillus cereus and *blaOXA-100* in *Acinetobacter baumannii*. Following PEG precipitation, two water samples tested positive for Betacoronaviruses by RT-PCR; however, confirmation was not possible because Sanger sequencing results were identical to both the SARS-CoV-2 positive control and the Wuhan reference genome, suggesting a potential contamination.

We found that brown rats were in direct contact with the water in all positive cases, suggesting they were the primary source of the pathogens. Taken together, our findings demonstrate that this novel non-invasive method is a feasible and suitable option for conducting wildlife research studies within the One Health framework.

Keywords: Non-invasive, wildlife, PEG precipitation, AMR, pan-Betacoronaviruses

Acknowledgement: As a recipient of an Erasmus Mundus Scholarship, I would like to express my sincere thanks to the European Commission for their financial support.

P116. Supplementary feeding, when combined with finch abundance and seasonality, has driven finch trichomonosis outbreaks

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Human activities increasingly shape wildlife disease risk by altering when and where pathogen transmission and outbreaks occur. Understanding these human-wildlife interactions is therefore essential for effective wildlife conservation and disease management. Finch trichomonosis, caused by the protozoan parasite *Trichomonas gallinae*, illustrates this challenge. The disease has driven significant population declines in Greenfinch (*Chloris chloris*) and, more recently, Chaffinch (*Fringilla coelebs*) in Great Britain, with outbreaks frequently detected in gardens where birds congregate at supplementary feeding sites.

We use national-scale garden wildlife surveillance data, combining weekly bird abundance and feeding observations from Garden BirdWatch (www.bto.org/gbw) with veterinarian-validated finch trichomonosis reports from Garden Wildlife Health (www.gardenwildlifehealth.org) to link garden-level information on bird numbers, feeding activity and disease occurrence to assess the localised conditions under which finch trichomonosis outbreaks (FTOs) occur. To assess the ecological and human-mediated factors associated with FTOs, we used generalised linear mixed models in a case-control study to compare FTO with disease-free periods from gardens statistically matched for location and garden type as counterfactuals.

We show that, at supplementary feeding sites, FTOs are primarily structured by seasonal and density-dependent processes. Disease risk peaked during the post-breeding period (July-October) and increased with local finch abundance, particularly numbers of Greenfinch. Within this elevated-risk ecological context, supplementary feeding – measured as the number of seed-based food types provided - independently increased outbreak odds.

These findings suggest that supplementary feeding is a key underlying risk factor but can also further amplify outbreak risk under specific ecological conditions, leading to changes in recommended feeding practices. More broadly, our findings highlight can how everyday human behaviours influence pathogen transmission in wildlife populations within increasingly human-dominated ecosystems.

Keywords: *Trichomonas gallinae;* garden bird feeding; supplementary feeding; citizen science

P117. Wild bird species found infected with WNV in Vojvodina Province of Serbia: results of WNV surveillance program from 2014 to 2025

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West Nile virus (WNV) is a neurotropic mosquito-borne flavivirus considered to be one of the most widespread arboviruses in the world. The natural infection cycle involves mosquitoes, mainly *Culex* spp. as virus vectors and birds as natural hosts, while horses and humans are considered to be dead-end hosts. After some historical data, the first data on the presence of WNV in Serbia was obtained by serological testing of healthy backyard pigs sampled during 2006/2007 and horses sampled during 2009/2010 in Vojvodina Province, the northern part of the country. WNV circulation was also confirmed by 8/82 (9.8%) WNV RNA positive tissues from 134 wild birds collected during 2011/2012 at the same territory. The aim of this study is to present the data of WNV detection in wild birds obtained during the period of 11 years, i.e. from the start of the integrated national WNV surveillance program implementation in Vojvodina Province (Serbia) in 2014 until 2025.

In total, from 2014 to 2025, samples of 4778 wild birds (pharyngeal swabs from live captured, or tissues samples from found dead or shot wild birds) were tested by RT-qPCR for WNV presence in Serbia, from which 929 were from the territory of Vojvodina Province.

WNV was detected in 170/4778 (3.56%) and 55/929 (5.92%) wild birds tested in Serbia and Vojvodina province. By years, 2/992 (0.2%) & 2/111 (1.8%), 8/720 (1.11%) & 6/76 (7.89%), 2/388 (0.52%) & 1/107 (0.93%), 31/365 (8.49%) & 5/111 (4.5%), 16/557 (2.87%) & 6/73 (8.22%), 44/347 (12.68%) & 12/114 (10.52%), 25/431 (5.87%) & 10/59 (16.85%), 26/527 (4.93%) & 4/69 (5.80%), 16/451 (3.55%) & 4/78 (5.13%) as well as 5/131 (3.85%) wild birds were found WNV positive in 2014, 2015, 2017, 2018, 2019, 2021, 2022, 2023, 2024 and 2025 from the territory of Serbia & Vojvodina Province respectively. Tested wild birds (929) from Vojvodina Province, belonged to 18 orders and 91 species. Most of the wild birds belonged to the orders Passeriformes, Accipitriformes, Strigiformes and Falconiformes (37, 7, 7 and 5 species). WNV was detected in 20 wild birds' species, mostly from *Corvidae* (21/309; 6.77%), *Accipitridae* (9/117; 7.62%) and *Falconidae* (7/123; 5.69%) families. Interestingly quite high number (3/30; 10%) of white storks and owls (9/108; 8.33%) were found positive for WNV presence in Vojvodina province that should be considered as an endemic area for WNV. As a rarity, WNV was also detected in one Humboldt penguin and one cormorant.

It could be concluded that birds from order Passeriformes, and especially of the Corvidae family, are highly susceptible to WNV infection as already described in literature and found in practice. However, further testing of different wild birds' species, besides those that are already known as WNV natural hosts and highly susceptible to WNV infection should be done in the to define the other most competent wild bird's species for WNV surveillance at the specific region.

Keywords: West Nile virus, wild birds, active and passive WNV surveillance, prevalence, Vojvodina Province, Serbia

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P118. Human West Nile Neuroinvasive Disease as an Indicator of Zoonotic Transmission: Spatiotemporal Patterns and Implications for One Health Surveillance in Vojvodina, Serbia

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West Nile virus (WNV) is a mosquito-borne virus maintained in a complex ecological cycle involving birds and mosquitoes, while humans represent dead-end hosts. For over a decade, Serbia has had Europe's highest West Nile fever incidence, and the northern province of Vojvodina is an endemic area. Human West Nile neuroinvasive disease (WNND) is the most severe clinical form of WNV infection that serves as a sentinel indicator of intensified WNV circulation in the area. This study aimed to analyze long-term spatiotemporal patterns of WNND in Vojvodina, Serbia, to enhance preventive strategies.
A retrospective population-based study was conducted using surveillance data on WNND reported in Vojvodina between 2012 and 2025. Cases were retrieved from the surveillance database and classified according to national case definition criteria. Incidence and mortality rates of WNND, as well as case-fatality rate (CFR) were analyzed by year, age group, and place of residence. Spatial distribution of cases was mapped to identify geographic clustering in study area.
During the study period, 1337 suspected cases were investigated, of which 557 (41.7%) fulfilled the case definition for WNND. The majority of cases (98.9%) were autochthonous. During the study period, WNND incidence showed a moderate upward trend, while mortality slightly declined. The mean annual incidence was 2.17 per 100,000 population (95% CI: 0.60–3.75), with pronounced interannual variability and epidemic peaks in 2013, 2018 (10.31/100,000), and 2022. The mean mortality rate was 0.28 per 100,000 population, and the overall CFR was 12.9%. Cases showed strong seasonal clustering, occurring predominantly between epidemiological weeks 31 and 34, corresponding to the period of highest mosquito activity. Individuals aged ≥70 years experienced the highest disease burden. Spatial analysis revealed heterogeneous distribution of cases across the province, consistent with ecological conditions favorable for WNV circulation. During peak years, cases were reported in all districts, with the highest WNND incidence and mortality recorded in the South Banat.
WNND remains a significant public health concern in Vojvodina, marked by recurring epidemic peaks, pronounced seasonal clustering, and substantial mortality. The observed spatiotemporal patterns highlight the value of integrating human, veterinary and entomological surveillance within a One Health framework. Coordinated monitoring of mosquitoes, birds, horses, and human cases can enhance risk assessment, strengthen early warning systems, and improve preparedness for emerging vector-borne diseases.

Keywords: West Nile virus; One Health

P119. Antimicrobial resistance patterns in *Escherichia coli* isolates from wild boar across a gradient of human impact in north-eastern Spain

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Antimicrobial resistance (AMR) is a growing global public health concern. Understanding the mechanisms that drive the emergence and spread of AMR is essential for developing effective surveillance programs, earlier detection and improved response strategies. Given the widespread distribution of wild boar in Spain, this study aims to determine whether resistance patterns in this species vary across a gradient of habitat and anthropogenic characteristics.

A total of 183 *Escherichia coli* isolates were obtained from 220 wild boars hunted during the 2023/2024 season in 45 hunting grounds in north-eastern Spain. These hunting grounds were categorised into three main zones according to human impact. The isolates were then grouped using a principal component analysis and a hierarchical cluster analysis. Differences in the prevalence of each cluster by zone, sex, and age were assessed using Fisher's exact test.

The analysis showed 3 clusters of AMR, but no significant differences were found between zones ($p=0.21$), sex ($p=0.22$), or age ($p=1.00$).

Our results suggest that AMR is widespread across the study area, indicating that resistant bacteria are not confined to human-impacted environments but have also spread into more natural and less disturbed ecosystems. In this regard, wild boar may play an important role as both sentinels and potential vectors in the dissemination of AMR, given their wide-ranging behavior, habitat overlap with human activities, and frequent interaction with multiple environmental sources of bacteria.

Keywords: *Sus scrofa*, animal husbandry, One Health, Antimicrobial resistance, health surveillance

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P120. Widespread antimicrobial resistance in red foxes (Vulpes vulpes) from northern Italy

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Antimicrobial resistance (AMR) is a major One Health concern, with wildlife playing a relevant role in the spread of antimicrobial-resistant genes (ARGs) and bacteria by acting as a bridge between natural and anthropised environments. The red fox (*Vulpes vulpes*) is a highly synanthropic species that frequently coexists with humans, making it a potential sentinel and source for AMR and ARGs. This study aimed to investigate major AMR factors, such as extended-spectrum beta-lactamases (ESBL) and carbapenemases, in red fox faeces across areas with different levels of anthropisation.
Between January and February 2026, 67 faecal samples were collected from red fox carcasses in 22 municipalities in Lombardy, Italy. These municipalities cover an area of 448 km^2, with a median population density of 425 inhabitants (range 69–1040) and 278 livestock (range 5–2462) per km^2. Samples were cultured on MacConkey agar supplemented with 1 mg/L cefotaxime and on ChromID® CARBA SMART agar to screen for ESBL- and carbapenemase-producing bacteria. Phenotype-positive colonies were identified using MALDI-TOF mass spectrometry and tested by MIC assays. PCR assays were used to test for ARGs associated with ESBL, carbapenemases and also colistin resistance. The effects of fox sex, human density and livestock density on the occurrence of resistant isolates were assessed using logistic regression models.
A total of 47 resistant bacterial isolates were recovered from 32 of the 67 foxes analysed (47.8%). Phenotypic screening identified 17 ESBL-producing isolates (36.2%), 29 carbapenemase-producing isolates (61.7%) and one isolate that grew on both selective media (2.1%). Among ESBL producers, the most prevalent ARG was *bla*$_{CTX-M}$ (8/18; 44.4%) and the most frequent genus was *Escherichia* (11/18; 61.1%), with one isolate also carrying the *mcr-1* gene. Among carbapenemase producers, only one tested positive by PCR (*bla*$_{NDM}$, 1/30; 3.3%) and *Pseudomonas* was the most prevalent genus (18/30; 60%). The occurrence of AMR was independent of fox sex, human density or livestock density.
Despite the limited sample size, these results suggest that AMR and ARGs are widespread among foxes. The lack of association between AMR and anthropisation may reflect the species opportunistic behaviour and widespread distribution in the area. Notably, this study provides one of the few reports of bacteria harbouring the *mcr-1* and *bla*$_{NDM}$ genes in red foxes, highlighting the importance of wildlife as a sentinel for the environmental spread of clinically relevant ARGs.

Keywords: enteric bacteria, wildlife, *mcr-1*, *NDM,* AMR, resistance genes

Funding source: MT was funded by the Italian Ministry of Health (Ricerca Finalizzata GR-2021-12374932).

P121. Microbiome and Resistome Characterisation in Loggerhead Sea Turtle Eggs: Insights for Environmental AMR Surveillance within the Tarta-Net Project

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Marine ecosystems are increasingly affected by anthropogenic pressures, including antimicrobial resistance (AMR) dissemination. Sentinel species such as the loggerhead sea turtle (*Caretta caretta*) can provide valuable insights into environmental health risks within a One-Health framework. Within the Tarta-Net project, this study investigates whether unhatched and non-embryonated egg swabs can serve as an effective and non-invasive matrix to monitor microbial communities, potential pathogens, and AMR determinants. The objective is to assess their suitability as early warning indicators for ecosystem and public health threats.

Egg swabs were collected from multiple nesting sites in Sicily (Ionian and Tyrrhenian coasts). Microbial community composition was analysed using molecular approaches, while resistome profiling focused on the detection and classification of antimicrobial resistance genes (ARGs), prioritised according to the WHO AWaRe classification. The study characterised (i) the overall microbiome, (ii) the potentially pathogenic fraction (pathobiota), and (iii) the resistome. Statistical analyses were performed to explore relationships among these components and to evaluate spatial differences. A composite AMR risk index was also developed to synthesise the findings.

Unhatched egg swabs hosted structured and non-random microbial communities, with a core microbiota shared across approximately 70% of samples, including genera such as *Alcaligenes*, *Pseudomonas*, *Nitratireductor*, and *Devosia*. A diverse pathobiota was identified, including genera with potential relevance for human health (e.g., *Klebsiella*, *Enterobacter*, *Citrobacter*), showing variability across sampling sites. The resistome was broad and included numerous ARGs spanning multiple antibiotic classes, including those of high clinical importance under the WHO AWaRe classification. A core resistome of 51 ARGs was detected in the majority of samples. No direct correlation was observed between pathogen richness and resistome diversity; however, the resistome was significantly associated with the overall microbial community rather than solely with the pathogenic fraction. Spatial differences between sampling areas were also observed. The AMR risk index enabled integrated interpretation of these patterns.

Unhatched loggerhead turtle eggs represent a promising matrix for environmental AMR surveillance. The strong association between resistome and the overall microbial community highlights the importance of considering the entire microbiome in AMR monitoring, rather than focusing exclusively on pathogens. These findings support the role of *Caretta caretta* as a sentinel species and contribute to the development of integrated One Health surveillance systems for early detection of environmental and public health risks.

Keywords: Antimicrobial Resistance, One Health, Resistome, Sea Turtles, Environmental Surveillance

Funding source & Acknowledgement: Supported by WHOA under the project: TARTA-NET: A Tool to monitor Antibiotic Resistance (AMR) genes in loggerhead sea Turtle (*Caretta caretta*) and create a NETworkfor biodiversity protection

P122. Tarta-Net: A One Health approach to monitor antimicrobial resistance in loggerhead sea turtles (*Caretta caretta*) and strengthen a Mediterranean network for biodiversity protection

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Marine ecosystems are increasingly impacted by anthropogenic pressures, including antimicrobial resistance (AMR) dissemination. Migratory marine species may act as reservoirs, sentinels, and early warning indicators of emerging health threats at the human–animal–environment interface. The Tarta-Net project aims to strengthen the capacity to understand the circulation of AMR determinants while supporting biodiversity conservation through a One Health approach. The project focuses on the loggerhead sea turtle (*Caretta caretta*), a recognized sentinel species in the Mediterranean, to investigate the spread of resistance determinants as proxies for ecosystem and public health risks. Led by IZSSi in collaboration with IZSVe, the project also supports capacity building in one recovery and monitoring centre in Tunisia and two in Morocco. The project is structured into multiple work packages including: (i) upgrading recovery and monitoring centres in North Africa; (ii) integrated field surveillance activities, including turtle and nest monitoring and systematic sampling; (iii) microbiological and resistome analyses using advanced molecular approaches; and (iv) data integration, modelling, and dissemination. Activities combine field sampling and laboratory analyses (including Next Generation Sequencing and ddPCR) to characterise microbial communities and AMR gene circulation. This integrated approach supports the development of harmonised surveillance frameworks and contributes to early detection of environmental and zoonotic risks.

To date, key activities have been successfully implemented. Governance and coordination structures have been established, including regular online meetings and a shared digital platform for protocols and training materials. Capacity-building activities have been delivered through two online sessions and one in-person training, covering clinical management, sampling procedures and microbiology AMR assessment. Standard operating procedures for nest inspection and egg sampling have been developed. A laboratory assessment has been done in all the involved centers. Field activities have been initiated, including the sampling of approximately 38 sea turtle nests, with morpho-biometric and microbiota analysis. Communication and dissemination actions have also been launched to enhance awareness and stakeholder engagement.

Tarta-Net contributes to the development of an integrated One Health surveillance system in which resistome analysis in sentinel wildlife can act as an early warning tool for ecosystem disturbance and emerging public health threats. Future activities will include expanded field sampling, resistome characterisation, and advanced modelling to support risk assessment, early warning systems, and evidence-based policy-making. By strengthening transnational collaboration and surveillance capacity, the project supports preparedness for emerging risks and contributes to biodiversity conservation and global health security.

Keywords: Antimicrobial Resistance, One Health, Early Warning, Sea Turtles, Wildlife

Funding source & Acknowledgement: "A Tool to monitor Antibiotic Resistance (AMR) genes in loggerhead sea Turtle (*Caretta caretta*) and create a NETwork for biodiversity protection" A project financed by Italian Ministry of Health and supported by WOAH project

P123. Use of recently regurgitated pellets to monitor the role of plastics in antibiotic resistant bacteria carriage in white storks (*Ciconia ciconia*)

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Plastic pollution and antimicrobial resistance (AMR) each on its own but even more so combined represent a global threat to human and livestock and ecosystem health, as plastics can act as substrate for biofilm formation and thus enhance the horizontal transfer of resistance genes.
This study evaluated the role of plastics in the acquisition of AMR through the non-invasive analysis of 31 freshly regurgitated pellets of white stork (*Ciconia ciconia*) nestling collected from the nest in colonies associated to landfills (n=18) or located in natural habitats (n = 13). We compared the load of anthropogenic debris and the presence of antibiotic-resistant Enterobacterales, particularly those carrying carbapenem (Carba) and extended-spectrum β-lactamase (ESBL) resistance using MacConkey agar and selective media.
Prevalence of pellets containing plastic was high (24 out of 31 / 77.4%) and plastic was found both in pellets from landfill associated colonies and natural habitat albeit higher in landfills. Predominantly pellets contained fibers, filaments, and solid fragments in landfill-associated colonies. Microbeads, likely originating from cosmetic products, were also detected, highlighting their environmental persistence. Enterobacterales were detected in 38.7% (12/31) of the pellets and 29% (9/31) carried enterobacterales with multiresistant (MDR) phenotypes although none showed carbapenem resistance or ESBL phenotypes. The weight of "potential plastics" in the pellets was associated with the presence of enterobacterales with MDR phenotypes. Also a statistically significant association was observed between "films" and "potential plastics" with AMR phenotypes, although mixed-effects models (GLMM) accounting for colony aggregation, suggest a multifactorial relationship.
The results reinforce the value of the white stork as a bioindicator and potential vector of AMR across ecosystems and support the use of recently regurgitated pellets as a means of noninvasive monitoring of plastic exposure and antimicrobial resistant bacteria carriage.

Keywords: plastics, antimicrobial resistance, *Ciconia ciconia*, biofilms, pellets, One Health

P124. *Salmonella* occurrence in wildlife in a high-density farmed area of Northern-Italy

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Salmonella is a zoonotic bacterium with a broad host range, including livestock, companion animals, and wildlife, increasing the risk of human exposure. This risk is amplified at the wildlife–livestock interface, especially in high-density farming areas where interactions are more frequent. Although host adaptation has been described for some serovars (e.g., *S.* Dublin in cattle), the role of wildlife in *Salmonella* ecology remains poorly understood.
This study investigated the occurrence of *Salmonella* in wild mammals and birds from the provinces of Parma and Reggio Emilia (Emilia-Romagna Region, Northern Italy) between 2023 and 2024. The aim of the study was to assess whether the *Salmonella* strains observed in wildlife co-circulated in livestock in the same area. To assess *Salmonella* co-circulation, the study isolates were compared to the Salmonella isolates obtained during diagnostic activities in livestock.
During postmortem examination of wild animals' carcasses, 238 intestine samples were collected to be analysed for *Salmonella* detection following ISO 6579:2002. Strains were characterized phenotypically using the serum agglutination test according to the Kauffmann–White scheme. Additionally, a Whole Genome Sequencing (WGS) was performed. Furthermore, a comparative genomic analysis based on core-genome MLST (cgMLST) was conducted between *Salmonella* strains isolated from wildlife and strains obtained from livestock.
Out of 238 samples from wild mammals and birds, 26 tested positive for *Salmonella*. Hedgehogs were the most frequently positive species (12 isolates), followed by foxes (5). *S.* Enteritidis was the most commonly observed serovar (11), followed by *S.* Typhimurium (4) and *S.* Bovismorbificans (3). The comparison through WGS with livestock isolates identified three *Salmonella* strains (2 of *S.* Typhimurium, 1 of *S.* Bovismorbificans) co-circulating among wild mammals and bovine farms.
Salmonella includes over 2500 serovars widely distributed across environments, humans, and animals, indicating complex transmission pathways. Our study highlighted, in a high-density farming area, the possible contribution of wildlife-derived strains to livestock cases of salmonellosis. On the other hands, the detection of livestock-associated strains in wildlife highlights the need for improved biosecurity measures to reduce contact between farmed and wild animals and limit pathogen transmission.

Keywords: *Salmonella*, wildlife–livestock interface, Genomic cluster

P125. Host-specific coronaviruses in bats of Bosnia and Herzegovina

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Bats are important natural hosts of diverse viruses, including coronaviruses of potential zoonotic relevance. The aim of this study was to determine the composition of viromes of bats living in publicly accessible caves in Bosnia and Herzegovina, with a particular focus on the coronaviruses.
Live bats were captured using mist nets and determined to the species level using a morphological key. Anal and oral swabs were collected from each bat before release, and guano samples were additionally collected from cave floor deposits. All samples were transported to the laboratories of UNSA-VF. Nucleic acids were extracted and subjected to sequence-independent single-primer amplification (SISPA) protocol on a MinION Mk1C. Furthermore, the bat species identification was confirmed by COI sequencing on the same platform. All sequences were assembled using Minimap2 and Geneious Prime, and phylogenetic analysis was performed with MEGA11 and reference sequences retrieved from NCBI. The presence of subgenus *Sarbecovirus* was confirmed by RT-PCR.
Coronaviridae virus reads, representing 10,4% of total virus reads, were detected in anal swabs and guano samples, but none were detected in oral swabs. The anal swabs and guano associated with the same bat species showed a highly concordant virome composition. Sequencing enabled the assembly of ORF1ab, E and M gene sequences of multiple coronavirus species. Both the Alphacoronavirus (subgenus *Decacovirus*) and Betacoronavirus genus (subgenus *Sarbecovirus*) were detected, but the presence of both genera was only recorded on one sampling site. The detected alphacoronaviruses showed apparent host association: a *Rhinolophus* bat alphacoronavirus was detected only in the guano of *Rhinolophus* bats, while the *Miniopterus* bat alphacoronavirus was detected solely in the guano of *Miniopterus schribersii*. These Alphacoronavirus species were not detected in same localities nor in other bat species. Betacoronaviruses were detected only in *Rhinolophus* bats, and the phylogenetic analysis demonstrated >96% sequence identity with previously described bat-associated sarbecoviruses.
Bat guano appears to be a useful non-invasive sample type for monitoring bats and bat-borne viruses, and metagenomic sequencing represents a valuable approach for virome characterization and the detection of coronaviruses of potential zoonotic relevance. These findings support continued surveillance of *Rhinolophus* spp. and *Miniopterus schreibersii* populations within a One Health framework.

Keywords: bats, coronaviruses, virome, sequencing, Bosnia and Herzegovina

Funding source: This study is the result of the project "Studying biodiversity and health status of bats on the territory of FBiH" (Bosnian: Istraživanje biodiverziteta i zdravstvenog statusa šišmiša na području FBiH), funded through the Environmental Fund of the Federation of Bosnia and Herzegovina (bosnian: Fond za zaštitu okoliša FBiH) and University of Sarajevo – Veterinary Faculty (Grant No. 01-09-2-312/2025).

P126. Rethinking bat surveillance: environmental sampling in a One Health context

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Interest in bats as carriers of zoonotic microorganisms has increased following COVID-19, leading to intensified sampling for research and surveillance. While essential, these efforts may cause disturbance to bat populations, potentially affecting infection dynamics and pathogen shedding. Novel environmental sampling offers a promising non-invasive alternative, but its application in wildlife disease surveillance requires standardized and validated approaches to ensure sensitivity and repeatability. The CABLES (INTERREG ITAT 27 011) project aims to develop and evaluate a structured and sustainable surveillance framework that minimize the need for bat capture while maintaining diagnostic performance and optimizing resource use.

From 2025 to 2026, we combined active surveillance based on bat capture and individual sampling with several environmental approaches across four mixed colonies of *Myotis myotis/Myotis blythii* in Italy. Individual sampling followed a standardized protocol, including collection of faeces, salivary swabs, patagial swabs, ectoparasites and blood. Bat capture was authorized by the Italian Ministry of Agriculture, performed by highly trained personnel. We performed non-invasive faecal collection using chart paper (30 pooled samples) and overshoes to maximize viral recovery, alongside air sampling (Coriolis® Compact) and entomological sampling using manual aspiration and CO_2 traps. We compared laboratory workflows for environmental sample pre-treatment and nucleic acid extraction to optimize detection of viruses, bacteria, parasites and fungi. Samples were analysed using metagenomic and broad-spectrum molecular approaches.

Environmental surveillance enabled standardized sampling of pooled faeces that mimicked seasonal patterns seen in individual samples and increasing the probability of pathogen detection. Blood-feeding arthropods were effective for investigating microorganisms with a haematic phase, while air sampling and collection of guano using overshoes detected agents shed via respiratory and gastrointestinal routes. Environmental samples also allowed identification of bat species within colonies, supporting ecological monitoring.

Standardized environmental surveillance can complement and potentially reduce capture-based approaches, requiring limited technical expertise for sample collection while reducing disturbance to bat populations.

Keywords: *Myotis sp.*, environmental sampling, One Health approach

P127. Seals as sentinels – detection of a novel Orthonairovirus in the Baltic ecosystem

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Wildlife disease surveillance can serve as an important early warning system for emerging pathogens, including zoonoses, that may threaten animals, humans and ecosystems. The *Orthonairovirus* genus is a rapidly expanding group of RNA viruses that typically are tick-borne and can infect a broad range of mammals and birds. Many species cause febrile disease in humans. Here we provide an example of how general disease surveillance of marine mammals in Sweden identified a novel, potentially zoonotic, Orthonairovirus in the Baltic Sea ecosystem.

A grey seal pup (*Halichoerus grypus*) found dead in Östhammar municipality on the east coast of Sweden April 2020, was examined by necropsy. The animal was in poor nutritional condition and had infected facial bite wounds. Microscopic findings suggestive of viral hepatitis prompted deep sequencing of the liver, spleen, kidney, lung and brain. Following the detection of Orthonairovirus, a tailored RT-qPCR was developed to investigate wider virus occurrence in stranded seals (n = 49) from the Baltic coast. Additionally, because ixodid ticks generally are not found on seals, seal lice (*Echinophthirius horridus*) were screened from 46 seals to identify potential virus vectors.

Metagenomic analyses identified *Orthonairovirus* (GenBank accession numbers PX251549-51) in all tissues except brain of the stranded seal, with highest levels in the liver. The virus showed closest similarity (amino acid identity ranged from 74.7-90.2% depending on the virus segment) to Yezo virus, which causes febrile illness in humans. The Orthonairovirus was genetically distinct enough to be proposed as a new species: Östhammar virus, *Orthonairovirus östhammarense*. Screening of additional stranded seals and seal lice did not result in any other positive findings.

The discovery of a novel Orthonairovirus, provisionally Östhammar virus, through general disease surveillance illustrates how wildlife can act as early warning sentinels for emerging viruses. The high viral load in the liver of the stranded seal coupled with severe liver lesions suggest that this novel virus can be pathogenic for seals. No virus was detected in any other seals or seal lice, so this finding may represent a sporadic spillover infection. However, other Orthonairoviruses recently have been found in ticks in Latvia and Poland, supporting circulation of potentially pathogenic and zoonotic Orthonairoviruses in northeastern Europe. Further investigations into the occurrence of Orthonairoviruses around the Baltic Sea, the host range and significance for wildlife hosts, and regional cases of unexplained human febrile illness are highly warranted.

Keywords: Wildlife disease surveillance, marine mammal, *Orthonairovirus*

Funding source & Acknowledgement: Sweden's health and disease surveillance program for marine mammals is funded by the Swedish Agency for Marine and Water Management as part of Sweden's environmental monitoring.

P128. Pump up the volume: including the game surveillance system component in the assessment of bovine tuberculosis surveillance sensitivity and freedom from disease in Dutch wildlife

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Bovine tuberculosis (bTB) is a zoonosis caused by *Mycobacterium tuberculosis* complex, including *Mycobacterium bovis*, that can have cattle and wildlife reservoirs. The Netherlands are tuberculosis-free since 1999. However, incidentally, bTB cases have been detected in imported cattle, highlighting the need for continuous surveillance in wildlife. Both the wildlife disease passive surveillance system component (passive SSC) and the game meat chain surveillance system component (game SSC) contribute to surveillance for bTB in wildlife. This study aimed to calculate how likely these surveillance systems are to find a case if bTB is present in Dutch wildlife (sensitivity), and how probable freedom from bTB is in absence of positive samples.
Scenario trees were developed for both SSCs for wild boar (*Sus scrofa*) and three cervid species (red deer *Cervus elaphus*, roe deer *Capreolus capreolus* and fallow deer *Dama dama*). Relevant risk factors for bTb infection at the population level were defined through literature. Numbers of animals investigated annually were obtained from the Dutch Wildlife Health Centre (2008-2023) and a hunter association (2014-2023). The sensitivity of the diagnostic procedures was obtained from literature and, for the game SSC, through a questionnaire distributed to hunters to quantify the probability of a diseased animal being referred for bTB diagnostics. The final model included all scenario trees and preexisting trees for the Eurasian badger (*Meles meles*) and was implemented stochastically.
Literature search showed that age category and sex were relevant risk factors for bTB infection at population level. The numbers of animals investigated per year in the game SSC were 500-fold higher than in the passive SSC. Questionnaire results suggested that hunters would refer one-fifth of the suspect cases to the competent authority for diagnostic testing, resulting in a four-fold lower likelihood of detecting a bTB infected animal through the diagnostic steps in the game SSC than in the passive SSC. At the lowest design prevalence (0.1%), the sensitivity of the total model was 99.9%, and probability of freedom-from-bTB in Dutch wildlife 98.5%. The high sensitivity was driven by the high animal numbers in the game SSC.
By including game species in bTB surveillance it was possible to achieve near-perfect sensitivity and a high probability of freedom-from-disease, showing the crucial role game meant chain stakeholders can play in detecting bTB in wildlife. It also shows the importance of training hunters on bTB lesions and the importance referring suspect cases.

Keywords: Bovine tuberculosis, surveillance, scenario tree, game meat chain, wildlife

P129. At the wildlife, free-roaming cat, and humans interface: understanding the risks for European public health.

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Urban expansion and shifting cultural perceptions of cats, from utilitarian pest controllers to companion animals, have contributed to increased abandonment and stray populations across Europe. Despite this, unclear legal frameworks and inconsistent regulation have enabled the persistence of free-roaming cats in urban and peri-urban environments, posing risks to both public health and biodiversity. While trap-neuter-return programs dominate current management strategies, their population-level effectiveness lacks scientific consensus, and they may favour the maintenance of potential disease reservoirs in urban and peri-urban areas where 79% of Europeans reside.
This perspective is a call to action for European authorities, examining the wildlife-free-roaming cat-human interface as an emerging epidemiological concern. Systematic literature analysis reveals critical knowledge gaps regarding cats' role as bridge hosts for pathogens shared between wildlife and humans. This contrasts with the wide ecological niche cats occupy, interconnecting rural and urban areas, and with their high contact rates with epidemiologically relevant wildlife, such as birds, rodents, and bats. Avian influenza exemplifies how their predatory behaviour and susceptibility to both avian and mammalian virus create opportunities for viral adaptation.
Free-roaming cats represent an underrecognized public health risk requiring integrated monitoring within multidisciplinary and evidence-based regulatory frameworks at the European level to protect public and ecosystem health.

Keywords: stray cats; feral cats; cat colonies; urban zoonosis; One Health; mixing vessels.

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P130. PigViroScope: Synthesising Evidence of the Global Pig Virome with Artificial Intelligence

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Pigs (*Suidae*) play essential roles in agriculture and serve as important models for infectious disease research due to their physiological similarity to humans. Swine virology is thus a key domain within the One Health framework, particularly regarding emerging infectious diseases, zoonotic spillover, and pandemic risk. Yet, no comprehensive inventory of the global pig virome currently exists, limiting disease surveillance, pandemic preparedness, and food system resilience. Moreover, the virological literature is extensive, fragmented, and distributed across decades and disciplines, making conventional manual synthesis infeasible.

To address this gap, we conducted a systematic literature review supported by natural language processing to identify and catalogue all viruses reported to infect pigs. We developed Evidence Unification through Language-model Evaluation (EULE), a hybrid workflow integrating a locally hosted large language model (LLM) into established systematic review methodology. The pipeline was implemented in R, with Llama 3.3 70B deployed locally for literature screening, information extraction, and downstream visualization.

Using EULE, we screened over 56,000 literature records, of which more than half were classified as relevant to swine virology. Across these, we identified over 700 unique virus species spanning more than 30 viral families. The most frequently represented viruses were African swine fever virus (ASFV), porcine reproductive and respiratory syndrome virus (PRRSV), porcine circovirus (PCV), classical swine fever virus (CSFV), and swine influenza A virus.

Our findings highlight major viral priorities in swine research while revealing the broader diversity of less frequently reported pig-associated viruses worldwide. By applying artificial intelligence to systematically synthesize the known pig virome from scientific literature, we provide a foundational resource for cross-species pathogen monitoring at the human–animal interface and demonstrate the broader value of large language models for large-scale biological knowledge synthesis in support of pandemic preparedness.

Keywords: Porcine Viruses, Viral Taxonomy, Systematic Literature Review, Large Language Models, Literature Mining

Funding source: This project, part of the European Partnership on Animal Health and Welfare, is co-funded by the European Union's Horizon Europe Project 101136346 EUPAHW

Session 8

Emerging and re-emerging zoonotic pathogens & diseases in wildlife

Oral Presentations

Invited lecture

Hidden in plain sight: Are "new" zoonotic cestodes truly emerging in the Western Balkans?

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Historically, well-known zoonotic cestodes such as *Taenia solium* and *Taenia saginata* have been recognised as important public health threats, while *Echinococcus granulosus* has been responsible for the majority of human disease burden in the Western Balkans. Although the incidence of cystic echinococcosis has declined in recent decades, the epidemiological landscape is shifting with the increasing detection of so-called "new" zoonotic cestodes. These parasites are primarily associated with expanding populations of wild carnivores, including red foxes, golden jackals, and martens, whose abundance and ecological plasticity are increasing across the region. Their growing presence in peri-urban and urban environments is intensifying contact with humans, domestic animals, and synanthropic hosts, thereby creating new opportunities for parasite transmission.

Currently, *Echinococcus multilocularis*, the causative agent of alveolar echinococcosis, represents one of the most significant emerging zoonotic threats. Its prevalence in red fox populations can reach up to 30% in certain areas, and it has also been confirmed in golden jackals, indicating a broader host range and potential for further spread. The routine application of molecular methods has significantly improved detection capacity and revealed the presence of additional zoonotic species, including *Taenia crassiceps* and *Taenia martis*, both of which have been associated with severe human infections, including cases of neurocysticercosis. More recently, *Spirometra mansoni*, the causative agent of sparganosis in humans, has been molecularly confirmed for the first time in golden jackals in Croatia, highlighting the previously unrecognised diversity of zoonotic cestodes circulating in wildlife hosts in the region.

This presentation will provide an overview of the current distribution, host range, and epidemiological significance of zoonotic cestodes in the Western Balkans, with a particular focus on wildlife reservoirs and the wildlife–human interface. Special emphasis will be placed on the role of molecular diagnostics in uncovering hidden parasite diversity and redefining our understanding of transmission cycles.

Finally, key knowledge gaps will be identified, including limited data on human exposure, underdiagnosis, and insufficient integration of wildlife surveillance into public health frameworks. Future research directions will be discussed, particularly in the context of climate change, host population dynamics, and the need for a strengthened One Health approach to better assess and mitigate emerging zoonotic risks.

Keywords: zoonotic cestodes, wildlife reservoirs, One Health

Environmental Risk Mapping of *Echinococcus multilocularis* Infections in Wild Carnivores on Rügen Island

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Alveolar echinococcosis (AE) is a rare zoonotic disease in Germany, caused by the endemic tapeworm *Echinococcus multilocularis*. The complex life cycle of this parasite involves red foxes (*Vulpes vulpes*) and raccoon dogs (*Nyctereutes procyonoides*) as definitive hosts, which shed *E. multilocularis* eggs in their faeces. Accidental ingestion of eggs can lead to fatal AE in humans. The prevalence of the disease in Germany is rising, with cases emerging in previously unaffected regions. However, the underlying wildlife ecology and environmental risk factors that contribute to the distribution of *E. multilocularis* remain poorly understood.

Here we conduct a spatial analysis of diagnostic findings from the 'Wildlife disease monitoring in Mecklenburg-Western Pomerania (MV) for One Health' project (WiMoPOH), to identify environmental risk factors for *E. multilocularis* infection in wild carnivores. WiMoPOH is supported by the local hunting community to facilitate the collection and diagnostic parasite testing of wild carnivores on Rügen Island over a three-year period. Since the start of the study in November 2023, diagnostic results from 392 foxes and 203 raccoon dogs up to June 2025 have been included in the analysis so far, confirming the presence of E. multilocularis in foxes on Rügen Island. By utilising geospatial landcover information from OpenStreetMap, as well as detailed biotope and land use type mappings from the competent state authority, we created disease risk maps and conducted initial analysis of landscape factors by multivariable logistic regression. We found that increasing proportions of farmland in proximity of fox capture sites correlated with an increased risk of *E. multilocularis* infection ($P < 0.01$). By contrast, increasing proportions of woodland area ($P < 0.05$), but greater distances to nearest woodland ($P < 0.1$) protected from infection. Our findings uncover distinct roles of landscape composition on *E. multilocularis* infection in carnivores on the island of Rügen.

Keywords: Echinococcus multilocularis, wildlife disease surveillance, red foxes, wildlife ecology, spatial analysis, environmental risk factors

Funding: The study is part of the One Health project Wildlife disease monitoring in Mecklenburg-Western Pomerania through an integrated One Health surveillance-response system (WiMoPOH) funded by the "Initialisierungs- und Vernetzungsfonds für Infektionsforschung" managed by the Helmholtz Institute for One Health

Echinococcus multilocularis in red foxes in the Netherlands: current situation and comparison of detection methods for surveillance

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Echinococcus multilocularis is a zoonotic tapeworm with foxes as the main definitive host and rodents as intermediate hosts. Infection can lead to the life-threatening disease alveolar echinococcosis (AE) in humans. After the first detection in foxes in the provinces of Limburg and Groningen in 1996, prevalence in foxes has increased and multiple autochthonous human AE cases have occurred. The first objective of this study was to assess the current prevalence and spread of *E. multilocularis* in foxes in Limburg. Given that existing diagnostic methods are labor-intensive, there is a need for alternative tools to improve the efficiency of large-scale surveillance. Therefore, the second objective was to compare two conventional methods (colon content qPCR and the sedimentation and counting technique (SCT)) and one new method (qPCR on rectal swabs) for detection of *E. multilocularis* in foxes. 278 fox carcasses were collected from Limburg in October-April 2024-2025 and 2025-2026. During necropsy, colon content, the small intestine and rectal swabs were collected. *E. multilocularis*-specific qPCR was performed on colon content and rectal swabs. SCT was performed on the small intestine of all qPCR-positive foxes and a sample (n = 85) of qPCR-negative foxes. Performance of the methods was compared using a Bayesian approach.
42/278 foxes (15%) were *E. multilocularis*-positive; all positives except one originated from South Limburg (local prevalence 25%). Worm burdens of positive foxes ranged between 1 and ~20,000. We found a significant negative correlation ($p < 0.001$, $R^2 = 0.45$) between mean Cq value of the colon content qPCR and worm burden as determined by SCT. Colon content qPCR proved to be the most sensitive detection method (sensitivity 96%), compared to SCT (93%) and rectal swab qPCR (51%).
Though the prevalence of *E. multilocularis* in foxes remains high in Limburg, geographic expansion of the endemic area appears limited. Given its high sensitivity and the possibility of Cq-based estimation of the worm burden as a proxy for infection intensity, we propose colon content qPCR as the primary tool for *E. multilocularis* surveillance. This can potentially replace the more labour-intensive SCT for routine monitoring, though SCT remains valuable when precise quantification of worm burden is needed. While qPCR on rectal swabs showed lower sensitivity, it could be a practical alternative for large-scale screening, provided that the lower sensitivity is taken into account in sample size calculation and prevalence estimation.

Keywords: *Echinococcus multilocularis,* red fox, zoonosis, parasite, surveillance

Shared transmission pathways of zoonotic helminths at the wildlife–domestic interface: evidence from Serbia

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Wild canids represent important reservoirs of zoonotic helminths and maintain diverse parasite communities in natural ecosystems. Domestic dogs may act as epidemiological interfaces where wildlife-derived parasites are selectively maintained or filtered, potentially enabling spillover into human-associated environments. Within this context, the SURF-PAW project aims to investigate potential changes in the transmission dynamics of key zoonotic helminths at the wildlife–domestic interface in Serbia. This study aimed to assess helminth infections in domestic dogs from rural Serbia and evaluate their relationship with previously characterized helminth communities in red foxes and golden jackals.

A total of 59 fecal samples from owned dogs were examined using coprological techniques, multiplex PCR, and sequencing for the identification of Taeniidae species. Results were interpreted in relation to our previously generated dataset from wild canids (foxes and jackals) from northern Serbia, representing an ecological baseline of helminth circulation.

Wild canids exhibited high overall helminth prevalence (red foxes: 79.8%; golden jackals: 57.8%) and harbored a diverse parasite community, including *Alaria alata*, *Echinococcus multilocularis*, *Taenia* spp., *Mesocestoide*s spp., *Toxascaris leonina*, *Toxocara canis*, and *Uncinaria stenocephala*. Domestic dogs showed lower overall prevalence (49.2%) but also diverse parasite community, composed of *E. multilocularis* (1.69%), *Taenia hydatigena* (6.77%), *Taenia pisiformis* (5.08%), *T. canis* (8.47%), *U. stenocephala* (22.03%), *Ancylostoma* spp. (11.8%), *Trichuris* spp. (10.2%), and *Capillaria* spp. (11.8%). %). Importantly, the taxa shared between wild and domestic canids included key zoonotic species such as *E. multilocularis* and *T. canis*, together with *Taenia* spp. and *U. stenocephala*, indicating overlapping transmission pathways across host groups.

The detection of *E. multilocularis* in a domestic dog represents the first record of this parasite in dogs in the region and indicates potential spillover at the wildlife–domestic interface. These results, together with the rising number of human cases of echinococcosis, emphasize the need for continued surveillance of zoonotic helminths in domestic dogs in relation to wildlife reservoirs within a One Health framework.

Keywords: zoonotic helminths; dogs; wild canids; Echinococcus; One Health

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First confirmed case of Aujeszky's disease in a grey wolf (*Canis lupus*) in Central Europe

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Aujeszky's disease (AD), caused by Suid herpesvirus 1 (pseudorabies virus, PRV), is a highly contagious viral disease of swine, with wild boar acting as the main reservoir in Europe. Spillover infections to non-suid species, including carnivores, are rare but usually fatal. Reports in free-ranging apex predators remain exceptional. This study reports the first confirmed case of AD in a grey wolf (*Canis lupus*) in Central Europe and aims to characterize the detected virus.

An approximately 8-month-old grey wolf was found moribund in the Carpathian Mountains in southeastern Poland, showing acute neurological signs. The animal was humanely euthanized. Necropsy and tissue sampling were performed. PRV DNA was detected using real-time PCR, virus isolation was conducted in cell culture, and whole-genome sequencing followed by phylogenetic analysis was performed.

No pathognomonic gross lesions were observed. PRV DNA was detected in examined tissues, and infectious virus was successfully isolated. Phylogenetic analysis classified the isolate within genotype I, the predominant PRV genotype circulating in Europe. Limited availability of PRV genome sequences from European wildlife prevented precise determination of the virus origin.

This study documents the first confirmed case of Aujeszky's disease in a grey wolf in Central Europe, expanding the known host range of PRV. The findings support wild boar as the most likely source of infection and highlight the risk of PRV spillover to apex predators. The case underlines the need for enhanced PRV surveillance in wildlife and expanded genomic databases.

Keywords: Aujeszky's disease, pseudorabies, suid herpesvirus 1, wolf

Serosurvey of shrew-associated parahenipaviruses in white-toothed shrews and potential contact animals

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In recent years there has been an increased interest in insectivorous species such as shrews (family Soricidae) as potential pathogen hosts, ultimately leading to the identification of several previously unknown shrew-associated microorganisms. However, there are still knowledge gaps regarding the ecology of shrews and the interface between shrews and potential contact species. In a previous metagenomic study on white-toothed shrews (genus *Crocidura*) from Central Europe, we identified Hasua virus (HasV) in lesser white-toothed shrews (*Crocidura suaveolens*). HasV is closely related to Langya virus (LayV), which was first identified in China and is considered to be potentially zoonotic. HasV and LayV are members of the genus *Parahenipavirus*, a new genus of mainly shrew-borne viruses within the *Paramyxoviridae* family. They are closely related to the highly pathogenic fruit bat-borne henipaviruses, such as Hendra virus and Nipah virus. To assess the rate of potential spillover to other animal species, we conducted a serosurvey of predators (cats, wild carnivores) and other potential contact species (horses, shrews) sampled between 2002 and 2025 across the distribution range of *C. suaveolens*. We expressed the putative immunogenic attachment (G) proteins of HasV and LayV in an Expi293F expression system and established a multi-species enzyme-linked immunosorbent assay (ELISA) with HRP-labelled Protein A/G as secondary antibody to detect parahenipavirus-reactive antibodies. Additionally, the occurrence of HasV-RNA within its putative reservoir population was assessed by RT-qPCR of kidney tissues.
As part of the ongoing serological testing, 10/240 shrews (lesser, greater and bicolored white-toothed shrews), 7/520 cats, 1/380 horses and 0/20 wild carnivores (foxes, raccoons, badgers, raccoon dogs) demonstrated a reaction in the HasV G-based ELISA. HasV-RNA was present in 30% of the *C. suaveolens* and all sero-positive *C. suavoelens* had a positive RT-qPCR signal. Interestingly, cross-reactivity between LayV G and HasV G was only observed in three samples, which already had a strong response in the HasV G ELISA. Therefore, cross-reactivity between parahenipaviruses may be limited and cannot be assumed solely on the basis of the phylogenetic relationship. In this case, the amino acid similarity between HasV G and LayV G was 71.8%.
In future, we will assess the zoonotic potential of these viruses by testing human sera as well as the ecology and behaviour of shrews within an interdisciplinary One Health framework.

Keywords:

Prion Protein Gene (*PRNP*) Diversity in European Cervid Populations–A Review

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The Prion Protein gene (*PRNP*) plays a key role in susceptibility to Chronic Wasting Disease (CWD), a prion disease affecting cervids. Since the detection of CWD in novel contagious and sporadic forms in Fennoscandia, investigation of *PRNP* sequence variation became a major component in disease management throughout Europe. Considering potential spread of CWD, this study aims to review *PRNP*-sequence-data of European cervids to estimate the potential impact of CWD on population dynamics.

Over 5.100 samples of published and unpublished *PRNP*sequence-data were considered for this study. The dataset includes red deer (*Cervus elaphus*), roe deer (*Capreolus capreolus*), fallow deer (*Dama dama*), moose (*Alces alces*), reindeer (*Ragnifer tarandus*), sika deer (*Cervus nippon*), sika-red deer hybrid and white-tailed deer (*Odocoileus virginianus*, WTD) samples from France, Germany, Denmark, Poland, Finland, Sweden, Norway, Scotland, England, the Czech Republic, Italy, Spain and Portugal. We performed a phylogeographical and statistical analysis of this dataset.

Throughout Europe, roe and fallow deer were predominantly monomorphic for the wildtype. However, some roe deer populations showed geographically confined synonymous mutations and one non-synonymous mutation. While Polish moose only carried the wildtype-allele, the Swedish moose population presented a low *PRNP*variability. In contrast, in Norwegian reindeer and European red deer a high *PRNP*variability was found. The phylogeographical investigation of the red deer dataset even suggests the occurrence of "*PRNP*-lineages", as several alleles were only found in distinct geographical regions. Sika deer were mostly monomorphic for the wildtype allele, while Finish WTD presented a moderate *PRNP*-variability, similar to its originating population in North America.

Over the last centuries, many European deer populations have experienced genetic bottlenecks or even regional extinction, mostly due to wars and overhunting. Today, this still has an influence on regional diversity of *PRNP*-variability (e.g. in red deer) or lack thereof (e.g. in roe deer), as local populations were re-established from very few individuals. This is the first overview on an European wide phylogeographical and statistical analysis of cervid *PRNP*-variability. Based on European and NorthAmerican outbreak data and CWD-susceptibility studies, our data suggest that potential CWD outbreaks would pose a high risk to native populations, as most cervids are probably highly CWD-susceptible. The results of this study built the basis for future *in vitro* research identifying the alleles impact on CWD-susceptibility. This studies knowledge is essential for detailed risk assessment and management of disease control efforts, including the future implementation of tailored control measures in Europe.

Keywords: Chronic Wasting Disease, Cervids, deer, prion protein, genotype, genetics

Session 8

Emerging and re-emerging zoonotic pathogens & diseases in wildlife

Poster Presentations

P131. A One Health, pan-European network strengthening surveillance, clinical management and control of zoonotic hepeviruses

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Zoonotic hepevirus infections represent a significant yet still underestimated public-health challenge in Europe. *Paslahepevirus balayani*, commonly known as hepatitis E virus (HEV), is currently the leading cause of acute viral hepatitis in many European countries. Despite this, the true burden of disease remains obscured by heterogeneous surveillance systems, uneven diagnostic capacity, and substantial underdiagnosis. Beyond the human clinical setting, HEV is recognised by the European Food Safety Authority (EFSA) as a priority food-borne pathogen. However, surveillance across animal reservoirs, farms, wildlife, food products and the environment remain fragmented and poorly harmonised. The recent identification of *Rocahepevirus ratti* (ratHEV) as a cause of acute and chronic hepatitis in humans in several European countries has expanded the known spectrum of zoonotic hepeviruses with human pathogenic potential.

In response to these scientific, clinical and policy gaps, ONWARD (One Health Zoonotic Hepevirus Network; COST Action CA24140) brings together experts from 32 European countries, encompassing virology, hepatology, infectious diseases, clinical microbiology, veterinary medicine, food safety, epidemiology, ecology, bioinformatics, public health and health policy. ONWARD is structured into five thematic Working Groups that address the full continuum of zoonotic hepevirus research and control: (i) diagnostic harmonisation and molecular characterisation; (ii) clinical research and therapeutic management; (iii) integrated surveillance across humans, animals, food and the environment; (iv) communication, training and dissemination; and (v) alignment with European initiatives and policy development.

A core objective of ONWARD is to harmonise diagnostic and surveillance strategies for HEV and ratHEV across Europe by aligning serological and molecular testing algorithms, standardising partial and whole-genome sequencing protocols, and extending surveillance to non-canonical samples and reservoirs. In parallel, the network strengthens clinical management through shared research frameworks, prioritisation of antiviral development, and the adoption of standardised outcome measures, while advancing the identification of diagnostic, prognostic and treatment-response biomarkers to improve patient stratification and long-term follow-up, particularly in vulnerable populations. At the animal, food-chain and environmental levels, ONWARD is mapping key transmission routes and identifying risk factors related to livestock production, wildlife exposure, hunting practices, culinary habits and environmental contamination. Communication, training, and dissemination are central to ONWARD's mission. The initiative bridges the gap between research and practice through the development of shared clinical guidelines and educational resources.

ONWARD establishes the first coordinated pan-European framework integrating molecular surveillance, clinical evidence generation and preventive strategies for zoonotic hepeviruses under a *One Health* approach. Its outputs are designed to inform European public-health agencies, strengthen outbreak preparedness, and support the development of harmonised European standards for surveillance, clinical management and prevention.

Keywords: Hepatitis E, Zoonoses, Rat Hepatitis E, Surveillance, One Health, Network, COST Action CA24140 (ONWARD)

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P132. Serological detection of CCHFV and RVFV in Zambian wildlife using multiple assays

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Emerging infectious diseases increasingly threaten global health, with many originating from zoonotic sources. Vector-borne viruses such as Crimean–Congo hemorrhagic fever virus (CCHFV) and Rift Valley fever virus (RVFV) are of particular concern. CCHFV, primarily transmitted by ticks, is typically asymptomatic in animals but can cause severe hemorrhagic disease in humans. RVFV, transmitted by mosquitoes, affects both livestock and humans, causing abortion storms in animals and a range of clinical manifestations in humans. The fact that diseases are spread via arthropod vectors, alongside direct transmission from domestic and wild animals, poses significant challenges for prevention and control. Reliable diagnostics and a thorough knowledge of potential wildlife reservoir hosts are therefore essential for better understanding of zoonotic disease outbreaks. Zambia's extensive and ecologically rich landscapes provide habitats for diverse wildlife while also supporting intensive livestock farming. Data on the occurrence of CCHFV and RVFV in wildlife are extremely limited making Zambia a suitable study area.

More than 250 serum samples were collected in Zambia from various wild ruminants (African buffalo, Eland, Red Lechwe, Puku, Impala, Kudu) and warthogs using darting under full anaesthesia. Samples were tested for antibodies against CCHFV and RVFV using two commercial ELISA kits (ID Screen CCHF Double Antigen Multi-species and ID Screen Rift Valley Fever Competition Multi-species). All ELISA-positive samples and selected negatives were subsequently analyzed using Luminex bead-based serology, and results were compared. Additionally, selected RVFV-positive samples were tested by serum neutralization test (SNT), which serves as the gold standard for RVFV serology.

Ongoing statistical analyses suggest that African buffalo, in particular, exhibit a high seroprevalence for both RVFV and CCHFV. For RVFV, isolated positive cases have been detected in other species, while for CCHFV, aside from buffalo, only warthogs appear to have tested positive.

The preliminary results suggest that buffaloes exhibit a notable seroprevalence for CCHFV and RVFV and may play an important role in maintaining both viruses. Buffaloes are generally known as reservoirs for various pathogens without showing severe symptoms. There is generally a lack of recent data on CCHFV serology in wildlife, and together with a study from Kenya using the same commercial ELISA, the present study is one of the few to demonstrate a high CCHFV seroprevalence in African buffalo.

Keywords: Zambia, CCHFV, RVFV, wildlife, serology

P133. First molecular-genetic detection of *Rocahepevirus* in wild living animals from Slovakia

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Hepatitis E virus (HEV) is an emerging zoonotic pathogen that belongs to family *Hepeviridae*. In two decades, the genus *Paslahepevirus* has been frequently detected in main reservoirs – pigs and wild boars, moreover with serious manifestation of infection in human population. In recent years, the genus *Rocahepevirus* (RHEV) has been isolated in rodents, foxes and many other species. Zoonotic potential of this genus has been confirmed recently with increasing number of human cases reported worldwide. Presence of genus *Paslahepevirus* has been confirmed in human and animal population in Slovakia, but presence status of genus *Rocahepevirus* was unknown until now. The aim of this study was to determine the presence of RHEV in wild living animals from Slovakia.

Detection of RHEV RNA was performed in liver samples collected from seven different animal species: red fox (*Vulpes vulpes*), European badger (*Meles meles*), brown rat (*Rattus norvegicus*), house mouse (*Mus musculus*), common vole (*Microtus arvalis*), striped field mouse (*Apodemus agrarius*) and brown bear (*Ursus arctos*). Total RNA was extracted with the QIAamp Viral RNA Mini Kit by robotic station QIAcube (QIAGEN GmbH, Germany). All samples were screened individually using a nested broad-spectrum RT-PCR targeting the 332 bp in ORF1 according to Johne et al. (2010).

Presence of RHEV RNA was confirmed by molecular-genetic methods for the first time in samples from wild living animals from numerous localities in Slovakia.

This is the first molecular-genetic detection of RHEV RNA in animal population from Slovakia. The circulation of *Rocahepevirus* in wildlife population raises the question of the possible zoonotic transmission to human in Slovakia. The limited data on this zoonotic virus underscores the importance of strengthening of viral surveillance and control within the One Health framework.

Keywords: *Rocahepevirus*, zoonotic virus, wild living animals, molecular-genetic methods

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P134. Aujeszky's disease seroprevalence in wild boars in Serbia: the results of some serological studies conducted from 2013 to 2024

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Aujeszky's disease, caused by Aujeszky's disease virus, is endemic in many parts of the world. In Serbia, a national surveillance program for classical swine fever and African swine fever in wild boars was initiated 15 years ago. This program also includes serological testing of 20% of hunted animals and all found dead wild boars for the presence of antibodies against Aujeszky's disease virus during each year. The aim of this study was to summarize the results of the presence of antibodies against Aujeszky's disease virus in wild boar blood sera samples tested at the Virology Department of the Scientific Veterinary Institute Novi Sad, over an eleven-year period from 2013 to 2024.

During 2013–2015, in addition to samples from Vojvodina Province – northern part of Serbia, samples from seven districts of central Serbia were also tested. In subsequent years, only samples from Vojvodina Province were included. Overall, 38.36% of the 3,793 animals tested by commercial competitive ELISA test were found positive for anti-glycoprotein E antibodies for Aujeszky's disease virus.

The number of samples tested each year depended on the total number of hunted and dead wild boars, ranging from 127 to 485. A high prevalence was observed, ranging from 34.91% to 44.88% annually throughout the study period.

These results highlight the high prevalence of Aujeszky's disease virus in wild boar population all over the country and the real risk for domestic pigs and intensive pig production. In addition, the obtained results point on necessity of further surveillance for the future establishment of Aujeszky's disease control program based on risk assessment in Serbia.

Key words: Aujeszky's disease, wild boar, ELISA, surveillance program, Serbia

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P135. Serological and virological survey of hepatitis E virus in wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*) populations in Serbia

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Hepatitis E virus (HEV) is an emerging zoonosis, with pigs and wild boars considered as the main reservoirs of zoonotic HEV-3 and HEV-4 genotypes. In Europe, autochthonous human hepatitis E cases, linked with consumption of raw or undercooked pork, wild boar and dear liver/meat, have increased in recent decades. This study investigated the prevalence and circulation of HEV in wild boars and roe deer in Serbia during the 2010/2011 and 2011/2012 hunting seasons.
A molecular and serological survey was conducted in wild boar (*Sus scrofa*) and roe deer (*Capreolus capreolus*) populations. Anti-HEV IgG antibodies were detected using a commercial indirect ELISA (PrioCHECK HEV Ab porcine, Prionics) and an in-house ELISA based on baculovirus-expressed ORF2 recombinant proteins, while HEV RNA was identified using TaqMan one-step RT-qPCR.
During 2010/2011 hunting season, 201 blood and 298 liver samples were collected from culled wild boars from 27 hunting grounds located on the territory of 7 districts of Serbia. The overall HEV seroprevalence rate found was 34.33% (69/201) but ranged greatly between different hunting grounds (0 - 93.33%) and districts analyzed (4.55% - 48.65%). RT-qPCR analysis revealed a relatively high prevalence of 9.40 % (28/298) of HEV positive animals with regional differences. Phylogenetic analysis of partial ORF1 sequences from wild boar confirmed the HEV genotype 3 presence and heterogeneity, revealing presence of different strains (3a, 3g) circulating. In the 2011/2012 hunting season, 333 blood samples were collected from wild boars originating from 52 hunting grounds in 13/25 Serbian districts. HEV antibodies were detected in 16.82% (56/333) tested samples, again varying greatly between different hunting grounds (0 - 46.67%) and districts (0 - > 20%) with higher rates in districts with intensive pigs' production. Additionally, 91 serum collected from roe deer shot on the territory of 30 hunting grounds from 5 /7 districts of Vojvodina Province during hunting season 2011/2012, only 1 (1.1%) sample reacted positively on the presence of HEV antibodies indicating very low general prevalence of HEV in roe deer population despite high prevalence in wild boar population in those areas (20% – 48%). The high prevalence of HEV found in wild boars' population in Serbia may represent a risk for human health through human alimentary infection after consuming undercooked wild boar livers/meat. Contrary to the risk connected to the wild boars, our results suggests that roe deer population in Vojvodina Province of Serbia doesn't represent human health risk regarding HEV infection.

Keywords: hepatitis E, wild boar (*Sus scrofa*), roe deer (*Capreolus capreolus*), HEV serology and virus prevalence, zoonosis, Serbia

Acknowledgement: This research was supported by the Ministry of Science, Technological Development and Innovation of Republic of Serbia, Contract No: 451-03-33/2026-03/200031

P136. Camera traps reveal a high prevalence and seasonal variation of sarcoptic mange in red foxes across Croatia

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Sarcoptic mange, caused by the mite *Sarcoptes scabiei*, is a globally distributed parasitic disease affecting a wide range of mammals, with the red fox (*Vulpes vulpes*) as the most significant host. It may occur endemically or cause severe epizootics with substantial population declines. Traditionally, the prevalence of mange in wildlife has been researched using carcasses, but recently automated camera traps have been used to monitor diseases that manifest through changes visible in photographs.
We analysed camera trap photographs collected at 200 locations in Croatia from 2018 to 2024, to assess the prevalence of skin lesions probably caused by *S. scabiei*. Red fox images were classified as without skin lesions, with lesions, or undetermined. Only reliably assessed individuals were included and data were processed in R. For each station-month combination, fox detections (total, without skin lesions, with lesions), sampling effort (camera-days), and mean monthly temperature were analysed. Seasonal and climatic effects on infection probability were modelled using generalized linear mixed models (GLMMs) with a binomial error distribution and logit link, including station as a random effect. Model selection was based on Akaike's Information Criterion (AIC). Spatial structure was assessed using Moran's I.
Total sampling effort amounted to 57,101 camera-days (range 5,932 - 12,650 camera-days annually), with a total of 4,722 independent red fox detections. Overall, 53.2% of detections (n=2,510) were included in analyses. Among these, 12.8% of detections (n=320) showed skin lesions indicative of mange. Mange prevalence varied between years, with the lowest values in 2023-2024 (6.3% and 4.0%), and the highest between 2020 and 2022 (18.2-22.3%). Strong seasonal variation was observed, with low prevalence in winter (<3%) and peaks in early summer (35-47%). After accounting for seasonality, mean monthly temperature had a significant negative effect on infection probability ($\beta = -0.97 \pm 0.32$ SE, $p = 0.003$). Inclusion of the temperature variable improved model fit ($\Delta AIC = -7.9$). No spatial pattern was detected. This study highlights the value of camera-trapping as a non-invasive approach for long-term and large-scale wildlife disease monitoring.

Keywords: *Vulpes vulpes*, *Sarcoptes scabiei*, camera traps, health monitoring

Funding: Croatian Science Foundation, grant IP-2025-02-1750

P137. Unprecedented epidemic outbreak of *Suttonella ornithocola* in Eurasian blue tit (*Cyanistes caeruleus*) in Sweden

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In late March – early April of this year, an unusually high number of dead Eurasian blue tits (*Cyanistes caeruleus*) were reported to the Swedish Veterinary Agency (SVA). In 2024 and 2025, 7 and 15 dead or diseased blue tits were reported respectively between March 1 and April 30, while in 2026 the number of birds from March 1 to April 20 has reached 501 and counting. Reports and submissions are primarily from the south and central parts of the country, but also from northern counties. Previous outbreaks with high mortality in blue tits have been associated with *Suttonella ornithocola*, a bacteria causing severe, necrotizing pneumonia and sepsis in Passeriformes.

In the ongoing outbreak, the public describe 1-10 dead or sick blue tits per report, mainly noted at feeders in gardens. Affected blue tits show signs of unspecific illness, including lethargy, sitting with eyes closed and fluffed-up plumage. Concurrently, there are scattered reports of 1-2 sick passerines of other species with similar signs of acute disease, including Great tit (*Parus major*), European robin (*Erithacus rubecula*), Eurasian siskin (*Spinus spinus*) and Eurasian bullfinch (*Pyrrhula pyrrhula*). The public was asked to submit dead birds to SVA. By April 20, seven blue tits have been necropsied with subsequent histology. From each submission of dead blue tits, lungs from at least one of the birds was submitted for bacteriology.

Blue tits necropsied were adults in good body condition, displaying congested lungs with a mottled gross appearance. At bacteriology, *Suttonella ornithocola* was cultivated from lung samples. No *Salmonella* could be detected in lung or intestines, even with selective cultivation. Results from the histologic evaluations and whole genome sequencing of bacterial isolates are pending.

The large number of dead blue tits reported in 2026 is unprecedented in wildlife disease surveillance in Sweden. In 2020, when Germany described a large outbreak of *Suttonella ornithocola* with thousands of dead blue tits, Sweden accumulated 11 reports of ill or dead blue tits and subsequently confirmed the first case of the bacteria. The media attention in 2026 has in part skewed the data of observed ill birds as the awareness of the disease and reporting has increased. Even so, the current outbreak encompasses almost the entire country, indicating a massive spread with high transmission. As the outbreak is ongoing, results will be updated.

Keywords: epidemic outbreak, passerines, Eurasian blue tits, *Suttonella ornithocola*

P138. Case Report of Infectious Coryza in Pheasants under Semi-Intensive Rearing Conditions

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Infectious coryza, caused by the bacterium *Avibacterium paragallinarum* (formerly *Haemophilus paragallinarum*), is an important respiratory disease of poultry and birds. Although it is most frequently reported in chickens, its occurrence in pheasants is of particular relevance, especially in semi-intensive or semi-open rearing systems that simulate natural conditions and increase the risk of exposure to environmental sources of infection. The aim of this study was to present a case of infectious coryza in pheasants kept in a semi-open pheasantry system and to analyze its clinical and epizootiological characteristics.

The outbreak was recorded in May 2023 in a pheasantry with a capacity of 25,000 birds. Disease occurrence was observed in two age groups, 58-week-old and 6-week-old birds. Samples from dead birds were collected for laboratory examination. Bacteriological analysis confirmed the presence of *A. paragallinarum*. The final diagnosis was based on clinical examination and pathological findings, which revealed characteristic lesions. Following confirmation, control measures were implemented, including antimicrobial therapy, reinforcement of biosecurity procedures, and restriction of contact with potential infection sources.

Respiratory signs of varying severity were observed in both affected flocks. Clinical manifestations included serous to mucopurulent nasal discharge, marked swelling of the infraorbital sinuses, conjunctivitis, dyspnea, and reduced activity. Morbidity was approximately 50%, while mortality reached 9.7%. Pathological examination revealed catarrhal to fibrinopurulent inflammation of the nasal mucosa, infraorbital sinuses, and conjunctiva, accompanied by subcutaneous edema in the facial and submandibular regions. Extensive exudate accumulation led to atrophy and deformation of skull bones, with protrusion toward the nasal cavities and hard palate. Epizootiological assessment suggested that infection likely originated from the external environment, particularly through contact with wild birds and contaminated materials.

The implemented control measures resulted in a gradual reduction of clinical signs and stabilization of flock health status. This case highlights the importance of continuous health monitoring and strict biosecurity in semi-intensive pheasant production systems, as well as the potential role of wild birds as reservoirs of *A. paragallinarum*.

Keywords: Infectious coryza, *Avibacterium paragallinarum,* pheasants, respiratory disease, biosecurity.

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P139. Survey of *Echinococcus multilocularis* and *Echinococcus granulosus* in wild and feral carnivores from Northeastern Spain

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Alveolar and cystic echinococcosis are globally significant zoonotic diseases. In Europe, *E. granulosus* (EG) is predominantly associated with a domestic cycle mainly maintained between dogs and livestock, whereas *E. multilocularis* (EM) is primarily linked to a sylvatic cycle, involving red foxes as its main definitive host. EM has never been reported in animals in Spain, but it has significantly expanded its range in southern Europe over the past two decades. In contrast, EG is endemic in several regions of the country. This study aimed to investigate the occurrence of both parasites in wild and feral definitive hosts in northeastern Spain.

Samples from wild and feral carnivores were collected in transects and carnivore monitoring programs between 2019-2025, across Aragon (n=86) and Catalonia (n=714). These included molecularly identified 494 red foxes (*Vulpes vulpes*), 46 wolves (*Canis l. italicus*), 192 European wildcats (*Felis silvestris*) and 50 domestic dogs (*Canis l. familiaris*) and 18 domestic cats (*Felis catus*). A SYBR Green-based real-time qPCR assay targeting the mitochondrial *ND1* gene was used to detect EG sensu lato and EM in DNA extracted from the surface of the faeces. A 10×10km grid was used to pool red fox results as unique observations to avoid pseudoreplication and estimate 95% confidence intervals in Catalonia. All samples tested negative for EG and EM. In Catalonia, sampling was spatially extensive, including all 42 counties, but less representative in Aragon and covering 12/32 of the counties. Among red foxes, a 95% confidence interval (CI) for EM were 0.0–2.0% in Catalonia.

This study provides the first comprehensive survey of EM and EG among wild and feral carnivores in northeastern Spain. The broad coverage in Catalonia and large sample size supports the absence of EM in the region, although continued surveillance remains important. In contrast, the lack of detection of EG is consistent with current knowledge of its domestic cycle.

Keywords: echinococcosis; real-time qPCR; parasitology; tapeworms; zoonosis

P140. Monitoring the occurrence of gastrointestinal nematodes in selected areas in northeastern Slovakia

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Gastrointestinal nematodes represent a significant part of the parasitofauna of cloven-hoofed game and consequently affect the health status and epidemiological situation in livestock farms. Infections caused by these nematodes often have a subclinical course but represent a significant stress factor that reduces the physiological fitness and reproductive potential of the hosts. The most important pathogens of ungulates include nematodes of the *Trichostrongylidae* family, whose pathogenicity is mainly associated with hematophagy and disruption of the abomasal mucosal integrity. The aim of the monitoring was to determine the prevalence and intensity of infection of representatives of the *Trichostrongylidae* family in wild ungulates in selected locations in Slovakia, with the emphasis on the invasive species *Ashworthius sidemi*.

During continuous monitoring conducted throughout the period 2024–2026, a total of 24 abomasal samples obtained from wild ruminants were examined. The analyzed material comprised red deer (*Cervus elaphus*; n = 9), fallow deer (*Dama dama*; n = 1), roe deer (*Capreolus capreolus*; n = 1), and mouflon (*Ovis aries musimon*; n = 2). Samples collected in the Žilina Region included 13 specimens, whereas 11 additional samples of red deer originated from the Prešov Region.

Parasitological examinations were performed using the gravity sedimentation method. The overall prevalence reached 83.3%, with *Ashworthius sidemi* being the dominant species (75%) and *Haemonchus contortus* was present in 45.8% of the individuals. Mixed infections occurred in 37.5% of the individuals.

The results confirm the necessity of continuous monitoring of invasive parasitoses due to the risk of transmission to domestic ruminants. The results indicate a high level of infestation of the monitored sites with the invasive species *Ashwortius sidemi*, which requires increased attention in terms of game population management.

Keywords: *Ashworthius sidemi*, invasive parasite, *Haemonchus contortus*, cervids, abomasum

Funding source: This study was supported by the Slovak Grant Agency VEGA project No. 1/0452/25

Session 9

Endemic, neglected and non-communicable diseases

Oral Presentations

Unexpectedly prolonged half-life of neutralising antibodies against Crimean-Congo haemorrhagic fever virus infection in red deer

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The Crimean-Congo haemorrhagic fever virus (CCHFV), a zoonotic tick-borne virus with few therapeutic options and no vaccine for humans, is the only BSL-4 pathogen in Europe. In Spain, red deer and *Hyalomma lusitanicum* interactions maintain CCHFV and may underlie some human cases. Understanding the interactions between CCHFV *H. lusitanicum* and red deer could improve our ability to predict high-risk areas and seasons, and identifying recent infections is essential to understanding these dynamics. This study was based on the hypothesis that the level of neutralising antibodies could be a good indicator of recent infection in red deer.
We collected sera from a cohort of 20 red deer aged between 3 and 32 months in an enzootic area for CCHFV in Spain and tested them for antibodies against CCHFV (ID Screen® CCHF Double Antigen Multi-species ELISA, Idvet, France). We selected 37 ELISA-positive and 18 ELISA-negative sera to estimate the level of neutralising antibodies against CCHFV using viral neutralisation tests (VNT) with two virus strains (IbAr 10200, G-III; Kosova Hoti, G-V) in a BSL-4 laboratory.
None of the 18 ELISA-negative sera showed neutralising activity for CCHFV G-III and G-V, while 21 of the 37 ELISA-positive sera (56.8%) showed VNT ND_{50} values ≥8, mainly against G-III (ND_{50} ranging 8-42.5). Four out of nine 3-month-old ELISA-positive animals presented VNT ND_{50} values ≥8, but all nine were ELISA and VNT-negative four months later, indicating the maternal origin of these antibodies. We observed strong viral neutralising activity in three 7-month-old animals that was still evident six months later, indicating probable infection at the autumn peak of adult *H. lusitanicum*. A fourth animal (ELISA and VNT-negative at 3 and 7 months of age) presented an increase in neutralising antibodies at 13 months of life, after the spring peak of *H. lusitanicum*. Three of these four animals again presented neutralising activity at 19 months of age, suggesting re-infections during the autumnal peak of *H. lusitanicum*. In two of them, the neutralising antibodies persisted 6 months later.
The results of the VNTs and similar findings in France demonstrate the specificity of the commercial ELISA for CCHFV in western Europe. Further, they suggest that neutralising antibodies may be good indicators of recent infections as initially hypothesized, being potentially useful to precisely identify recent CCHFV infections.

Keywords: *Cervus elaphus*, incidence, *Orthonairovirus haemorrhagiae,* wildlife.

Funding source ^ Acknowledgement: EU-ISIDORe ISID_8a02, EU & MICIU/AEI (CGL2017-89866-R) and SBPLY/19/180501/000321-JCCM/EU-ERDF.

Implication of *Clostridium botulinum/baratii* in paretic syndrome of yellow-legged gulls on Salvora Island in the Atlantic islands National Parc in Spain: a field study

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Paretic syndrome impacts gull and other marine bird species in the Baltic and Mediterranean seas but also on the Atlantic coast of Spain. Recently type C toxin botulism has been postulated as the cause in rehabilitation centre admitted gulls in Portugal, while in the Baltic, botulism and vitamin B1 deficiency are under debate. The island of Salvora foremost the most important breeding colony of yellow legged gulls (*Larus michahellis*) hosts now only 10% of its former breeding population. Our objective was to assess the implication of *Clostridium* (*C.*) *botulinum* and *baratii* by comparatively studying healthy and diseased individuals from the Salvora yellow-legged gull breeding colony.
During the 2024 breeding period diseased and deceased individuals were collected during daily control rounds on the colony edges (n = 166) and 59 healthy gulls (23 chicks, 36 adults) were sampled during ringing activities. Biometry, cloacal swab, blood and contour feather samples were collected from live gulls and tissue samples for histopathology and large intestine and liver samples from deceased birds. Culture for *C. botulinum/baratii* and PCR based detection of expression of genes for production of neurotoxins C, E and F7 were carried out on cloacal swab, intestinal and liver samples in addition to histopathology and stable isotope signature quantification in feathers.
Of the 225 gulls, 128 allowed for clostridium culture. Overall prevalence of *C. botulinum* was 32.8% (32/128) and it was present in both healthy and sick/deceased gulls. Expression of type C neurotoxin gene was only detected in two diseased individuals and type F7 neurotoxin gene from *C. baratii* in 33 both healthy and sick/deceased gulls. While *C. baratii* F7 neurotoxin gene presence was not related to paretic syndrome, *C. botulinum* presence was significantly higher in gulls with paretic syndrome than in healthy gulls, and a more carbon rich stable isotope contour feather signature indicating landfill foraging was weakly associated with a higher *C. botulinum* prevalence. A cluster of highly decomposed individuals from the colony collected at the end of the breeding season revealed a concomitant H5N1 high pathogenicity avian influenza virus outbreak.
Our results show association of paretic syndrome to presence of *C. botulinum*, albeit limited C toxin, but also threats such as high pathogenicity H5N1 AIV. Future investigations should study point sources and the role of vitamin B1 deficiency along the marine food web and other factors.

Keywords: Paretic syndrome, yellow-legged gull, *C. botulinum, C. baratii*, landfills, stable isotopes

Long-term seroepidemiology of European Brown Hare Syndrome in European and Italian hares in Tuscany (Italy), 2003 to 2019

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European Brown Hare Syndrome (EBHS) is a highly contagious disease caused by a virus in the Lagovirus genus, family Caliciviridae (EBHSV – Lagovirus GII.1). First identified in Italy in 1988, it has since spread and become endemic, affecting various species within the Leporidae family. Notably, it has affected the European hare (*Lepus europaeus*), a common species in North and Central Italy, and the Italian hare (*Lepus corsicanus*), a species of conservation concern, due to its endemism in Central and South Italy. This study aimed to determine the presence and to assess the occurrence of EBHS in the province of Grosseto (Tuscany, Central Italy), through a longitudinal survey conducted from 2003 to 2019.
The diagnostic investigation was carried out using a competitive ELISA on blood samples from 479 brown hares and 58 Italian hares that had been captured and released to restock hunting areas. Descriptive statistics were used to provide an overview of the distribution of positive anti-EBHSV titres, stratified by age class, sex, species, years of sampling, and the type of establishment where individuals were caught. A generalised linear model with a binomial distribution and a logit link function was used to estimate EBHSV prevalence, including four fixed effects: sex, age, year of sampling, and month of sampling from October to March.
The results showed that the disease is apparently more widespread among European hares than among Italian hares. A higher prevalence was found in adults than in young individuals, with no differences between males and females. Most sera had low antibody titres, indicating endemic EBHSV circulation and a high level of population-level protection. The sex effect was not significant, whereas the age effect influenced the probability of infection, which was higher in adults than in young individuals. The winter months mainly influenced the probability of EBHSV infection. Years did not influence infection, and no clear trend was observed, which might be related to an unbalanced experimental design.
The data from this survey, spanning over 15 years, contribute to a better understanding of the dynamics of EBHS in an endemic area. Therefore, they may inform intervention strategies and improve the management of hunting areas.

Keywords: hare, EBHS, serology, surveillance, Tuscany

Do clusters of tumour-like disease in wild red squirrels suggest a common cause?

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Background and objectives: Atypical histiocytosis (AH) is a tumour-like condition in wild red squirrels (*Sciurus vulgaris*) first identified in Scotland in 2017 (Smith et al). Nine cases have now been detected in Cumbria, England, since 2019 (Duff et al 2026). This oral presentation describes their occurrence clustered at two locations (with 3 and 5 confirmed and suspected cases respectively); each cluster occurring at two separate locations in a short time span of several months. Neoplasia (if this proliferative condition is neoplastic) is unusual in wild animals and, more generally, clusters of neoplastic disease is significantly more unusual and moreover can indicate a common cause. Work to try and elucidate a cause for the condition is in progress (Next Generation Sequencing and IHC) and available results will be reported at the conference.

Keywords: histiocytosis, wild, squirrel, cluster

Funding – Defra, UK government

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Session 9

Endemic, neglected and non-communicable diseases

Poster Presentations

P141. Sero-surveillance for Diseases of Livestock in Wild Deer in England

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In landscapes where wild deer live in close proximity to livestock, they are often perceived as contributors to the transmission of common livestock diseases. In Great Britain, deer have been implicated in the persistence and/or spread of diseases such as Johne's disease (caused by *Mycobacterium avium* subspecies *paratuberculosis* (MAP)), Q fever (infection with *Coxiella burnetii*) or infection with Schmallenberg virus (SBV). However, despite known outbreaks of diseases such as Johne's disease in farmed deer, little is known about these diseases in wild deer in GB. This study used samples from culled deer to investigate the presence of antibodies to diseases of livestock in wild deer. Blood samples were obtained from 585 deer culled for reasons unrelated to this study across two spatially distinct areas of England during autumn/winter of 2022/23 and 2023/24. The sampled deer represented multiple species and were located in close proximity to livestock farms. Serum samples were analysed using enzyme-linked immunosorbent assay to detect antibodies to SBV, *C. burnetii* and MAP.

No antibodies to *C. burnetii* or MAP were detected in any samples throughout the study. In contrast antibodies to SBV were detected in 21% of samples collected in 2022/23 and 38% of samples collected in 2023/24. Seropositivity to SBV was observed across all wild deer species common to the UK with no apparent association with deer life-stage or sex.

The absence of seropositivity to MAP and *C. burnetii*, despite sampling from areas with known Johne's disease and Q fever in livestock and other wildlife, does not support a hypothesis that wild deer act as reservoirs for these diseases in these areas. The spatial and temporal separation of these sample groups prevents robust conclusions being drawn regarding changes in SBV seropositivity over time; however, the observed increase coincided with a rise in SBV cases in livestock during the winter of 2023/24. Further research is needed to clarify any role of deer as potential reservoirs for SBV, and to assess any clinical effects of SBV infection on wild deer populations. While limited pathogens were included for testing in this study, the engagement with the deer management community in sample collection demonstrates the value of close working relationships between government and wildlife management professionals. This study has shown the potential of sero-surveillance using bloods from culled deer in assessing regional disease statuses.

Keywords Deer, SBV, MAP, Q fever

P142. Evidence of increased transmission of Aujeszky's disease virus in wild boar in Catalonia, NE Spain

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Aujeszky's disease virus (ADV; pseudorabies virus) is a suid *alphaherpesvirus* maintained in wild boar across Europe, posing a persistent threat to domestic pigs and other susceptible species. Despite its enzootic status and the constant spill-over risk, changes in transmission intensity over time remain poorly understood. This study aimed to assess temporal trends and age-related patterns of ADV seroprevalence in wild boar in Catalonia (northeastern Spain).

Between 2011 and 2025, 21,381 wild boar sera were analyzed using commercial ELISAs. Seroprevalence was modelled using binomial generalized additive mixed models (GAMMs), including age as a categorical predictor and a smooth function of year stratified by age. Sampling zone was included as a random effect to account for spatial variation.

Overall seroprevalence was 19.71%. It remained relatively low between 2011 and 2020 (ranging from ~6–14%), followed by a marked increase from 2021 onwards, reaching 30.43% in 2024. Adults showed higher seroprevalence (25.51%) than subadults (11.17%) and juveniles (10.91%), consistent with cumulative exposure in horizontal transmission. The GAMM confirmed a strong age effect, with adults showing significantly higher odds of seropositivity compared to juveniles ($\beta = 1.10$, $p < 0.001$; OR ≈ 3.0), while subadults showed lower odds than juveniles ($\beta = -1.10$, $p = 0.046$; OR ≈ 0.33) after accounting for temporal and spatial effects. Temporal trends were significant across all age classes ($p < 0.001$), indicating an overall increase in exposure over time. A strong spatial effect was also detected ($p < 0.001$), indicating marked variation in seroprevalence among sampling areas.

ADV infection in wild boar in Catalonia shows an increasing transmission pattern over the study period, consistent with intensifying viral circulation in an enzootic system. The strong age-related differences in seroprevalence support cumulative exposure as a key driver of infection dynamics. These findings suggest a recent increase in transmission, which aligns with growing concern among local hunters and reports of cases in hunting dogs in recent years. Continued long-term surveillance is essential to monitor trends and improve understanding of the drivers of ADV transmission.

Keywords: Aujeszky's disease virus, wildlife epidemiology, seroprevalence dynamics

P143. A survey of feline viral pathogens in free-living European wildcats (*Felis silvestris*) in Serbia

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Abstract

The European wildcat (*Felis silvestris*) is a native felid distributed across much of Europe. While some populations remain stable, others face habitat loss, fragmentation, and interactions with free-ranging domestic cats (*Felis catus domesticus*). Compared to other wild felids, European wildcats have received limited conservation and health-related attention, particularly in Eastern and South-Eastern Europe. Previous studies indicate exposure of wildcats to common feline viruses; however, no data are available for Serbia. Therefore, the aim of this study was to investigate the exposure of Serbian wildcats to major pathogenic feline viruses commonly found in domestic cats. Between 2019 and 2022, blood (or blood exudate from thoracic/abdominal cavities) and tissue samples (spleen, liver, kidney, lungs, mediastinal and mesenteric lymph nodes) were collected from 36 wildcats that were shot or found dead across 14 of 25 districts in Serbia. Samples were tested for feline coronavirus (FCoV/FIP), feline immunodeficiency virus (FIV), feline leukemia virus (FeLV), and feline parvovirus (FPV). Serological testing was performed using immunochromatographic assays for antibodies and antigens, while molecular detection was conducted using PCR/RT-PCR and qPCR/RT-qPCR assays. In total, blood /blood exudate samples of 21 wildcats were tested for the presence of antibodies for FIP and FIV and viral antigens for FeLV, as well as tissues homogenates samples from 36 animals were tested for FCoV (FIP), FPV, FeLV and FIV genomes presence. All tested samples were negative for FIV by serological and molecular methods. By contrast, the highest prevalence (8/35, 25.71%) was found for the feline parvovirus (FPV) presence in tissue samples, followed by FeLV virus presence in tissue samples (3/35, 8.57%) and FeLV antibodies in blood samples (1/21,4.76%). Feline coronavirus (FCoV/FIP) was detected in 2.86% (1/35) tissue samples and antibodies were found in 9.52% (2/21) of wildcat blood samples. FPV presence in wildcats was found in 5 (Srem, Rasina, Bor, Pomoravlje and Belgrade), FeLV in 3 (Srem, South Banat, and Belgrade), and FIP (FCoV) in 2 (Srem and South Backa) out of 25 districts of Serbia respectively. This study confirms that wildcats in Serbia are commonly infected with the major viruses of the domestic cat, except for FIV. Close contact between wildcats and free-ranging domestic cats is likely an important factor contributing to viral transmission. Besides the influence on health, these contacts strongly influence on the biodiversity of wildcats in Serbia due to the crossbreeding between these animal species.

Keywords: European wildcats (Felis silvestris), FCoV (FIP), FPV, FeLV and FIV presence, Serbia

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P144. Subcutaneous cysts in alpine birds from Picos de Europa National Park (Spain): increasing prevalence and first detection of *Collyriclum faba*

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Long-term scientific bird ringing enables syndromic surveillance by systematically recording of visible clinical signs in wild populations, allowing the early detection of emerging health threats and assessment of temporal trends. Within this framework, the Iberian Ringing Group (GIA) has monitored alpine passerine communities in Picos de Europa National Park (PENP, Spain) since 2003. Subcutaneous cysts have been consistently observed across several passerine species. These lesions are conspicuous, protruding structures of 4-10 mm, occasionally with a small external opening. In this study, we assessed cysts prevalence and temporal trends over more than two decades and investigated their etiology.

Field campaigns were conducted during the breeding season (June-August) in alpine sites across the central and eastern massifs of PENP. A total of 2,281 records from six bird species (2003-2025) were included: *Prunella collaris*, *Anthus spinoletta*, *Montifringilla nivalis*, *Oenanthe oenanthe*, *Phoenicurus ochruros*, and *Linaria cannabina*. Cysts prevalence was analyzed by species, age, sex, capture area and year. In 2025, two cysts were punctured and their contents examined microscopically; parasite identification was performed by sequencing ITS1, ITS2, and ND1 genes.

Overall cyst prevalence was 2.4% (95% CI: 1.8-3.1), with 1-15 cysts per affected individual. Significant interspecific differences in prevalence were observed (Fisher's exact test, $p<0.01$), ranging from 0.3% in *M. nivalis* to 11.7% in *P. ochruros*. No effects of age or sex were detected. Temporal trend analysis using a binomial logistic regression model on a representative subset (2003-2024; n=1,653) revealed a significant increase in prevalence over time (OR per year = 1.12; 95% CI: 1.05-1.2; $p<0.001$); species and area did not significantly improve model fit. Molecular analysis confirmed the diagnosis of the trematode *Collyriclum faba*, genetically identical to Central European isolates.

Collyriclum faba is a widely distributed trematode infecting a broad range of avian hosts across Eurasia, Africa, and the Americas. This is the first description of the parasite in an alpine passerine community. The observed increase in cyst prevalence over the past two decades highlights the need for further research to clarify transmission dynamics and assess potential impacts on fragile alpine bird populations.

Keywords: alpine passerines, *Collyriclum faba,* syndromic surveillance, trematode

P145. Presence of *Skrjabingylus nasicola* in American Mink (*Neogale vison*) in Catalonia, NE-Spain

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Skrjabingylus nasicola is a metastrongyloid nematode that parasitizes the frontal sinuses of mustelids, potentially causing cranial lesions associated with osteolytic processes. Although its distribution is well documented across several European mustelid species, information on its presence in the Iberian Peninsula remains limited. This study aims to analyze the presence of the parasite in the exotic invasive species American mink (*Neogale vison*) in Catalonia, NE-Spain.

Sixty *N. vison* skulls collected in Catalonia between 2025 and 2026 were analyzed for the presence of *S. nasicola*. Parasite detection involved macroscopic examination, inspection for black dots, and flushing of frontal sinuses, with recovered material examined under a stereomicroscope.

No adult nematodes, larvae, or eggs were detected in any sample. Minor alterations were observed, including muscular lesions in seven individuals, black dots in three skulls, and a single instance of cranial bone lesion.

These findings indicate either the absence or a very low prevalence of *S. nasicola* in *N. vison* populations in Catalonia. The absence of parasites contrasts with higher prevalence reports in other European mustelids, suggesting that *N. vison* may play a limited role as a host in Mediterranean environments. Further studies incorporating a larger sample size and additional mustelid species are recommended to confirm these results and better understand the epidemiology of this parasite.

Keywords: *Skrjabingylus nasicola*; metastrongyloid nematode, mustelids; cranial parasites; Catalonia

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P146. A case of hydrocephalus in a gray wolf (*Canis lupus*) cub

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Hydrocephalus is a neurological condition characterized by an abnormal accumulation of cerebrospinal fluid within the brain's ventricles. Treatment of hydrocephalus in wild animals is questionable, hence the importance of an accurate diagnosis.
A gray wolf cub, approximately two months old, was found near human settlements in southern Poland. All attempts to return the cub into its natural habitat were unsuccessful; thus, it was transferred to the rehabilitation center. The cub was mildly dehydrated and weak. *Toxocara* sp. and *Anaplasma sp.* infestation, as well as iron deficiency anemia, were diagnosed. Appropriate treatment was administered. After a week, it began walking in circles and appeared to be losing vision on one side. Due to suspicion of hydrocephalus, the Computed Tomography scan was performed. The CT findings were most consistent with severe internal obstructive intraventricular hydrocephalus with secondary brain atrophy and formation of periventricular diverticula. Due to the lack of detection of infectious agents congenital/developmental stenosis or obstruction of the mesencephalic aqueduct was suspected as the underlying cause. Because there was no possibility of treating the cub and releasing it back into the wild, a decision was made to perform euthanasia. It is advisable to conduct a comprehensive panel of necessary additional diagnostic tests on animals admitted to rehabilitation centers, as having the test results enables making the most accurate decision regarding the animal's further management. Because information available on hydrocephalus in wild animals is scarce, presenting this case is essential, especially in the context of decisions made in wildlife rehabilitation centers.

Keywords: hydrocephalus, gray wolf, congenital, developmental defects

Session 10

Threats to ectotherms, urban wildlife, wild pets, fish and exotic animals

Oral Presentations

Betanodavirus Infections in Mediterranean and Atlantic Groupers: Epidemiology, Host Interactions, and Conservation Implications

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Mass mortality events in groupers (*Epinehelus marginatus*) and other marine fish in the Mediterranean and Atlantic are increasingly linked to betanodavirus infections, raising major ecological and conservation concerns. These impacts are critical for grouper populations already under pressure from fishing and habitat degradation. This study synthesizes current knowledge on betanodavirus epidemiology, emphasizing virus–host–environment interactions and the roles of wild and farmed fish.
This work was conducted by a multidisciplinary expert group from Italy, Greece, Spain, Croatia, and Portugal, led by Dr. Toffan (IZSVe), who have monitored and characterized this disease over the past decade (Toffan et al., 2026). Their approach integrates field observations, diagnostics, and epidemiological analyses across Mediterranean and Atlantic ecosystems.
Betanodaviruses comprise multiple genogroups with strong reassortment capacity, generating variants with different host range and virulence, leading to dynamic epidemiology. Mortality events are driven by interactions between aquaculture and wild populations, with farms acting as amplifiers and sources of spillover. Impacts are particularly severe in marine protected areas, where high densities of susceptible species can result in significant losses, especially in already stressed wild populations. Climate changes and particularly hatwaves are under investigation amongst foctors triggering these mortality ourbreaks.
Betanodavirus poses a significant threat to Mediterranean grouper populations. Surveillance and monitoring are essential, alongside preventive mesurés such as vaccination and the maintenance of broodstock under high biosecurity to preserve genetic diversity. Integrated strategies combining epidemiology, conservation, and aquaculture management are crucial to mitigate risks.

Keywords: betanodavirus, grouper mortality, aquaculture–wildlife interactions

Refence: Toffan, A., Volpe, E., Zrnčić, S., Mylonas, K. and Katharios, P. 2026. "Nodavirus in Wild Fish: Addressing the Mediterranean Grouper (Epinephelus Spp) Mortality Crisis." Bulletin of the European Association of Fish Pathologists, February 27. https://doi.org/10.48045/001c.158446

Amphibian scanning disease surveillance for threat detection: Bufonid herpesvirus 1 infection in common toads (*Bufo bufo*) in Great Britain

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Skin disease associated with Bufonid herpesvirus 1 (BfHV1) infection was recently described in common toads (*Bufo bufo*) in Switzerland, Germany, and Luxembourg, yet the distribution and health impact of BfHV1 across the species range is uncertain. In Great Britain (GB), scanning disease surveillance for amphibians is conducted through the Garden Wildlife Health (GWH) project with the objective to identify endemic and emerging diseases that may affect native species

Reports of sick and dead amphibians in GB have been solicited from the public through GWH since 2013. Since November 2023, multiple reports of common toads with skin lesions consistent with BfHV1 infection were received from a toad patrol volunteer from a single site in England. Of these, twelve carcases, found between February 2024 and March 2025 inclusive, were submitted for investigation. Systematic post-mortem examinations (PMEs), including histopathology where possible, were conducted, and samples collected for BfHV1 PCR screening and whole genome sequencing (WGS). Photos of GWH disease incident and PME reports (2013-2025) of common toads were retrospectively reviewed, and archived skin tissues from historic PMEs where BfHV1-like lesions were noted were screened by PCR.

While the proximate cause of death for all 12 toads was road traffic collision, skin lesions of varying severity were observed in each case and tested BfHV1 PCR positive. Dermatitis and parakeratosis were identified histopathologically, consistent with BfHV1 skin disease. Finally, we confirmed a 99% genome identity to the original BfHV1 strain (FO1_2015) described in Switzerland by WGS. Retrospective review of disease incident and PME photos identified multiple historical cases with skin lesions suggestive of BfHV1 infection, and BfHV1 was PCR confirmed by PCR in skin lesion from a common toad examined in 2014.

Here we describe the first confirmation of BfHV1 in common toads in GB. Whilst further surveillance is needed to better understand BfHV1 occurrence, distribution and potential impact on common toad health, our findings suggest that BfHV1 is not a recent emergence in GB, but likely an overlooked cause of amphibian skin disease. Our study demonstrates the utility of scanning disease surveillance for disease detection, and the value of long-term datasets and tissue archives, to establish if they represent recent emergent events or previously missed infections.

Keywords: citizen science, amphibian health, common toad, bufonid herpes, skin disease

Parasitic spillover in endangered fresh water turtles in France

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Invasive species constitute a major driver of global biodiversity loss, with pathogen spillover representing a particular threat. In Europe, several cases of parasitic spillovers from exotic to native turtle species have been documented. In particular, in Switzerland and Spain, the red-eared slider (*Trachemys scripta elegans*) is strongly suspected to be responsible for the transmission of the exotic blood parasite *Spirorchis elegans* to the European pond turtle (*Emys orbicularis*). As a result, significant mortality events have been recorded in this endangered species, which is also subject to conservation measures in several European countries. More recently, in France, abnormal mortality events were reported in captive European pond turtles and Mediterranean pond turtles (*Mauremys leprosa*) prompting investigations into the causative agents and their epidemiology.
Between November 2023 and February 2025, a total of 9 captive freshwater turtles originating from a sanctuary, including 6 European pond turtles, 2 Mediterranean pond turtles and 1 razor-backed musk turtle (*Sternotherus carinatus*), were submitted to the National Veterinary School of Toulouse for diagnostic investigation due to the onset of increased mortality. Following the initial necropsy findings, 15 eastern mosquitofish (*Gambusia holbrooki*) sharing the same pond of the turtles examined, were collected, euthanized and processed for histopathology.
Necropsy revealed pulmonary congestion, haemorrhages, and consolidation, with 2-6 cm long yellow-white worms found in the respiratory tract of all turtles. Histopathology revealed bronchointerstitial pneumonia and the presence of organisms morphologically consistent with adult pentastomes, within the bronchial lumen. PCR targeting the 18S rRNA gene (18A1F and 1800R) of arthropods and Sanger sequencing strongly supported the involvement of *Levisunguis subaequalis*. Histopathological examination of mosquitofish from the same pond revealed pentastome nymphs in 2 specimens, confirmed by molecular analysis. In addition, *Spirorchis* sp. eggs and adults were also identified in both native turtle species.
To our knowledge, this is the first documented case of pentastomiasis in European freshwater turtles. A spillover event from exotic turtle species is suspected, given the previous detection of this pentastomid in soft-shell turtles in the USA, the cohabitation of a variety of turtle species at the sanctuary and the presence of a competent intermediate host, the eastern mosquitofish

Keywords: invasive species, turtles, spillover, pentastome

Is urbanization a driver of differences in bacterial communities among native and invasive rodents in Northern Senegal?

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Urbanization is a major cause of environmental disturbances responsible for reshaping the composition and dynamics of host-associated microbial communities (viruses, bacteria, helminths and protozoans, including pathogenic taxa). These changes may influence host health in multifaceted ways, including altered host condition, infection patterns, and population dynamics. As highly anthropophilic and widespread components of urban fauna, rodents are particularly exposed to urban-induced environmental changes, with strong implications for public health as some rodent species are known as major zoonotic reservoirs. Yet, in West Africa where urban transition is among the fastest throughout the world, the effects of urbanization on rodent microbial communities still remain to be investigated – particularly with respect to species status (native *versus* invasive) of rodent species as this region currently undergoes biological invasions by exotic rodents. Here, we investigate the links between ongoing urbanization and bacterial community dynamics within native and invasive rodent host populations in North Senegal. Specifically, we aim to test two alternative hypotheses, whereby urbanization may either reduce (*urban refuge hypothesis*) or increase (*urban burden hypothesis*) carriage of pathogenic bacteria by rodents.

We analysed samples from natural rodent populations collected between 2013 and 2025 across 31 urban or rural sites in North Senegal. Our dataset includes 1,430 individuals from two species: the invasive *Mus musculus domesticus* and the native *Mastomys erythroleucus*. We performed 16S metagenomics on spleen samples to characterize their bacterial communities based on Operational Taxonomic Units (OTU).

Our preliminary analyses identified ten bacterial genera, most of them shared by both host species. Interestingly, genus-level diversity was higher than previously reported. Based on a broad-scale classification of sampling sites, our analyses highlighted host-specific differences between urban and rural localities, suggesting patterns consistent with either *urban refuge* or *urban burden* hypotheses depending on the bacterial genus considered.

Our results provide preliminary signals that urbanization may reshape the composition of rodent microbial communities within host species, although further analyses including finer-scale landscape characterization are needed. In addition, the description of helminth communities will help exploring potential co-infection patterns.

Keywords: host-parasite interaction, community ecology, spatio-temporal survey, small mammals, zoonoses

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Respiratory disease in rehabilitating European hedgehogs (*Erinaceus europaeus*): Pathological and microbiological findings

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European hedgehogs (*Erinaceus europaeus*) are the most presented wild mammalian species for rehabilitation in Western Europe, with respiratory disease being a common morbidity. This study aims to describe potential aetiologies of respiratory disease in the species which may guide diagnostic and therapeutic options.
Fifty rehabilitating hedgehogs from England that died after exhibiting respiratory clinical signs and five controls underwent postmortem examinations. These were focused on the cardiorespiratory tract and included extensive histology as well as nasal and pulmonary microbiology.
Upper respiratory tract disease (URTD) and lower respiratory tract disease (LRTD) were almost equally prevalent, each affecting 50-60% of diseased animals, whereas cardiac disease was rare. URTD usually presented as exudative neutrophilic rhinitis, often with turbinate atrophy and luminal bacterial colonies. Underlying causes included trauma, foreign bodies, dental disease and fluke. *Pasteurella spp.* and *Morganella morganii* were only isolated from rhinitis cases, suggesting that they may be implicated in URTD. Approximately 40% of animals had moderate to severe tracheitis, often lymphoplasmacytic and associated with *Eucoleus aerophilus*. Several of these cases had secondary bacterial infection or strictures of the tracheal mucosa. Moderate to severe pneumonia was found in approximately 45% of hedgehogs, most of which constituted verminous pneumonia with the presence of *Crenosoma striatum* and/or less commonly *Eucoleus aerophilus*. Bacterial culture of lung tissue from pneumonia cases identified several gram-negative bacteria such as *Aeromonas, Morganella, Pasteurella and Bordetella spp.* and some infections presumably occurred following rhinitis and/or tracheitis. Three cases of diffuse alveolar damage with pulmonary oedema were associated with systemic salmonellosis. Two hedgehogs had pulmonary adiaspiromycosis associated with *Emmonsia crescens* but with questionable relevance.
Clinical respiratory signs in European hedgehogs can reflect URTD, LRTD or both. Making a distinction in live animals via radiography combined with other techniques can improve casualty care. Moreover, hedgehog postmortem examinations should routinely include assessment of the nasal cavity especially for animals with a history of respiratory clinical signs, given the high prevalence of URTD in this population.

Keywords: Hedgehog, rhinitis, pneumonia, lungworm, Morganella

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Session 10

Treats to ectotherms, urban wildlife, wild pets, fish and exotic animals

Poster Presentations

P147. Virus circulation in aquatic ecosystems: rethinking the role of wild organisms in fish disease dynamics

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Viral diseases of fish are a major constraint to the sustainability and biosecurity in Europe. Their epidemiology is shaped by complex interactions within open aquatic systems, where farmed fish, wild populations, and diverse aquatic organisms coexist. Continuous waterborne transmission facilitates pathogen exchange, blurring ecosystem boundaries. This study aims to synthesize current knowledge on fish viral epidemiology, focusing on virus circulation across aquatic communities and the diverse roles of organisms.

This study was conducted within the framework of SOA7 of the EURPA&W initiative. A comprehensive bibliographic review was carried out, followed by expert discussion and validation by members of the action to ensure robustness and consensus of the findings.

Fish virus circulation involves complex networks extending beyond aquaculture systems. In this study, a detailed analysis of the current knowledge on the main viral diseases affecting fish in Europe was conducted. While wild fish can act as reservoirs or sources of infection, they are often incorrectly regarded as primary culprits, whereas evidence shows they are frequently victims of spillover events from aquaculture, where viral amplification increases transmission pressure. Additionally, various aquatic organisms may act as carriers, vectors, or reservoirs, with roles that are highly virus-dependent. Environmental factors further modulate viral persistence and transmission dynamics.

Fish viral epidemiology is driven by complex and interconnected processes involving host, virus, and environmental factors. Recognizing wild populations as both potential sources and victims of infection is essential to avoid biased interpretations. A holistic, ecosystem-based approach integrating epidemiology, ecology, and virology is required to improve disease management and biosecurity in aquaculture.

Keywords: fish farming, viral diseases, aquatic wildlife

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P148. Circulation of Amphibian Herpesviruses in Common Frogs (*Rana temporaria*) and Common Toads (*Bufo bufo*) in Schleswig-Holstein, Northern Germany

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Amphibian population declines are attributed to multiple stressors, including infectious diseases. Herpesviruses such as the ranid herpesvirus 3 (RaHV3) and the bufonid herpesvirus 1 (BfHV1) have raised concerns due to their potential impact on native European amphibians. In Schleswig-Holstein, northern Germany, *Rana* species (common frogs, *Rana temporaria*; and moor frogs, *Rana arvalis*), and common toad (*Bufo bufo*) populations exhibit decreasing trends. Previous studies reported both herpesviruses occurrence in the region.

To elucidate herpesvirus dynamics through longitudinal data spanning multiple years and assess infection patterns across life stages, tadpoles and post-metamorphic individuals of common toads and *Rana* species were sampled at three sites across Schleswig-Holstein in 2025 and 2026. Skin swabs were collected from 157 metamorphosed individuals, while swabs targeting keratinized tissues were taken from 71 tadpoles according to their Gosner developmental stage. All samples were analysed via PCR for BfHV1 and RaHV3 detection.

Preliminary results showed BfHV1 detection in 75.0% (30/40) of common toads and 11.6% of common frogs (8/69), and RaHV3 in 36.2% (25/69) of common frogs. Among tadpoles, 11.4% (3/35) of common frog larvae tested positive for RaHV3. All moor frog samples tested negative for both herpesviruses during the study.

Our results indicate persistent circulation of RaHV3 and BfHV1 in common frogs and common toads in northern Germany over time. Detection of BfHV1 in common frogs suggests potential cross-species infection. Tadpole RaHV3-positivity supports infection during larval or embryonic stages. However, susceptibility of pre-metamorphic individuals, transmission pathways and population-level impacts of herpesviruses in native amphibians warrant further investigation.

Keywords: herpesvirus, amphibian diseases, common toad, common frog, tadpole

P149. Stranding monitoring of cold-stunned sea turtles along the coast of Northern Germany

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An increase in sea turtle occurrences along the European Atlantic coastline has been observed in recent decades, with stranding events likely to become more frequent under changing climatic conditions. Sea turtles are widely distributed in (sub)tropical waters. Temperatures below 10°C can cause severe hypo-thermia, leading to reduced metabolic activity and immobility, commonly referred to as "cold stunning". Monitoring provides critical information on spatiotemporal patterns and health statuses, linking individual welfare with broader biodiversity conservation.
This study focuses on 14 stranding events of live and deceased sea turtles during winter seasons between February 2022 and November 2025. Health assessments of live individuals included a full clinical examination, blood analyses and radiographic imaging. Necropsies encompassed macroscopic examinations, histopath-ologyical evaluations (where feasible), and screening for infectious agents in deceased specimens. Genetic analyses were performed on both live and deceased turtles.
Four live juvenile loggerhead turtles (*Caretta caretta*) stranded on Sylt, all exhibiting clinical signs and mild blood analyses abnormalities consistent with hypo-thermia. Three turtles were successfully rehabilitated, satellite-tagged and released nearby La Rochelle, France; one awaits release. In six juvenile loggerheads and one juvenile Kemp's ridley (*Lepidochelys kempii*), cold-stunning was the most likely cause of death, since only minor pathologies (mild pneumonia, gastritis, intestinal endoparasito-sis) were detected. An adult leatherback turtle (*Dermochelys coriacea*) showed signs of traumatic injuries. One loggerhead and one green turtle (*Chelonia mydas*) remained at their stranding sites without pathological examination. Five necropsied loggerheads were screened for herpesvirus of which all tested negative. Genetic analyses revealed three loggerheads with a genetic affinity to the Cape Verde population and one to Georgia, USA.
These findings highlight cold-stunning as the predominant driver of sea turtle strandings along the coast of Northern Germany, underlining the importance of systemic monitoring for early detection, rehabilitation, and health status analyses. Genetic data indicated transatlantic dispersal patterns, emphasizing their wide distribution range. Enhanced monitoring integrates health, welfare, and biodiversity data on sea turtle populations by providing vital baseline data to predict and prevent cold-stunning events.

Keywords: Sea turtle, stranding, cold-stunning, health monitoring, genetic analyses

P150. Post-release monitoring in rehabilitated wildlife: insights from a multi-species telemetry pilot study in Germany

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Wildlife rehabilitation centres admit increasing numbers of wild animals each year due to trauma, disease, or orphaning, requiring substantial personnel and financial resources. Animals often undergo prolonged periods in human care, yet post-release outcomes, such as survival and the ability to perform species-specific behaviors in the wild, frequently remain unknown. Evaluating release success is therefore essential for improving rehabilitation protocols and assessing their contribution to wildlife conservation and health. This pilot study examines whether telemetry-based monitoring can reliably assess post-release adaptation and survival across multiple species commonly presented to German wildlife rehabilitation centres, including common buzzards (*Buteo buteo*), European hedgehogs (*Erinaceus europaeus*), edible dormice (*Glis glis*), thrush species (*Turdus* spp.), and house sparrows (*Passer domesticus*).
A total of 93 individuals were tagged with telemetry devices over a two-year period (2024–2025). GPS transmitters were used for raptors, while smaller species were monitored using VHF tags in combination with automated antenna systems and complementary manual tracking. Nestboxes with Radio Frequency Identification (RFID) were additionally used to evaluate post-hibernation survival in edible dormice.
Key parameters included short-term survival, post-release activity patterns, circadian rhythms, space use, and the effects of soft release as release strategy. Species-specific methodological challenges required adaptive approaches, including addressing tag loss in hedgehogs, limited signal detection in ground-dwelling species such as dormice, and constraints in tracking small passerines.
Despite these challenges, the study generated valuable first insights across species. Telemetry data allowed initial assessment of post-release adaptation and survival, including indications of successful overwintering of hand-reared edible dormice released in autumn, a rapid re-establishment of circadian activity patterns in European hedgehogs, and potential implications for antiparasitic management in common buzzards. While analyses are ongoing, these preliminary findings highlight the potential of multi-species telemetry approaches to improve the evaluation of rehabilitation outcomes. The study further emphasizes the importance of systematic post-release monitoring and provides practical insights into both opportunities and limitations of telemetry in rehabilitated wildlife.

Keywords: wildlife rehabilitation, post-release monitoring, telemetry, animal welfare

P151. Urban wildlife: Perils of the built environment and modified ecosystems

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Artificially created water bodies and altered natural landscapes can attract and sustain populations of water birds. Although some are created primarily for human recreational purposes, they can also result in habitat suitable for wildlife. However, variable conditions can result in sub-optimal habitats leading to disease in wildlife. Mortalities in town recreational lakes or wildlife reserves result in heightened public awareness, and pressure on authorities to act. Deaths in birds were investigated to identify any causal factors relevant to the urban environments so advice could be given regarding control measures. Members of the public and bird reserve wardens are encouraged to report dead wild birds to the government for avian influenza screening. Many of these are collected and tested. As part of our surveillance for new and emerging wildlife diseases, a proportion are examined to determine the cause of death, but not all events can be investigated further. Here we report details of investigations into deaths of waterfowl on town lakes, often built in the Victorian era, and at a rare inland salt marsh ecosystem formed by human-induced subsidence due to salt mining. The investigation involved postmortem examination, laboratory testing, visits to collect samples and meetings with stakeholders to identify risk factors and plan control measures.

In one year at 12 locations described as town boating lakes or similar, avian botulism was suspected due to the clinical history and lack of pathological findings. What was unusual was the number of similar locations with similar outcomes in the same year which was the hottest on record for England. Correspondence with local authorities revealed similar histories of low rainfall, low water levels and poor water quality. Confirming the diagnosis was challenging due to the decomposition of carcases. In subsequent cases, visits were made to affected water bodies, including a wildlife reserve. Factors identified included silting up of lakes, suspect sewage ingress into the water, provision of excess feed by the public, rotting bird carcases, poor water level control, constraints on funds for maintenance and the difficulties managing a site with competing wildlife priorities.

Botulism in wild birds on urban lakes is not a new phenomenon, but hotter drier summers may increase incidents. The report illustrates the continued need for advice for stakeholders in the urban setting to provide evidence to support management operations to decrease the risk to wildlife.

Keywords: Avian botulism, poor water quality

P152. Dogs, Tourism, and Wildlife Disease: Mapping Transmission Potential at High-Visitation Natural Protected Areas

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The presence of domestic dogs in natural protected areas (NPAs) has become increasingly controversial. Dogs often engage in bidirectional interactions with wild carnivores, potentially posing a threat to biodiversity through the spread of pathogens. In highly visited NPAs, there exists a dearth of information regarding health status management of dogs and other pets accompanying visitors or roaming around visitors' accommodations. Our objective is to address knowledge gaps on the presence and potential impact of dogs (and cats in Doñana) on the health of wild carnivores in NPAs.
The study is part of a Pilot Study, including the parks La Mandria, in Italy and Doñana National Park, in Spain. Data on prophylactic measures against transmissible diseases were collected through interviews to dog owners in Paneveggio Pale di San Martino Natural Park (SMP), Italy, throughout a two-year period. Dogs and wild carnivores' droppings were collected from high- and low-tourist traffic transects (n=12) to detect relevant helminth parasites with copro-microscopic examination and major viral pathogens with biomolecular assays. Pathogens' detection frequency was calculated.
Data refer to the first year in SMP. Based on 357 interviews, at least 70% of dogs underwent prophylaxis for endoparasites, and 45-89% underwent vaccination considering different protocols. 199 dogs', 86 red foxes', 56 mustelids' and 6 wolves' droppings were collected through 56 transect repetitions. Positivity rates of helmintic infections were low in dogs (*Capillaria* spp., 3.0%; *Trichuris vulpis,* 0.5%; *Toxocara canis*, 0.5%). Wild carnivores showed moderate to low prevalence for *Capillaria* spp. (37.8%), *T. canis* (20.3%), *T. vulpis* (2.7%), and Taeniids (1,35%). Dogs were positive for: CCoV (2.52%), CanineCV (2.02%) and CPV (0.50%). Wild carnivores were positive for CCoV (0.65%) and AMDV (0.65%). All samples were negative for CAdV-1/2 and CDV.
In the SMP context the low positivity rates in dogs suggest a negligible role in transmitting pathogens to wild canids. Proper application of prophylactic measures in health management of owned dogs is a key element in reducing such impact.

Keywords: Wild carnivores, pathologies, dog health, EUPAH&W

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P153. Complete genome sequencing of Arctic-like canine distemper virus from puppies with acute neurological signs in Romania

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Canine distemper virus (CDV) is a highly contagious virus that poses a significant threat to domestic dogs and wild carnivores globally. Despite the long-term availability of vaccines, reports indicate a re-emergence of the virus in various regions. The Arctic-like lineage, commonly found in wild animals, has been increasingly identified in domestic dogs, demonstrating a broader global distribution. This study aimed to perform the genetic characterization of CDV lineage from two partially immunized puppies in Romania exhibiting severe neurological symptoms.

Brain samples were collected from two young dogs (2.5 and 3 months old) from Timișoara, Romania, presenting with seizures, ataxia, and lethargy in 2023. The CDV complete genomes were sequenced using an amplicon-based sequencing protocol on Oxford Nanopore sequencing platform. Phylogenetic analyses were conducted using complete genomes and H gene datasets.

Phylogenetic analysis clustered both Romanian sequences within the Arctic-like lineage of CDV. The two sequences were nearly identical, suggesting the local spread of the virus. The H gene of the study strains exhibited the highest genetic identity to an isolate from a Serbian golden jackal (*Canis aureus*) collected in the same year. These findings indicate ongoing circulation of Arctic-like CDV among in the wildlife within Balkans and a complex transmission network involving various carnivore species across Europe.

To our knowledge, these sequences represent the first two complete CDV genomes from Romania deposited in GenBank. The detection of CDV in partially immunized puppies highlights the risks of incomplete vaccination protocols. These genomic data provide valuable insights for monitoring CDV evolution and its circulation and impact in domestic and wild carnivores.

Keywords: *Paramyxoviridae*, *Morbillivirus*, *Morbillivirus canis*, Arctic-like lineage, Oxford Nanopore Technologie

P154. Circulation of CPV-2 in red foxes (*Vulpes vulpes*) in Slovakia: molecular detection, virus isolation, and the role of red foxes as reservoirs

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The transmission dynamics of CPV are influenced by ecological interactions between wildlife and domestic animals. Domestic dogs frequently encounter wild carnivores in forested habitats, during hunting, or near farms, and habitat loss and fragmentation further increase these contacts as carnivores adapt to human-modified landscapes and exploit anthropogenic food sources. Such adaptations may facilitate interspecies transmission and underscore the role of wildlife in CPV circulation.

To investigate CPV-2 circulation, we examined 221 red foxes (*Vulpes vulpes*). Small intestine samples (n = 72), rectal swabs (*n* = 84), and fecal samples (*n* = 65) were analyzed by real-time PCR. Positive samples were subsequently characterized by Sanger sequencing. For each sample, four overlapping amplicons were assembled to reconstruct the full-length *VP2* gene sequence (1,755 bp). Virus isolation was performed using MDCK cells.

CPV DNA was detected by real-time PCR in 24/221 (10.9%) red fox samples. Positive findings were recorded in 13/84 (15.5%) rectal swabs, 9/72 (12.5%) intestinal samples, and 2/65 (3.1%) fecal samples. Phylogenetic analysis identified CPV-2a in 7/24 (29.1%) samples, CPV-2b in 16/24 (66.6%), and CPV-2c in 1/24 (4.1%). CPV-2a and CPV-2b isolates clustered with European strains, whereas the CPV-2c isolate was assigned to the "Asian" lineage. Several sequences exhibited "Asian-like" molecular signatures (5G, 267Y, 324I, 370R), suggesting transboundary introduction of CPV and spillover into wild carnivores. Infectious virus was successfully isolated from all positive samples and produced characteristic CPV-associated cytopathic effects in cell culture.

This study provides the first evidence of CPV-2 circulation in free-ranging carnivores in Central Europe. The identification of CPV-2a, CPV-2b, and CPV-2c variants, including "Asian" lineages, demonstrates substantial genetic diversity and suggests that wild carnivores may contribute to virus dissemination, highlighting the risk of interspecies transmission and the need for continuous surveillance.

Keywords: canidae, carnivores, CPV-2, phylogenetic analysis, interspecies transmission

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P155. Progressive respiratory complications following presumed air sac rupture in a rehabilitated juvenile mute swan (*Cygnus olor*): from trauma to aspergillosis

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This case report describes the progressive clinical deterioration of a juvenile mute swan and discusses the endpoint decision-making process leading to euthanasia.
A juvenile mute swan *(Cygnus olor)* was admitted on 16 September 2025 following trauma in Cluj-Napoca city, Romania. Clinical examination followed by hematology, biochemistry, radiography, microbiology and coprology examinations were performed at multiple time points. Post-euthanasia gross necropsy and histopathological examination of tissue samples, using haematoxylin-eosin (HE) and periodic acid-schiff (PASS) staining, were performed to confirm the ante-mortem diagnosis.
On admission, the mute swan presented dehydrated and underweight (BCS ⅖), with mild neurological signs (astasia) and hypoglycemia. Subcutaneous emphysema indicative of abdominal air sac rupture was palpated on the left pre-femoral space. Coprological examination was positive for cestodes. Progressive weight loss to 5 kg necessitated assisted feeding (by gavage). On day 34, respiratory signs developed, nasal culture identified *Staphylococcus sciuri* and antibiotic therapy was initiated according to an antibiogram. Despite mild clinical improvement, repeated diagnostics on day 48 revealed persistent leucocytosis with heterophilia and monocytosis, worsening bilateral pulmonary infiltrates. Itraconazole (5 mg/kg PO) was initiated for suspected aspergillosis and administered for six weeks. During antifungal treatment, the animal was transferred to an outdoor aviary to reduce stress and allow physical activity. Discontinuation of the antifungal after partial improvement was followed by rapid clinical deterioration and weight loss. Necropsy confirmed bilateral pulmonary consolidation with multifocal haemorrhagic foci, caseous granulomas, and extensive airsacculitis. Histopathology revealed tissue-invasive hyphae with intact conidial heads, confirming disseminated aspergillosis with active sporulation.
After three months in captivity, release was contraindicated given the patient's failure to thrive, compromised physical condition, seasonal stressors, and high susceptibility to further infectious diseases after release. For wild waterfowl with clinical aspergillosis that rely on continuous antifungal therapy to maintain stabilisation, euthanasia followed by post-mortem diagnosis is likely the most humane and biologically justified endpoint. A bird unable to maintain condition without continuous medication is unlikely to survive the physiological demands of the wild.

Keywords: waterfowl, aspergillosis, decision-making, wildlife rehabilitation, necropsy

P156. Pathological changes of the yolk sac in mandarin duck (*aix galericulata*) naturally infected with avian pathogenic escherichia coli (apec)

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Wild waterfowl in aviculture may act as reservoirs of infectious agents. Avian pathogenic *Escherichia coli* (APEC) is an important cause of early mortality, primarily affecting the yolk sac and umbilical region. This study aimed to assess gross pathological changes in these tissues in naturally infected Mandarin duck (*Aix galericulata*) ducklings.

A total of 34 ducklings that died during the first ten days of life were included in the study. The ducklings originated from a private collection of 18 breeding pairs of Mandarin ducks. Each carcass was subjected to a detailed post-mortem examination, and gross pathological changes were recorded. External and internal examinations were performed, with particular emphasis on the umbilical region. Infection with avian pathogenic *Escherichia coli* (APEC) was confirmed using standard bacteriological methods.

External and internal examination of Mandarin duckling carcasses revealed pathological changes exclusively in the yolk sac and umbilical region. Necrotic changes in the umbilical region were observed in 21 dead ducklings (61.8%). Abnormal changes in colour, consistency, and odour of yolk sac contents were detected in 29 cases (85.3%). A patent (unclosed) umbilicus was recorded in 8 ducklings (23.5%). Petechial haemorrhages on the yolk sac wall were observed in 20 cases (58.8%), while vascular congestion of the yolk sac wall were present in 29 ducklings (85.3%).

The predominant pathological finding in deceased Mandarin duck (*Aix galericulata*) ducklings naturally infected with avian pathogenic *Escherichia coli* (APEC) was retention of the yolk sac accompanied by inflammation. Incomplete resorption of the yolk sac led to failure of umbilical closure, facilitating secondary infection and systemic dissemination of APEC. These findings suggest that clinically healthy adult breeding pairs may act as carriers and a potential source of infection for ducklings.

Keywords: Mandarin duck, *Aix galericulata*, APEC, yolk sac, omphalitis, mortality

P157. Multicentric Lymphoma with Concurrent Systemic Bacterial Infection in Two Captive Capybaras (*Hydrochoerus hydrochaeris*)

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Lymphoma is the most frequently diagnosed hematopoietic neoplasm in domestic carnivores, while reports in wild rodents are scarce. Here, we describe two cases of multicentric lymphoma in adult female capybaras, associated with systemic bacterial infections.
The first case involved a 5-year-old female capybara with a 7x4cm inguinal mass. Fine-needle aspiration (FNA) was not diagnostic revealing abundant fibrin and hemorrhages. After five months the animal died following moderate weight loss with inguinal and retroscapular lymphadenopathy. The second case involved a 6-year-old female capybara in good nutritional condition but with severe systemic pathology. Both animals died and fine-needle aspiration (FNA), gross examination, histopathology, immunohistochemistry (IHC) and bacteriological cultures were performed.
In the first case Post-mortem FNA showed a monomorphic population of large atypical lymphoid cells compatible with lymphoblasts, with necrosis and degenerate neutrophils. Gross examination revealed severe generalized lymphadenomegaly with lardaceous, haemorrhagic and necrotic lymph nodes, as well as serohemorrhagic abdominal, thoracic and pericardial effusions. Multifocal yellowish nodules were present in the liver and spleen. Additional findings included renal haemorrhages, pulmonary congestion and edema, meningeal vascular congestion, and caudal vena cava dilation. Histopathology of lymph nodes, spleen, liver, heart, brain, and lungs revealed replacement infiltration by large pleomorphic lymphocytes with moderate atypia, and mitotic activity (up to 2 mitoses per high-power field-2.73mm2). IHC performed on lymph nodes, spleen and liver demonstrated a T-cell phenotype, with up to 60% of neoplastic cells CD3-positive. Tumor-associated-macrophages (TAMs) were also investigated by means of CD204, CD168, iNOS and MAC387 IHC. *Salmonella typhimurium* was isolated from lymph nodes as well as liver. In the second case necropsy revealed diffuse lymphadenomegaly, splenomegaly, necrotic hepatic lesions, fibrino-hemorrhagic abdominal effusion, gastric ulceration, and intestinal lesions. Histology confirmed widespread infiltration of neoplastic lymphoid cells in lymph nodes, spleen, liver, intestine, brain, and vascular lumina, with moderate atypia and high mitotic activity (up to 4 mitoses per high-power field). Concurrent systemic bacterial infection was present with *Salmonella hessarek*, *Escherichia coli* and *Staphylococcus aureus* isolated from multiple organs. Neoplastic cells were moderately immunopositive for CD79a with IHC demonstrating a B-cell phenotype. TAMs were also investigated with IHC in this case.
These cases represent the first documented multicentric lymphoma in Italian captive capybaras, highlighting its aggressive behavior. Lymphoma-associated immune dysregulation likely promoted systemic bacterial infections. The cross-reactivity of commercial antibodies supports their diagnostic use in this species. Overall, findings stress the importance of pathological monitoring to better understand lymphoma in captive capybaras.

Keywords: *Hydrochoerus hydrochaeris,* capybara, multicentric lymphoma

P158. Endoparasite finding in European Hedgehog (*Erinaceus europaeus*) in two regions on north Serbia

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The European hedgehog is one of the most widespread animal species in nature. Its presence can be registered in nature (outside urban areas) but also in settlement areas, including cities. The way of eating (belongs to omnivores) and life of the European hedgehog, enables it to easily adapt to different environmental conditions, which has led to its noticeable presence in urban areas and their suburbs. Since urban hedgehogs can be considered omnivores with scavenging behavior (eating dead small animals and leftover food), monitoring the presence of hedgehog populations in the city, due to possible contact with humans, is also important for health reasons. Hedgehogs can be carriers of some biotic factors that can affect human health: dermatophytes, ectoparasites (fleas, ticks and mites) and bacteria (salmonella, listeria). As the subject of our work, our investigation is related to the parasitological analysis of hedgehog feces. The aim of the work is to determine whether endoparasites can be found in the European hedgehog in the urban environment, if there are any, which species are present and whether some of the found parasite species can endanger human health.
A total of 12 faecal samples collected over a year at two urban sites were examined. Hedgehogs were kept in an isolated area overnight for sample collection, after which they were returned to their primary habitat and released at the capture site. Coprological diagnostics were performed using standard parasitological methods (flotation and sedimentation) using a saturated sodium chloride (NaCl) solution.
The presence of endoparasites was detected in all 12 faecal samples examined (100%). Coccidia oocysts and endoparasite eggs were found: *Capilaria* sp. (*C. putori*), Cestodes (*Hymenolepis nana*), lung parasites (*Crenosoma striatum*).
The examination revealed the presence of eggs of two different species of nematodes and one species from the cestode class, as well as protozoan oocysts. Identified eggs of Hymenolepis nana can pose a threat to human health in a milder or more severe form. They belong to the group of dwarf tapeworms that can complete their life cycle in one host, which is why it spreads relatively easily and can most often endanger children.

Keywords: Key words: European hedgehog, endoparasites, human health

P159. Higher haemoparasite prevalence in the urban wall lizards *Podarcis muralis*

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Human-driven landscape transformation, especially urbanization, strongly affects ecosystems worldwide. In urban environments, both abiotic and biotic factors can be profoundly altered, including interaction between species. Although often overlooked, these changes can also impact host-parasite relationships, potentially leading to cascading effects on urban populations and ecosystems. Reptiles represent a particularly understudied system in this context.
We sampled haemoparasites (through blood smears) from the common wall lizard *Podarcis muralis* differentiating between urban (n=122) and non-urban (n=90) locations in Croatia. For each individual, we also counted the number of ticks present on the lizard and obtained the impervious surface area (ISA) as a proxy of urbanization level with a 25m buffer around capture location. We quantified the percentage of infected erythrocytes microscopically through blood smear screening.
We found a higher prevalence of infection in urban populations. While 62% of individuals in urban sites were infected, only 24% of non-urban lizards were infected. Prevalence was also higher with increasing ISA. Males were more often infected than females regardless of the habitat. All parasites were recognized as belonging to the genera *Karyolysus*, *Hepatozoon* or *Schellackia*. Infection intensities ranged from 0.02% to 1.6%, but infection intensity did not differ significantly between urban and non-urban lizards. Finally, there was no correlation between the numbers of ticks found on the individuals and the number of haemoparasites.
Lizards sampled at urban sites were significantly more likely to be infected compared to lizards living in non-urban areas. However, the parasitic load does not seem to correlate to the level of urbanization. Future studies should disentangle which factors affect parasite prevalence in urbanized sites and their influence onvector and host abundance and ecology.

Keywords: haemogregarines, reptiles, urbanization, anthropogenic pressure, parasitaemia

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P160. Spontaneous Neoplasia in Zoo Animals: Gross and Histopathological Findings from a Case Series

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Neoplastic diseases in zoo animals represent a growing area of interest in veterinary pathology. Tumors arise from complex evolutionary and ecological interactions between hosts and their environments, and their occurrence in captive wild species poses unique diagnostic and clinical challenges. Despite increasing reports of neoplasia in zoo collections worldwide, systematic case series remain scarce, particularly in European institutions. This work aims to contribute to the characterization of neoplastic lesions in zoo animals by describing a case series diagnosed at necropsy.
All cases were diagnosed at post-mortem examination. Gross pathological findings were recorded, and tissue samples were collected for histopathological analysis. Samples were fixed in 10% neutral buffered formalin, routinely processed, and stained with hematoxylin and eosin.
Four cases of neoplasia in zoo animals are reported. The first case involved an intestinal carcinoma in an African lion (*Panthera leo*). The second case concerned the co-occurrence of two distinct neoplasms in the same individual, a thyroid tumor and a laryngeal squamous cell carcinoma, in a South American sea lion (*Otaria flavescens*), representing a rare simultaneous presentation of multiple primary tumors. The third case described a fibroma in a common hippopotamus (*Hippopotamus amphibius*). Additionally, a disseminated carcinoma was identified in a wild mallard (Anas platyrhynchos), highlighting the occurrence of spontaneous neoplasia in free-ranging waterfowl.
This case series illustrates the diversity of neoplastic conditions affecting zoo animals across taxonomically distinct species. Post-mortem examination proved essential for the definitive diagnosis of all cases, underscoring the importance of systematic necropsy protocols in zoo medicine. These findings contribute to the growing body of knowledge on tumor pathology in captive and wild animals and highlight the relevance of comparative oncology for both animal and human health.

Keywords: neoplasia; zoo animals; necropsy; comparative oncology; captive wildlife

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