11th SYMPOSIUM OF THE BWDS

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16 October 2026

Royal Museum for Central Africa

Leuvensesteenweg 13, 3080 Tervuren

One World, One Wildlife Health

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AFRICA museum

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ABSTRACT BOOK
'One World, One Wildlife Health'

11th Symposium:
Belgian Wildlife Disease Society

16th of October 2026
Africa Museum, Tervuren, Belgium

Organizing and Scientific Committee:

Tim Adriaens, Kristof Baert, Valérie De Waele, Famke Jansen, Stefan Roels, Paul Tavernier, Naomi Terriere

Abstract book edited by Naomi Terriere & Kristof Baert

Introduction

Africa and Europe - with focus on Belgium - share a common controversial history. Worldwide, expanding intercontinental exchanges led to economic and cultural "globalization" by the end of the 20th century. In the same time period the world population boomed unprecedentedly. Together, these dynamics opened new interfaces for possible ecologic and health issues. On top of all this, rapid climate change and the ever stronger and more frequent El Niño events, are completing the list of ingredients for a real box of Pandora containing substantial threats to biodiversity and human and animal health. Many of the consequences became visible in the last decades. The dramatic level of biodiversity loss is thought to stand for the earth's 6th mass extinction event. Such events result in ecological reorganization, and differ from baseline extinctions, occurring more regularly in earth's history. In the health field, we witness large scale infectious disease outbreaks, some of them evolving to pandemics. Less highlighted threats are the far reaching effects of chemical pollution, many of which are not recognized or staying under the radar. Others came into the picture, like the microplastics saturation of the oceans, with a dramatic impact on marine life.

The surveillance tools to detect what goes wrong - or to predict what could go wrong - are widely available now, allowing to create awareness, which is the first step towards developing resilience strategies. But usually these alerts fail to reach those who should hear them, and lose their power by keeping on circulating amongst those who don't have to be convinced anymore. The ongoing One Health anomalies are still not enough considered as priorities. Moreover, global problems need global solutions, and this is beyond any doubt where we reach the limits of what can be done in trying to turn the tide. In a politically divided world full of conflicts, getting all noses pointed in the same direction appears utopic.

Despite the perhaps limited reach of this symposium, it offers an opportunity within our possibilities to keep the discussion animated, in line with the objectives of the BWDS. Hoping to get the message delivered to those who can make the difference is maybe too much "wishful thinking".

But never say never, "*The man who moves a mountain begins by carrying away small stones"* (*Confucius).* Wildlife health and wildlife-borne diseases are inherent in talking about biodiversity. Disturbances are linked to (past and present) interactions between man and environment. In this broad context, the Africa Museum represents

the perfect venue for a multidisciplinary "One world, One wildlife health" conference, a more appropriate location would have been hard to find. We are extremely grateful to the direction and staff of the Africa Museum for the privilege of having been able to organize our 11th Symposium here.

The subjects are arranged under four sub-themes: the trade in wildlife and its impacts, emerging viral diseases, the sustainable control of vectors to mitigate vector-borne diseases, and captive breeding projects for "rewilding". The subjects were selected in function of their relevancy for the Symposium theme, while trying to avoid the frequently highlighted topics. We insist on thanking the eminent speakers who accepted our invitation with much enthusiasm. A number of "free slots" in the program are reserved for poster presenters selected by our scientific committee, allowing them to present orally. Besides, the best poster presentation will be awarded.

Sepelá na mokolo oyo! We wish you all an enriching, thought provoking and convivial symposium!

For the organizing committee,
Paul Tavernier

Programme

09.00–09.30 Registration and coffee

Moderators: Tim Adriaens (INBO) & Naomi Terriere (BWDS)

09.30 Welcome: T. Huyse (Africa Museum) & S. Roels (BWDS)

Session 1: Wildlife Trade

09.40 Keynote – Cultural background of bushmeat, the anthropological approach (T. Trefon, Africa Museum, BE)

10.15 CITES: Wildlife trade from Africa and its impact (C. Ceusters, CITES, BE & A. Laudisoit, UA, BE)

10.40 Poster pitches: H. Broes, F. van der Wal & S. Leen

11.00 Coffee break + posters

Session 2: Old & New viruses marching in

11.25 Flaviviruses circulating in The Netherlands (J. Vd Brand, UUtrecht, NL)

11.50 Ebola, a re-emerging epidemic (S. Gryseel & C. Mande, UA, BE)

12.15 Drivers of paramyxovirus diversity in African small mammals (S. Gryseels, UA, BE)

12.40 Lunch + posters

Session 3: Living with vectors

13.40 Sterile Insect Technique in control of the Asian Tiger Mosquito: experiences and perspectives (A. Ignjatović Ćupina, UNS, RS)

14.05 Vector control in Belgium: current status and emerging solutions (W. Van Bortel, ITG, BE & V. Versteirt, ANB, BE)

14.30 Poster pitches: E. Goossens, L. Durán Illán & B. André

14.50 Coffee break + posters

Session 4: Conservation projects

15.20 Captive breeding projects at Antwerp Zoo/Planckendael (F. Verstappen & S. Lafaut, KMMA, BE)

15.45 Reintroduction of the Green Tree Frog in Wallonia (A. Robise, Natagora, BE)

16.00 Reintroduction of the Garden Dormouse (D. De Keukeleire, INBO, BE)

16.15 Poster pitches: D. Rockx-Brouwer, T. Cooreman & S. Schneemann

16.30–18.00 Final remarks, poster prize & reception

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  - Impact assessment and risk analysis
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Faced with the resurgence of infectious diseases, with damaging economic and social consequences, it is vital to have robust data available that reflects the reality in the field at any given time. For the authorities in charge of managing and resolving health crises, comprehensive scientific advice based on validated objective data is just as important.

Sciensano is a public scientific & research institute. Our strength lies first and foremost in our combined – and recognised – expertise in human, animal and environmental health. Furthermore, we are the only scientific institute for public health in Europe accommodating both human and animal health under the same roof to operate from a *One Health* perspective, which emphasises the interconnection between human health, animal health and the wider environment.

This inspires the work of our 1,000 employees, making Sciensano your privileged partner in uniting science, health and society.

PUBLIC HEALTH MISSIONS SERVING THE COMMUNITY

Sciensano's primary mission is to detect any elements likely to constitute a health risk, to monitor their evolution and to contribute to their elimination, based on knowledge and data. To achieve these goals, we align our priorities with those of the authorities and our stakeholders at national, European and international levels.

We carry out numerous research projects to ensure that our scientific expertise is continually evolving in line with the latest technologies and innovations. Our research activities are paramount to maintaining and consolidating the recognition of our expertise, both in Belgium and internationally.

In addition to supporting decision-makers and our motivation to improve scientific knowledge in our areas of expertise, our activities and missions are above all committed to anticipating future health challenges.

A WIDE RANGE OF SCIENTIFIC EXPERTISE AREAS

Sciensano's surveillance activities rely on 9 main areas of expertise: biological risks, quality control, infectious agents for humans and animals, chemical hazards, physical hazards, health data, public health, health systems, and support in the event of a health crisis.

Through these nine areas of expertise, Sciensano works to protect the health of the population and livestock by assessing and monitoring a wide range of risks. We also monitor the quality of health products and services, assess the status of health and healthcare in Belgium, and actively contribute to prevention and health promotion initiatives.

AN INTERNATIONAL OUTREACH

As Belgium's focal point in a wide range of fields, Sciensano works with the main international organisations on research projects, on human and animal surveillance activities, as part of partnerships, and by providing scientific services.

Some of the most important of these partnerships are with UN agencies (such as the World Health Organisation, the World Organisation for Animal Health and the Food and Agriculture Organization), the International Association of National Public Health Institutes, the Pasteur Network, and numerous European agencies.

Oral Presentations

Cultural background of bushmeat, the anthropological approach

T. Trefon
Royal Museum for Central Africa, Belgium

Abstract

Bushmeat is a complex and contested natural-resource issue in Central Africa. Far from being simply a question of wildlife conservation, the hunting, consumption and commercialization of wild animals are deeply embedded in local livelihoods, cultural practices, food security, markets and relations between rural communities and the state. Central to this conference, public health threats from zoonotic diseases need considerable new research. These interconnected priorities place the use of wild animals within the broader social, political and economic realities of the Congo Basin.

Drawing on extensive field-based research and a social-science perspective, my research challenges approaches that portray bushmeat primarily as an environmental threat or as the consequence of local ignorance and poverty. It instead asks how people understand, use and value wildlife, and how changing economic circumstances, demographic pressures, urbanization, infrastructure development and expanding markets are transforming patterns of hunting and consumption. Particular attention is given to the relationship between rural hunting and urban demand, showing how bushmeat moves through networks linking villages, traders, transporters, restaurants, brokers and consumers.

The *Bushmeat* book explores the governance of wildlife resources. Formal conservation policies, protected areas and hunting regulations frequently coexist with customary institutions, informal rules and locally legitimate practices. The resulting institutional pluralism generates tensions when conservation measures restrict access to resources on which communities depend. I place bushmeat governance within wider questions of state–society relations, political economy, local authority and benefit sharing.

Rather than offering a simple choice between conservation and consumption, *Bushmeat* highlights the need to understand the social systems that sustain wildlife use. It argues for approaches that take local knowledge and livelihood strategies seriously while addressing the commercial pressures that can drive unsustainable exploitation. The book ultimately presents bushmeat as both a conservation challenge and a significant social, economic and governance issue, requiring policies that reconcile biodiversity protection with the realities of the people who live in and around Central Africa's forests.

Short Bio

Trefon (PhD in African Politics, Boston University) has devoted his career to the political economy of natural resources, environmental governance, state–society relations, and social science research methods. An Emeritus researcher at the Royal Museum for Central Africa (Belgium), he is currently an Associate at The Policy Practice (UK), a consultancy firm specializing in Political Economy Analysis. Dr. Trefon has conducted more than 130 field-based assignments across Central Africa, encompassing research, project evaluation, programme coordination, and teaching. His work is grounded in qualitative, anthropological approaches that prioritize community perspectives on natural resource governance. A contributing editor to the Review of African Political Economy, he has authored numerous books and more than 100 scientific papers. He is fluent in English and French and has a solid working knowledge of Lingala.

CITES: wildlife trade from Africa and its impact. Beyond Border: wildlife trade, disease risks and policy blind spots

C. Ceusters; A. Laudisoit
Belgian CITES Authority, Belgium; University of Antwerp, Belgium

Abstract

Africa's wildlife trade includes live animals, trophies and animal products, but also timber, and plants. Through legal and illegal channels, specimens move within interconnected transport, permit, commercial and digital networks. Their consequences extend beyond biodiversity loss and animal welfare: trade also creates pathways through which pathogens, parasites, invasive species and contaminated materials can cross borders and affect wildlife, forests, agriculture, domestic animals and people. Drawing on CITES records, with particular attention to Belgium and evidence from trade flow from Africa, this talk asks how illegally or unsustainably sourced specimens enter apparently legal chains. CITES permits remain essential, but they cannot replace proof of legal acquisition, robust non-detriment findings, correct identification, traceability, importer due diligence or veterinary and phytosanitary safeguards. Illegal shipments usually bypass declared quarantine, inspection and treatment altogether. Even regulated shipments of plants, timber, trophies or live animals cannot be assumed free of hidden organisms: insects may remain inside wood or skulls, while soil, roots, bark and packaging may carry fungi, bacteria, nematodes, seeds or other invasive organisms. Treatment and visual inspection reduce specific risks but do not detect or eliminate every hazard. The Vantara case, trophy hunting, African timber, orchids and South Africa's rare succulents illustrate why documentary legality cannot automatically be equated with verified provenance, biological safety or conservation benefit. Digital platforms further stimulate demand and move transactions into private channels. Mpox provides another warning: legally traded animals contributed to a virus crossing species and continents. While zoonotic diseases, pests and invasive species are discussed under the CITES-convention, they remain outside of the scope of the convention and countries remain responsible for preventing zoonotic spillover. CITES-permitting, blanket bans or content removal cannot fully prevent the spread of zoonotics. This talk thus suggests a practical One Health and whole-of-government response connecting CITES, customs, veterinary and phytosanitary services, public health, forestry, conservation, law enforcement and digital authorities through risk-based inspection, testing, quarantine and treatment; documentary, biological and digital traceability; independent verification; animal-welfare safeguards; anti-corruption measures; and community engagement.

Short Bio

C. Ceusters is a biologist by training and studied at KU Leuven. For the past five years, worked as a scientific adviser for the Belgian CITES Authority, which is responsible for implementing the Convention on International Trade in Endangered Species of Wild Fauna and Flora. Within this role, he coordinates the Belgian CITES Scientific Committee and provides scientific advice on the import, export and transit of CITES-protected animal and plant species. He is responsible for the representation of the Belgian CITES Scientific authority to take part in related negotiations at national, European and international level, with the aim of strengthening the protection of these species and listing additional species under CITES. Given the presence of the Port of Antwerp, their work has a strong focus on tropical timber. However, as CITES covers a wide diversity of taxa and forms of trade, the team is occupied with many different topics.

A. Laudisoit is a wildlife biologist, eco-epidemiologist and a National Geographic Explorer, whose work focuses on neglected, emerging zoonotic and vector-borne diseases in remote and under-resourced environments. She holds a PhD in plague epidemiology from the Universities of Liège and Antwerp and has accumulated more than 20 years of experience investigating pathogen spillover and wildlife disease ecology at the human-wildlife interface. She has led numerous wildlife inventories, epidemic investigations, and conservation initiatives in under-explored areas of the northeastern Democratic Republic of Congo, contributing to documenting poorly known chimpanzee populations and improving surveillance for diseases such as plague, mpox, and onchocerciasis-associated epilepsy.

Flaviviruses circulating in The Netherlands

J. van den Brand
Utrecht University, the Netherlands

Abstract

Arboviruses such as Usutu virus (USUV) and West Nile virus (WNV) are emerging zoonotic diseases that are a threat for human and animal health. Eurasian blackbirds are highly susceptible to develop severe disease after natural USUV infection with high mortality. Other bird species show differences in the pathological patterns and outcome of disease after natural infection that may account for different roles in the USUV transmission cycle. The current outbreak of WNV in the Netherlands causes mortality in corvids and demonstrates the impact of emerging flaviviruses on wild animal species with a risk for human and animal health.

Short Bio

J. van den Brand is an associate professor, veterinary pathologist and director of the Dutch Wildlife Health Centre at the Division of Pathology in the Department of Biomolecular Health Sciences of the Faculty of Veterinary Science at the Utrecht University in the Netherlands. She is currently working on (emerging) zoonotic (viral) diseases such as Usutuvirus, West Nile virus, Coronavirus, Influenza virus, Lyssavirus and Bornavirus, with the focus on wildlife and is interested in the role of co-infections on the outcome of disease.

Ebola, a re-emerging epidemic

S. Gryseels; C. Mande
University of Antwerp, Belgium

Abstract

The biological and ecological mechanisms underlying filovirus emergence and zoonotic spillover remain poorly understood. Serological, molecular and genomic evidence demonstrates Orthoebolavirus and Orthomarburgvirus circulating among wildlife, livestock and humans, including recurrent Orthoebolavirus epizootics in wild non-human primates, particularly in African ecosystems with high biodiversity. Antibodies and viral RNA detected in diverse African bat species support their role as candidate reservoir hosts. Their mobility, longevity, social organisation and immune adaptations may favour viral persistence and influence viral-load dynamics, yet the determinants of infection and shedding remain unclear. This gap is particularly evident in the Democratic Republic of Congo, where our field investigations from Kikwit (1995) to Ituri-Haut-Uélé (2026) have not detected active infection in sampled wildlife despite recurrent human outbreaks, indicating that viral maintenance may depend on host and environmental factors that vary across space and time. How do host traits, physiological state and environmental conditions shape reservoir competence? This is a challenging yet crucial question, as most filovirus surveillance relies on reactive responses, underscoring the need for predictive approaches. We therefore propose coordinated sampling across Afrotropical ecosystems where filovirus spillover recurs, spanning Central, East and West Africa. A spatially structured and seasonally repeated design across wildlife hotspots, combined with molecular diagnostics, standardised bat sampling and opportunistic sampling of syntopic wildlife, including faecal material, rodents and arthropods, can elucidate potential cross-species transmission interfaces and reconstruct host-virus networks. Linking these data with host traits, habitat and landscape characteristics can improve spillover-risk predictions, supporting targeted surveillance, risk assessment and public-health preparedness.

Short Bio

S. Gryseels is an evolutionary biologist and affiliated with the Evolutionary Ecology group at the University of Antwerp and the Operational Directorate Taxonomy and Phylogeny at the Institute of Natural Sciences in Brussels. Her research focuses on uncovering the natural diversity of viruses in wildlife and assessing the risk of virus spillover. Alongside fundamental research on the evolutionary ecology of wildlife viruses and their hosts, she conducts applied research on the wild meat trade to inform policy.

C. Mande is a biologist and postdoctoral researcher affiliated with the Evolutionary Ecology Group at the University of Antwerp, Belgium, and the Biodiversity Monitoring Centre (CSB) at the University of Kisangani, Democratic Republic of the Congo. His research focuses on how land-use change affects wildlife communities, particularly bats, and habitat conditions for potential hosts of zoonotic pathogens. He further investigates the potential of bioacoustic approaches to support ecological monitoring, wildlife surveillance and zoonotic disease risk assessment.

Drivers of paramyxovirus diversity in African small mammals

S. Gryseels
University of Antwerp, Belgium

Abstract

Paramyxoviridae comprises 153 species of unsegmented, negative-sense RNA viruses in 23 genera and nine subfamilies, including major human pathogens (measles, mumps, parainfluenza viruses) and veterinary pathogens (Newcastle disease, canine distemper, peste-des-petits-ruminant viruses). Only a handful are known to be zoonotic: Hendra, Nipah, Menangle and Sosuga viruses from bats, and Langya virus from shrews. Yet paramyxoviruses are widespread in wildlife, and assessing their spillover risk requires knowing their natural diversity, how occurrence varies across hosts and regions, and in which situations host switching occurs most readily. We assembled published paramyxovirus detection data from mammals and combined these with our own screening of several thousand small mammals from the Democratic Republic of Congo, Tanzania, Mozambique and Rwanda, yielding over twenty thousand records of tested animals from six continents. Detection frequency varies widely within and between studies: taxa with high prevalence in one study show low prevalence in others, or at other locations. Different laboratory assays explain part of this variation, but locality effects persist even within studies, with prevalence in a single rodent species ranging up to 20-fold across sites. Across studies and methods, however, paramyxoviruses are detected most frequently in Eulipotyphla (predominantly *Parahenipavirus*), followed by rodents (*Jeilongvirus*), and least often in bats (*Henipavirus*, rubulaviruses); among well-sampled rodent genera, *Lophuromys* and *Acomys* greatly exceed *Mus* and *Praomys*. Phylogenetic analyses reveal strong host fidelity throughout the family, although host switching also occurs; because this pattern is consistent across the tree, spillover risk may be distributed evenly across lineages rather than concentrated in *Henipavirus*, *Parahenipavirus* and the rubulaviruses, as currently assumed. Multiple lineages, within and across genera and subfamilies, can co-circulate in the same host species and locality. Host species diversity is thus the largest driver of paramyxovirus diversity, and Eulipotyphla the most frequently infected host group.

Short Bio

S. Gryseels is an evolutionary biologist and affiliated with the Evolutionary Ecology group at the University of Antwerp and the Operational Directorate Taxonomy and Phylogeny at the Institute of Natural Sciences in Brussels. Her research focuses on uncovering the natural diversity of viruses in wildlife and assessing the risk of virus spillover. Alongside fundamental research on the evolutionary ecology of wildlife viruses and their hosts, she conducts applied research on the wild meat trade to inform policy.

Sterile Insect Technique in control of the Asian Tiger Mosquito: experiences and perspectives

A. Ignjatović Ćupina
University of Novi Sad, Serbia

Abstract

The Asian Tiger Mosquito (ATM) is one of the most important invasive vector species globally. During the last decades, this mosquito species was introduced in many European countries, including Serbia. Conventional mosquito control measures alone cannot provide sufficient effectiveness. With the support of the International Atomic Energy Agency (IAEA RER5026), the first pilot study on Sterile Insect Technique (SIT) in control of ATM was conducted in Novi Sad, Serbia in 2022 and 2023, at an area of 30 ha. Sterile males were produced at Centro Agricoltura Ambiente "Giorgio Nicoli", Crevalcore, Italy, shipped and released on weekly intervals (in total 4 rounds, 200 000 males in 2022; 8 rounds, 800 000 males in 2023). Males in each shipment were marked by different dye to enable their tracking. The study was conducted in two phases: i) Mark- Release-Recapture trial (2022), with releases done from the center of the area - to identify the flight range, longevity of sterile males and wild/ sterile male ratio; ii) Suppression trial (2023), with releases conducted at multiple points - to determine the effects of SIT. Adult samplings were performed at the post release days 1, 2, 4 and 6 (MRR trial) and once weekly (suppression trial), applying the electric aspirator for 5 min at each sampling point. Egg sampling was performed on a weekly basis, using ovitraps. Egg sterility was recorded after the hatching procedure. Induced egg sterility was determined based on differences of the hatching rate in the release and untreated area. The average flight range of sterile males was 53 m and 96.7% of recaptured sterile males could survive for at least one week. Wild/ sterile male ratio (1:7 in 2022; 1:8 in 2023) ensured competitiveness of sterile males. With only 8 release rounds in 2023, the induced sterility was already detected after the 3rd round, reaching the peak of 51.5% after the 7th round. The study results justified perspectives for the integration of SIT in the control of ATM.

Short Bio

A. Ignjatović Ćupina is Full Professor of Entomology, Head of the Centre of Excellence One Health- Vectors and Climate and Head of the Laboratory for Medical and Veterinary Entomology at the Faculty of Agriculture, University of Novi Sad, Serbia. Her research interests are mainly focused on bloodsucking Diptera (true flies), on mosquitoes (Culicidae) and blackflies (Simuliidae): identification, ecology, behavior, monitoring, species distribution, implementation and evaluation of environmental friendly control strategies. Over the past decades she participated in many national and international scientific projects, and as an invited expert teacher/trainer she was involved in several international training courses in Medical and Veterinary Entomology. She also participated to few regional and national projects - supported by the International Atomic Energy Agency (IAEA), and currently, one of her main scientific interests regards the Sterile Insect Technique (SIT) and its integration in the control of invasive mosquito species in Serbia.

Vector control in Belgium: current status and emerging solutions

W. Van Bortel; V. Versteirt
Institute of Tropical Medicine Antwerp, Belgium; Agency for Nature and Forests, Flemish Government, Belgium

Abstract

In recent decades, Europe has experienced important changes in the epidemiology and distribution of vector-borne diseases (VBD), driven by factors including globalization, trade, travel, climate change, and changes in land use. The increase in VBD emergencies highlight the growing importance of effective vector surveillance and control to prevent the introduction and transmission of vector-borne pathogens. However, implementing vector control is complex, involving multiple stakeholders and requiring coordination across public health, environmental, research, and governmental actors.

This presentation provides an overview of the current status of vector control in Belgium. It first considers the main vectors of public health relevance and discusses which control measures are currently feasible within the Belgian context. The presentation then focuses on mosquitoes, distinguishing between invasive Aedes species, which are increasingly reported in Belgium, and native Culex species, which present different ecological and epidemiological characteristics and therefore require different approaches to surveillance and control.

The role of biocides in current vector control strategies is discussed, including the regulatory and practical challenges associated with their use, such as product authorization, availability, environmental considerations, and coordination between stakeholders. Against this background, the presentation explores emerging and complementary solutions that could reduce reliance on biocides or avoid their use altogether. These include enhanced surveillance and early detection, source reduction and mass trapping.

Short Bio

W. Van Bortel is a medical entomologist with a PhD and over 30 years of experience researching vectors and vector-borne diseases across Europe, Africa, and Asia. He earned his master's degree in biology from the University of Antwerp, Belgium, followed by specialization in Medical Entomology at the Institut Pasteur in Paris. Between 2003 and 2010, he worked as a postdoctoral researcher at the Institute of Tropical Medicine. From 2010 to 2016, he served as Senior Expert on vector-borne diseases at the European Centre for Disease Prevention and Control (ECDC), also holding the role of Deputy Head of the Emerging and Vector-borne Diseases Programme. Since 2017, he has been a Senior Researcher at the Institute of Tropical Medicine Antwerp (ITM), contributing to both the Entomology Unit and the Outbreak Research Team. His work is dedicated to developing strategies for the prevention and control of vector-borne diseases in the context of public health.

V. Versteirt is a policy officer and project coordinator at the Agency for Nature and Forests (Flemish Government). She has a background in medical and veterinary entomology and worked for many years on the research and surveillance of vector-borne diseases, with expertise in invasive mosquitoes such as the Asian tiger mosquito. Today, she coordinates policy and nature management projects at the intersection of biodiversity, pollinators, invasive species and wildlife diseases. Veerle is actively involved in various national and European initiatives on nature conservation, monitoring and One Health collaboration.

Captive breeding projects at Antwerp Zoo/Planckendael

F. Verstappen; S. Lafaut
Zoo Planckendael and Zoo Antwerp, Royal Zoological Society of Antwerp, Belgium

Abstract

Zoos play an essential role in species conservation through population management, research, education, and international collaboration. This presentation highlights the European Ex Situ Programmes (EEPs) coordinated by Zoo Antwerp and Zoo Planckendael, with a particular focus on the bonobo (*Pan paniscus*) EEP and the EEP for the cinereous (Eurasian black) vulture (*Aegypius monachus*). The bonobo programme illustrates how coordinated population management supports the long-term conservation of one of our closest living relatives while contributing to research, education, and in situ conservation efforts.

The EEP for the cinereous (Eurasian black) vulture (*Aegypius monachus*) highlights the conservation potential of well-managed zoo populations. By combining innovative breeding strategies, genetic research, and support for reintroduction projects throughout Europe, the programme actively contributes to the recovery and long-term viability of wild populations. Together, these case studies illustrate how modern zoos connect ex situ population management with visible conservation outcomes, helping secure a future for endangered species both in human care and in their natural habitats.

Short Bio

F. Verstappen is Curator of Birds at Zoo Planckendael, where he oversees the management, welfare, and breeding of the bird collection. He has worked with birds since 1999 and has a particular interest in the conservation of the cinereous vulture (*Aegypius monachus*). Since 2023, he has served as EEP Coordinator for the species, supporting breeding, research, and reintroduction efforts across Europe.

S. Lafaut is Curator of Mammals at Zoo Antwerp and Zoo Planckendael. She specializes in great ape management and conservation and has been involved in international breeding programmes for threatened species since joining the Royal Zoological Society of Antwerp in 2007. She is the International Studbook Keeper and EEP Coordinator for the bonobo (*Pan paniscus*) and serves as Vice-Chair of the EAZA Great Ape TAG.

Reintroduction of the Green Tree Frog in Wallonia

A. Robise
Natagora, Belgium

Abstract

The distinctive call of the European tree frog unfortunately vanished from Wallonia's soundscape during the 1980s. This species, adapted to agricultural water bodies, suffered greatly from land consolidation policies, the filling and silting up of ponds, and a massive loss of ecological connectivity. However, a reintroduction program for the European tree frog in Wallonia was launched in 2019 on the initiative of committed citizens. This program is supported by Natagora's herpetological department (*Raînne*), and a working group was formed to initiate the official procedures and optimize the breeding protocol. In 2022, following this optimization phase and after obtaining official derogations between the partner regions, European tree frog clutches were harvested from robust populations in Flanders (the northern part of Belgium). These clutches were entrusted to the project's official partners for the breeding phase. The protocol involves raising the young tree frogs until they reach the metamorphosed stage, at which point they are reintroduced onto land. The first phase of this project took place between 2022 and 2024, with the tree frog being reintroduced to 4 sites. The second phase of the project began in 2025 with 4 new release sites. Alongside this reintroduction project, the implementation of a monitoring protocol has highlighted encouraging results, with more tree frogs heard each year at every site. Observations of clutches, tadpoles and juveniles also demonstrate successful breeding within the release sites. Today, more than 30 years after its extinction, the European tree frog has made a major comeback to the Walloon soundscape.

Short Bio

A. Robise was introduced to the world of herpetology 20 years ago through amphibian rescue operations. Since then, she has been an active volunteer within Natagora's herpetology department, Raînne, contributing to several working groups—most notably the tree frog reintroduction project in Wallonia. For the past eight months, she has officially joined Natagora to monitor amphibian populations across the Walloon region.

Reintroduction of the Garden Dormouse

D. Dekeukeleire
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Abstract

The road verges of the Brussels Ring Road (R0) form an important stronghold for the Garden dormouse (*Eliomys quercinus*), a highly threatened and legally protected species in Flanders. Infrastructure development can pose major challenges for the conservation of threatened species. INBO assessed the potential impacts of planned works along the Brussels Ring Road (R0) near Zaventem, Belgium, on this species. To reconcile species protection with the practical constraints of infrastructure development, we developed a decision-making framework. One part of this was a translocation and captive breeding programme. Successful implementation requires sufficient numbers of animals, suitable and connected release sites, consideration of genetic aspects, and intensive monitoring. This case study illustrates how a structured, phased approach can integrate species conservation into large-scale infrastructure projects.

Short Bio

D. Dekeukeleire is a mammal ecologist in the species conservation group at the Institute for Nature and Forest Research in Brussels. His work mainly focuses on small mammals that are threatened and protected, such as bats, dormice and shrews. Daan uses a variety of methods, such as passive acoustic monitoring, radio tracking and camera traps.

Pitch* & Poster Presentations

*Infectious pit stops: arbovirus prevalence and wild bird reservoirs at wintering and stop-over sites in the Gambia

H. E. Broes, N. C. Atama, T. van Mastrigt, J. van Irsel, C. M. Holicki, F. D. Chandler, M. Colley, M. P. G. Koopmans, R. S. Sikkema, H. van der Jeugd

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Abstract

Birds are important reservoirs and suspected disseminators of arboviruses such as West Nile virus (WNV), Usutu virus (USUV), and Sindbis virus (SINV), which are established in Africa and expanding into Europe. Wintering and stopover sites, where birds congregate and interact, may act as hotspots for arbovirus exchange. The Gambia, a major migratory bottleneck with high avian density, remains understudied for Culex-borne arboviruses. This study investigates exposure and infection patterns in birds at these sites. Birds were captured over 7-12 days in February 2023 and in November 2023 and 2025. Oropharyngeal and cloacal swabs, serum, and feathers were collected. Swabs were screened for WNV, USUV, SINV by RT-PCR using virus-specific primers. Sequences were determined where possible. Prior exposure to WNV and USUV was assessed by enzyme-linked immunosorbent assay (ELISA). Positives were confirmed using focus reduction neutralization tests. ELISA-negative samples were tested for SINV-neutralizing antibodies using plaque reduction neutralization tests. A total of 1,510 birds were sampled. To date, only February 2023 samples have been analysed. USUV was detected with a prevalence of 0.6% (4/662). Positive birds included 2 Yellow-fronted Tinkerbirds, 1 Yellow-crowned Bishop, and 1 Common Nightingale. No WNV or SINV was detected. Serology showed WNV exposure in 12 birds, including 4 Hooded Vultures and 1 Little Bittern. A Black-headed Weaver also tested seropositive for USUV. Flavivirus antibodies were detected in 5 additional birds. SINV seroprevalence was 9,9% (23/232), particularly in African Jacana (n = 13). Preliminary results show exposure patterns in sampled birds, helping identify species of interest for future arbovirus reservoir-host studies. Active circulation of USUV at wintering and stopover sites suggests these locations may facilitate viral exchange between resident and migratory birds, with implications for intercontinental spread.

*Multi-antigen serology of livestock and wildlife: proof of concept of species-independent bead-based multiplex detection of antibodies

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Abstract

The presence of antigen-specific serum antibodies indicates (past) infection with, or vaccination against, pathogens in humans and animals. Serology is therefore used in various surveillance programmes and can also be employed to screen for pathogen (re)emergence. However, serological assays often use species-specific conjugates, which are not available for all hosts. Goals of the research presented here are to show the proof of concept of species-independent multi-antigen serology for antibody detection in sera from multiple animal species. To this end, a multiplex immunoassay in the format of a bead-based suspension array was developed, encompassing twelve different beads carrying antigens derived from four influenzaviruses, five coronaviruses, and hepatitis E virus. Internal positive and negative controls were designed, along with a universal approach to calculate serum-specific cutoffs. To enable detection of serum antibodies from multiple animal species, protein A/G or a broad anti-chicken antibody were used. For sera with known serostatus, high diagnostic sensitivities and specificities were observed for antibodies against Influenza A, Influenza D, SARS-CoV-2, and Hepatitis E virus. Results obtained with several larger panels of mammalian sera showed presence of antibodies against various viruses, most notably IAV in seals and HEV in cattle. When testing >500 sera from domestic pigs over a 3-month period, results showed that ca. 2/3 carried IAV antibodies, followed by antibodies against HEV (ca. 1/3) and HCoV-OC43 (ca. 1/4), with sporadic signals for other coronaviruses and for IBV and IDV. The results demonstrate that species-independent multi-antigen bead-based serology may be a valuable tool for serosurveillance of wildlife and livestock.

*Development of LAMP assays for the detection of environmental *Vibrio* in a One Health context

S. Leen

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Abstract

Cholera and vibriosis are diseases caused by bacteria of the genus Vibrio and pose a significant threat to human health. Cholera, specifically, is caused by toxigenic strains of *Vibrio cholerae* and leads to severe watery diarrhea. It enters the body via ingestion of infected water or food and may result in death by dehydration if left untreated. Beyond their pathogenic lifestyle, Vibrio are abundant in aquatic ecosystems. Here, they interact with other species in the aquatic food web. All Vibrio are capable of degrading chitin, which is abundant in the environment as it makes up the arthropod exoskeleton. Furthermore, there have been numerous cholera cases caused by consumption of contaminated fish. Cholera is continuously present in the African Great Lakes Region. However, which lake organisms may interact with environmental *V. cholerae* is not known. Two fish species, *Limnothrissa miodon* and *Stolothrissa tanganicae*, are an important source of protein for people living around Lake Tanganyika. As they are planktivorous, they may bioaccumulate *V. cholerae* and be a source of cholera infection. In addition, through horizontal gene transfer, which is common among Vibrio species, environmental strains can acquire virulence genes and become pathogenic. As the transmission routes and evolution of environmental strains remain incompletely understood, there is a need to monitor environmental Vibrio strains in several layers of the food web. Effective field surveillance requires methods that are rapid, simple, and suitable for low-resource settings. Loop-mediated isothermal amplification (LAMP) provides fast results and eliminates the need for complex equipment. We designed and optimized colorimetric LAMP protocols for the detection of *V. cholerae*, *V. vulnificus*, *V. parahaemolyticus*, *V. mimicus* and *V. alginolyticus* in environmental samples and fish tissue. These tests will help decipher the possible role of Lake Tanganyika as a cholera reservoir.

*Invasive *Pseudosuccinea columella* enters the transmission cycle of an amphistome parasite infecting African buffalo

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Hasselt University, Belgium; Royal Museum for Central Africa, Belgium; Institute of Tropical Medicine Antwerp, Belgium; Bindura University of Science Education, Zimbabwe; KU Leuven, Belgium

Abstract

Parasite transmission and disease outcomes in African wildlife are increasingly shaped by anthropogenic environmental change, yet empirical data linking parasites, intermediate hosts and wildlife health remain scarce. Following an unexplained increase in mortality among wild ruminants at a Zimbabwean conservancy, we investigated the diversity, transmission and potential health relevance of snail-borne trematodes within this managed wildlife conservancy. We combined a post-mortem examination of an African buffalo (*Syncerus caffer*), standardized freshwater snail surveys, cercarial shedding experiments, DNA-based screening in snails, and morphological and molecular analyses of snails and parasites. The buffalo was infected with the liver fluke *Fasciola gigantica* and an amphistome identified as *Calicophoron* aff. *microbothrium*. Snail surveys revealed 4 gastropod taxa: invasive *Pseudosuccinea columella* and *Physella acuta*, and native *Radix natalensis* and a Lentorbis-like planorbid. The latter 3 species hosted trematode infections. Molecular screening linked *C.* aff. *microbothrium* infections in the buffalo to a shedding *P. columella*, providing the first evidence that this invasive snail is a competent intermediate host for this amphistome. No snails were infected with *F. gigantica*. Additional trematodes detected in snails included *Plagiorchis maculosus, Plagiorchis* sp*., Echinostoma* sp*.* and another species of the order Plagiorchiida. The presence of *P. columella* as a competent intermediate host, combined with its known role in Fasciola transmission in Africa, highlights the potential for parasite spillback and elevated disease transmission. Our findings underscore the value of integrated approaches and emphasize persistent taxonomic and ecological knowledge gaps that limit understanding of trematode-driven disease dynamics in African wildlife.

*Early West Nile Virus detection in Wallonia and Usutu virus dynamics in wild birds: building on national One Health surveillance

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University of Liège, Service de Santé et Pathologies de la Faune Sauvage, Belgium

Abstract

West Nile virus (WNV) and Usutu virus (USUV) are emerging avian flaviviruses whose circulation has intensified and progressively expanded northwards in Europe. USUV is now considered endemic in Belgium, while WNV was only detected for the first time in wild birds in 2025, through the national One Health for Surveillance (OH4S) program coordinated by Sciensano, which identified 7 infected corvids in Flanders (Sohier et al., 2026). Both as part of this national surveillance program and as part of an ongoing PhD project on flaviviruses in native wildlife in Wallonia, we implemented a surveillance scheme combining systematic necropsies of wild birds, RT qPCR testing on carcasses and on live birds admitted to wildlife rehabilitation centers, and serological screening in game mammal species. Between 2023 and 2025, USUV circulation in Wallonia was characterized by endemic persistence with changing patterns of host involvement and prevalence. In 2023 -2024, USUV showed high circulation across a broad diversity of bird species, particularly passerines, with Eurasian blackbirds (*Turdus merula*) already heavily affected and a typical summer-early autumn seasonal peak. By 2025, USUV prevalence had decreased, with a relatively higher proportion of cases in young birds and fewer affected adults. On 25 May 2026, the first WNV infection was detected in Wallonia in a Eurasian magpie (*Pica pica*), more than one month later than the first animal cases reported elsewhere in Europe during the 2026 season, which occurred mainly in Corsica and Italy in milder Mediterranean climates. This relatively early detection in a cooler climatic context, following the initial Belgian WNV discovery in 2025, supports the hypothesis of WNV overwintering in Belgium and highlights the sentinel value of wild birds, particularly corvids and birds of prey, within a One Health framework.

*BEYOND THE TRAP: Integrating environmental DNA, classical entomology and xenomonitoring to trace malaria vectors and transmission in Kimpese Health Zone, Democratic Republic of Congo

B. André, C. W. Wambui, L. Minga, P. Ansobi, J.-P. Banzolele, D. Bakadila, C. Mabaya, P. Mitashi, M. Jorissen, M. Bentahir, J. Zanga, J. Madinga, H. Gante, T. Huyse

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Abstract

Malaria transmission remains exceptionally high in the Democratic Republic of Congo, driven by weak and fragmented surveillance systems that limit timely responses. Conventional entomological methods may miss cryptic or low-abundance vector species, particularly within *Anopheles* species complexes. This study integrates environmental DNA (eDNA), larval dipping, and adult mosquito surveillance to characterise malaria vector communities, *Plasmodium falciparum* infection, and vector competence at village scale in the Kimpese Health Zone.

*A comprehensive evaluation of alternative source materials in wildlife serology

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Abstract

Background: Serological techniques are commonly used in wildlife disease studies to determine the presence of pathogen specific antibodies. They have the advantage that antibodies remain present long after the pathogen is cleared, in contrast to molecular assays. For serological assays, ideally serum from whole blood is used, but researching wildlife often involves opportunistic sampling of animals, which limits whole blood collection and necessitates the use of alternative materials to serum.

Aims: 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.

Methods: We performed a scoping review researching alternative source materials to serum collection for use in serological assays with a focus on wildlife. To facilitate comparison, we grouped the different alternatives in four different categories. Subsequently, we collected the most common alternative materials and serum from euthanized rats for a comparison study.
Results: The initial literature search resulted in 704 papers, of which 152 papers were finally included in the scoping review. These described the use of dried blood spots (n = 31), serum-like fluids (n = 40), meat extract (n = 19), meat juice (n = 47) or a combination of these materials (n = 15). In the analyzed papers, large livestock mammals were overrepresented, as well as the methods using meat juice or meat extract. Only a third of the papers made a direct comparison between serum and these alternatives, using paired samples from the same animal. Based on the review, we are currently performing a comprehensive comparison of serum and various alternative source materials in rats.

Conclusion: The anticipated final overview can be used as a guideline to determine what source material is best to collect for serology-based assays, considering animal size, ease of use for collection, processing procedure and transportation requirements.

*Anthropogenic land-use change shapes zoonotic risk in terrestrial small mammals from Maniema, Democratic Republic of Congo

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Abstract

Background: Human-driven environmental change is increasingly recognized as a major driver of emerging infectious diseases. Land-use change can alter wildlife communities and intensify human-animal interfaces, yet it remains unclear whether biodiversity loss and the introduction of non-native generalist species consistently increase or decrease zoonotic disease risk.

Methods: We investigated how anthropogenic land-use change affects pathogen transmission in terrestrial small mammal communities in Maniema Province, Democratic Republic of Congo. A total of 380 small mammals (rodents and shrews) were sampled across two villages and ten forest plots, and screened for DNA of five pathogen groups: *Bartonella*, *Leptospira*, Anaplasmataceae, *Hepatozoon*, and Orthoherpesviridae.

Results: In villages, mainly *Rattus rattus* was captured, whereas in forest plots, 26 different small mammal species were sampled. The most common detected pathogens were members of Bartonella genus (22% of samples), followed by *Hepatozoon* (5.8%), herpesviruses (3.9%), and Anaplasmataceae (0.8%). *Bartonella* spp. were significantly more common in animals captured in villages than in forests, whereas *Hepatozoon*, Anaplasmataceae, and herpesviruses were detected more frequently in forest-associated hosts. Phylogenetic analyses revealed strong host species associations for *Hepatozoon* and Anaplasmataceae, whereas *Bartonella* showed evidence of being shared among *R. rattus* and forest-associated hosts. Furthermore, Bartonella lineages detected in *R. rattus* were closely related to globally distributed Rattus-associated strains, suggesting pathogen introduction into remote areas via invasive host species.

Conclusion: These findings indicate that anthropogenic habitats may facilitate the amplification and spread of certain generalist pathogens such as *Bartonella*, possibly including lineages with potential zoonotic relevance, while other pathogens remain more strongly associated with forest-dwelling hosts.

*Advancing wildlife-borne pathogen surveillance by determining mammal species' vulnerability to land use change

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Abstract

Introduction: Anthropogenic land use changes (LUC) may alter transmission dynamics of wildlife-borne pathogens through effects on e.g. local species assemblage composition (i.e. which wildlife species are present and at what abundances). This study aims to identify areas and species of increased interest for wildlife-borne pathogen surveillance based on expected shifts in pathogen transmission dynamics in wild terrestrial mammals under different LUC scenarios.

Methods: 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 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. Species scoring high for both exposure and sensitivity were classified as highly vulnerable or potentially adaptive depending on their adaptive capacity scoring.

Results: In all three analyses, nearly all species classified as highly vulnerable or potentially adaptive were species of the order Chiroptera. Potential hotspots for 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.

Conclusion: 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.

Turning awareness into action - A communication campaign on the tiger mosquito in Flanders

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Abstract

The Asian tiger mosquito (*Aedes albopictus*) is spreading across Europe and has repeatedly been detected in Belgium, highlighting the need for effective prevention and control measures. In addition to surveillance and control, public awareness and behavioural change are essential to reduce breeding sites, limit mosquito nuisance and prevent the transmission of mosquito-borne diseases such as dengue, chikungunya and Zika. To support these efforts, the Flemish Department of Care developed a communication campaign targeting the general public, local authorities, health professionals and travellers. The campaign promotes key preventive behaviours, including the removal of standing water, reporting suspected tiger mosquitoes through the national surveillance platform, personal protection measures and travel-related prevention advice. A central feature of the campaign is a scenario-based communication approach. Key messages, actions and communication materials are adapted to the local mosquito situation, which is visualised on a semi-real-time scenario map. Local authorities receive tailored guidance and communication support, facilitating rapid and coordinated responses when tiger mosquitoes are detected. To maximise reach and engagement, a broad range of materials has been developed, including social media content, videos, posters, leaflets, informative articles and educational tools. This poster describes the campaign strategy and communication framework, demonstrating how integrated risk communication can strengthen community engagement and contribute to the prevention of mosquito-borne diseases.

The impact of urban greening on hedgehogs, ticks and pathogens

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Abstract

Urban greening initiatives are increasingly implemented in cities. They offer a wide range of health benefits but can also unintentionally increase the diversity and abundance of vectors, reservoir hosts and pathogens. The European hedgehog (*Erinaceus europaeus*) is an important host for ticks and (zoonotic) pathogens. However, the impact of urban greening on hedgehog condition and tick-borne disease risk along an (urban) greening gradient remains unknown. To better understand these relationships, we are currently collecting data and ear biopsies from hedgehogs in 7 Dutch wildlife rehabilitation centers. These ear biopsies will be tested for the presence of different tick-borne pathogens (e.g., *Borrelia burgdorferi sensu lato*, *Anaplasma phagocytophilum, Rickettsia* spp., *Babesia* spp.). The lab results will be combined with the collected data on hedgehog body condition, tick burden and greenness of the location where the hedgehog was found. In this way, we can gain insight into the specific interactions between hedgehogs, ticks, and tick-borne pathogens along an urban greening gradient. With this analysis, we aim to study the impact of urban greening on hedgehog condition and tick-borne disease risk.

Lassa fever disease risk: a socioecological study of the human-rodent-virus interface

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Abstract

Lassa fever is a potentially fatal haemorrhagic disease caused by the zoonotic virus *Lassa mammarenavirus* (LASV). It is endemic to West Africa, where the primary rodent reservoir *Mastomys natalensis* thrives in human-dominated landscapes. Spillover from this wildlife reservoir to humans occurs through contact with infected rodents and their excretions, leading to an estimated 900,000 infections and 18,000 deaths each year. In the absence of a vaccine, reducing spillover risk relies on limiting human-rodent contact. However, the ecological and behavioural dynamics shaping this interaction, and what drives them, remain poorly understood.

We investigated the socioecological drivers of LASV exposure risk in Sierra Leone, combining concurrent rodent trapping, human mobility tracking, and surveys to characterise the shared space-use between *M. natalensis* and rural communities, and the transmission risk it creates. Fieldwork was carried out across four villages in the dry and wet seasons of 2025. Rodents were trapped in and around each village and tested for LASV RNA and antibodies. We simultaneously recorded the movement patterns of 240 participants and conducted interviews to gauge demographic and behavioural drivers of disease.

In 2026, we collected blood samples from these participants to test for LASV-specific IgG and IgM antibodies, providing the missing link between reservoir-host spatial overlap and actual human exposure risk. Serological work is currently underway in Sierra Leone. Here we present preliminary results, with the aim of identifying who is most at risk, when and where exposure occurs within the local landscape, and the socioecological factors driving these patterns.

Land use shapes host–pathogen networks and disease hazard in small mammal communities in the Netherlands

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Abstract

Human-driven land-use change is recognized as a major driver of zoonotic disease emergence by altering interactions among hosts, vectors, and pathogens. In the Netherlands, landscapes are expected to undergo substantial transitions in response to population growth, biodiversity conservation, and societal well-being. To assess the potential consequences of future landscape transitions, it is necessary to understand how disease hazard is currently distributed across dominant land-use types. We investigated host–pathogen associations and disease hazard across three Dutch land-use types representing different levels of anthropogenic disturbance: forests, farmlands, and urban areas. We characterized host–pathogen community structure by examining host communities and evaluating the contribution of individual host species to pathogen circulation. We also quantified variation in disease hazard and pathogen infection probability among land-use types at both the community level and within *Apodemus sylvaticus*, a widespread habitat-generalist rodent. We captured 1,621 small mammals belonging to 10 host species. Although *A. sylvaticus* was associated with the greatest number of pathogens, *Clethrionomys glareolus* was disproportionately important in maintaining pathogen communities in forests, while *Microtus arvalis* played a similar role in urban habitats. Disease hazard for tick-borne pathogens was highest in forests, whereas *Leptospira* spp. and *Toxoplasma gondii* were more prevalent in anthropogenic habitats.

Hidden viral diversity in wild and domestic meat imported by air passengers into Belgium

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Abstract

The international movement of animal-derived products through passenger luggage represents an under-recognized pathway for the introduction of animal pathogens and zoonotic agents. Wildmeat trade and consumption are increasingly recognized as hotspots for pathogen emergence, yet surveillance of imported meat products remains limited. Within INTERCEPT, the potential health risks associated with meat products illegally entering Belgium through passenger baggage was characterized. Meat products confiscated during customs inspections at Brussels Airport were sampled, primarily targeting flights arriving from West Central Africa and East Asia. A total of 628 meat samples were collected, with 509 identified to species/genus level using DNA-barcoding. 36 distinct animal species were identified. ~1/4 specimens originated from wild animals (mainly greater cane rat and African brush-tailed porcupine), and ~1/3 of these derived from protected species, e.g. duikers, pangolins and non-human primates. Metagenomic screening revealed a diversity of RNA and DNA viruses in both wild and domestic animal products, e.g. a novel orthohepadnavirus strain, peste-des-petits-ruminants, avian influenza and chicken anemia viruses. Several of these viruses are of veterinary and/or zoonotic relevance and were detected in cooked meat products. These findings demonstrate that passenger-imported meat products can harbor a wide diversity of animal viruses and may contribute to the transboundary movement of pathogens. By combining inspections by customs, DNA-based sp identification, and metagenomic pathogen surveillance, the project provides a practical One Health framework for monitoring biological risks associated with the illegal movement of animal products across borders. Strengthening coordinated surveillance systems and data sharing between scientific institutions and governmental agencies is essential to improve risk assessment and preparedness against emerging infectious diseases.

Lack of detectable anti-diphtheria toxin antibodies in European hedgehogs from a *Corynebacterium ulcerans* hotspot

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Abstract

Corynebacterium ulcerans is a zoonotic pathogen that can cause diphtheria-like disease, including cutaneous lesions. The bacterium has been reported in several wild and domestic animal species, causing sporadic infections or outbreaks. In Belgium, *C. ulcerans* appears to have emerged from an endemic state in the European hedgehog (*Erinaceus europaeus*) population, resulting in hedgehog diphtheric disease (HDD). HDD is characterized by abscesses and ulcerative lesions, mainly affecting the head and limbs, and is associated with *C. ulcerans* infection. However, little is known about the humoral immune response of European hedgehogs to *C. ulcerans* and its diphtheria toxin. This study investigated whether wild European hedgehogs from an HDD-endemic area have detectable antibodies against the diphtheria toxin. In spring 2025, 11 hedgehogs admitted to a wildlife rehabilitation center were euthanized due to severe clinical conditions. Swabs from abscesses, present in nine of 11 hedgehogs, and from the oral cavity of all animals were cultured and bacterial isolates identified using MALDI-TOF. *C. ulcerans* isolates were screened for the diphtheria toxin gene (toxE) using a duplex PCR assay. Blood was collected to assess anti-diphtheria toxin antibodies using a plasma neutralization test with Vero cells. Nine hedgehogs exhibited HDD-like lesions, of which five were confirmed positive for *C. ulcerans*. Four of these harbored toxigenic strains. None of the 11 hedgehogs had detectable anti-diphtheria toxin antibody titers. These findings suggest that European hedgehogs in HDD-endemic regions do not appear to mount a detectable humoral response. Future studies with larger sample sizes, including healthy wild hedgehogs, should investigate whether protective anti-diphtheria toxin immunity develops and how underlying health conditions may influence this response.

The potential role of *Ixodes ricinus* in the transmission of *Corynebacterium ulcerans*

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Abstract

Ticks are important vectors of a wide range of bacterial, parasitic, and viral pathogens affecting both animals and humans. In Europe, *Ixodes ricinus* is a widely distributed tick species that transmits pathogens such as tick-borne encephalitis virus, *Borrelia burgdorferi sensu lato, Babesia divergens*, and *Anaplasma phagocytophilum*. Wild animals play an important role in tick ecology by serving as hosts and reservoirs, helping to maintain and spread these pathogens. The European hedgehog (Erinaceus europaeus) is currently under considerable pressure. In Belgium, increasing mortality has been associated with hedgehog diphtheric disease (HDD), a severe cutaneous disease caused by the zoonotic bacterium *Corynebacterium ulcerans*. The high prevalence of *C. ulcerans* in Belgian hedgehogs raises the possibility that ticks feeding on infected hedgehogs may pick up the bacterium and contribute to its transmission among wildlife and potentially to humans. This study aims to assess the potential role of *I. ricinus* in the transmission of *C. ulcerans*. A total of approximately 600 *I. ricinus* larvae were artificially fed on blood contaminated with *C. ulcerans*, while approximately 300 larvae were fed on uncontaminated blood as controls. Before molting to the nymphal stage, ticks were tested for the presence of *C. ulcerans* to determine whether the bacterium was acquired. Subsequently, the potential transmission of *C. ulcerans* by infected nymphs during a second blood meal will be assessed. The study is ongoing. Preliminary results confirm successful exposure of larvae to *C. ulcerans* following the artificial blood meal. Further analyses will assess bacterial persistence and potential transmission by infected nymphs.

Eco-detection dogs for new targets in the field: feasibility check

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Abstract

For monitoring purposes ecological detection dogs can, in some cases, offer a viable solution. The central question is always: Is this detection target feasible for dogs, and under which conditions? Is it possible to realise the project goals with the proper dogs, handlers and trainers? We are developing an evidence based, systematic feasibility protocol to answer this question. Through iterative consultation rounds with international experts, we integrate technical parameters, ecological context, animal welfare considerations, legal constraints, operational feasibility, and economic cost benefit analyses. The goal is to produce a generic checklist capable of evaluating new detection targets, including those that are understudied or entirely novel. A preliminary set of criteria was applied to three ongoing pilot-cases: the invasive flatworm *Obama ungara*, the invasive marbled crayfish *Procambarus virginalis*, and nests of red wood ants *Formica rufa*. We present possibilities and limitations for each case. The safe availability of training material is a specific challenge for invasive species. There is sufficient evidence supporting further development for each case, including the quantification of the hitherto apparent added value compared to classical detection methods.

Movement and pathogen transmission in feral pigeons

B. Vanden Broecke, V. A. Kiss, A. Martel, L. Lens, W. Müller

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Abstract

Feral pigeons (*Columba livia*) are among the most abundant birds in cities worldwide and are known reservoirs for zoonotic pathogens, including *Chlamydia psittaci* and antimicrobial resistant *Escherichia coli*. Yet little is known about how individual pigeons move within urban landscapes, and how this shapes the spatial spread of pathogens across a city. Understanding these movement patterns is essential for predicting disease risk within a One Health framework. We fitted around 100 feral pigeons across multiple neighbourhoods in Antwerp, Belgium, with lightweight Bluetooth tags operating on the Apple Find My network. Tag detections were used to estimate individual home ranges and connectivity between neighbourhood subpopulations. A subset of birds was screened for *Chlamydia psittaci* and antimicrobial resistant *E. coli*. Preliminary results show strikingly small home ranges and very limited connectivity between neighbourhoods, indicating that pigeon subpopulations remain largely isolated from one another. This restricted movement corresponds with large spatial variation in the prevalence of both *Chlamydia psittaci* and antimicrobial resistant *E. coli*, suggesting that fine scale spatial structuring, rather than free mixing across the city, drives urban disease heterogeneity. These findings suggest pathogens are unlikely to spread easily across a city through pigeon movement alone, instead accumulating locally within relatively closed neighbourhood populations. This highlights the value of combining fine scale tracking with pathogen surveillance to understand urban disease ecology.

Detection of sarcoptic mange in red foxes (*Vulpes vulpes*) during wildlife disease surveillance in Brussels (Belgium) 2023-2025

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Abstract

Epidemics of sarcoptic mange in wildlife are characterized by high morbidity and mortality depending on the host species, with implications for the entire ecosystem. Contributing factors influencing disease introduction and spread are largely unknown, however – despite the limited understanding of interspecies transmission – sarcoptic mange is considered a One Health concern. Clinical manifestations can range from localized lesions to extensive crusted dermatitis with systemic effects eventually leading to death. Management of mange in wildlife is challenging, requiring consideration of contributing factors, animal welfare, and potential impacts on humans, domestic animals and the wider ecosystem. During this retrospective analysis we tried to determine the extent and factors contributing to disease severity during a recent epidemic of sarcoptic mange in foxes in the Brussels Capital Region. Autopsy reports and laboratory analyses from 282 fox cadavers collected during a wildlife disease surveillance program from 2023 to 2025 were analysed. *Sarcoptes scabiei* was detected in the Brussels fox population by the end of 2024 and has persisted ever since. Mange prevalence was estimated at 3.45% based on gross pathology lesions of foxes with traumatic lesions consistent with vehicle collision. Significant contributing factors on disease presence were cachexia and *Toxocara canis* co-infection. Mange was significantly less prevalent among foxes with lesions consistent with vehicle-related mortality. Our study findings support the classification of sarcoptic mange as an emerging disease in the Brussels Capital Region, and identified comorbidities such as cachexia and *T. canis* infections as important contributing factors to disease severity and mange-related death.

Avipoxviral lesions in two dunnocks (*Prunella modularis*)

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Abstract

Background: Avipoxvirus infection is frequently reported in passerine birds such as Great Tits and typically causes proliferative, nodular cutaneous lesions. Although dunnocks (Prunella modularis) have been reported with pox-like lesions, confirmed cases remain poorly documented, likely reflecting their relatively secretive behaviour.

Case description: Two dunnocks were admitted as nestlings to a wildlife rescue centre and subsequently developed rapidly progressive, extensive cutaneous nodules. In the first bird, a 1.3 × 1.0 cm nodule was present on the right wing, showing central necrosis, ulceration and haemorrhage. The second bird developed large, alopecic nodules measuring 1.2 × 0.7 cm on the chin and 1.0 × 1.0 cm on the left side of the neck. The lesions increased markedly in size over several days and initially did not resemble typical poxviral lesions. Attempts to control the nodules by ligation were unsuccessful. Due to the severity and progression of the lesions, both birds were euthanized and submitted for necropsy through the wildlife disease surveillance programme of the Agency for Nature and Forests.

Histopathology: Histological examination revealed marked epidermal hyperplasia with swollen keratinocytes showing ballooning degeneration. Numerous keratinocytes contained large (10–30 µm), eosinophilic intracytoplasmic viral inclusion bodies consistent with Bollinger bodies. A serocellular crust containing basophilic bacterial colonies covered the affected epidermis. The findings were consistent with avipoxviral dermatitis with secondary bacterial infection.

Discussion and conclusion: Avipoxvirus infection can result in extensive and rapidly progressive cutaneous lesions in dunnocks, potentially compromising welfare through ulceration, secondary infection and interference with feeding or vision. Although severe disease may occur, infection does not necessarily have a fatal outcome, as spontaneous remission has been reported in dunnocks. The marked ulceration and bacterial colonisation observed in these cases may have been facilitated by pruritus and self-trauma. Seasonal clustering of Avipoxvirus cases has been described in other passerines and in dunnocks during hot summer periods, as observed in the present cases. Mosquitoes may possibly contribute to transmission. These two histologically confirmed cases highlight the importance of wildlife disease surveillance, particularly in less conspicuous passerine species such as the dunnock.

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