JOINT SYMPOSIUM

13 OCTOBER 2022
UNIVERSITY
OF UTRECHT, NL

WILDLIFE DISEASES GOING VIRAL

BWDS
&
DSWH

RESEARCH INSTITUTE
NATURE AND FOREST

The C.T. De Wit Graduate School PE&RC
PRODUCTION ECOLOGY & RESOURCE CONSERVATION

Abstract book - Wildlife diseases going viral

2nd Joint Symposium:
Belgian Wildlife Disease Society
&
Dutch Society for Wildlife Health

BELGIAN WILDLIFE DISEASE SOCIETY (BWDS)

DSWH
Dutch Society for Wildlife Health

13 October 2022, Utrecht University, The Netherlands

Organizing and Scientific Committee:

Judith van den Brand, Miriam Maas, Helen Esser, Anne ten Berge, Erik Kleyheeg, Famke Jansen, Paul Tavernier, Myriam Logeot, , Leen Claes, Rosario Volpe, Kristof Baert, Stefan Roels

Abstact book edited by Kristof Baert & Miriam Maas

Introduction: "Wildlife diseases going viral"

After the first successful joint Symposium of the BWDS and DSWH in Antwerp (2016), titled 'Wildlife crossing borders', it became clear that wildlife health and disease cannot be discussed only within countries but need a broader view. Therefore, organising a second joint BWDS-DSWH symposium became evident.

Originally planned to take place in 2020, it is needless to say that the initial plans were hampered by the COVID19 pandemic forcing the event to be postponed to the present day, October 13, 2022. Although usually a difficult task, the choice of an appropriate theme to cover a selection of relevant subjects in the field of wildlife health in an era of corona and influenza viruses going around all over the place, was quite obvious.

"Wildlife diseases going viral" brings together a number of talks, not only about "hot" viruses from wildlife, but also about possible health risks from animal species (re)appearing in a viral-like way in our environment, including in urban wildlife. A pleasant surprise for the organizing committee was the number and diversity of the submitted abstracts, of which two were selected as a short communication.

We thank you for your participation and interest, and wish you all a pleasant, convivial, and scientific enriching day.

Sincerely,
DSWH & BWDS board members.

Programme

Moderators : Wim Van der Poel (WBVR, Nl) & Tim Adriaens (INBO, Be)

09:30 - 10:00 Registration and coffee

10:00 - 10:15 Opening (Prof. dr. A.D.C. Jaarsma, UU, Nl) & Welcome (Judith van den Brand, DSWH -Stefan Roels, BWDS)

Session 1: Viruses
10:15 - 11:00 Losing the upper hand: Establishment of highly pathogenic avian influenza in wildlife (Thijs Kuiken, Erasmus MC, Nl) (Keynote)
11:00 - 11:20 Sars-CoV-2 transmission to the wild fauna (Steven Van Gucht, Sciensano, Be)
11:20 - 11:40 The role of wildlife and wildlife surveillance in public health response towards arboviruses (Reina Sikkema, Erasmus MC, Nl)
11:40 - 12:00 African Swine Fever management (Valerie de Waele, SPW DEMNA, Be)
12:00 - 12:20 Bat or Bad Coronaviruses? (Lineke Begeman, Erasmus MC, Nl)

Poster session (on site) & Lunch

Short communications
13:40 - 13:50 Zoonotic pathogens linked with hedgehog diphtheric disease (Naomi Terriere, Ghent University, Be)
13:50 - 14:00 Ticking off the ungulate box – the role of different ungulate species in the ecology of tick-borne pathogens (Nannet Fabri, Utrecht University, Nl)

Session 2: Animal species
14:00 - 14:20 Marine mammal strandings research (Lonneke IJsseldijk, UU, Nl)
14:20 - 14:40 Wolves returning to the Low Countries: a closer look at the Hechtel-Eksel pack (Jan Gouwy, INBO, Be)
14.40 - 15.10 Raccoons: an invasive alien species with public health significance (Valerie de Waele, SPW DEMNA, Be & Miriam Maas, RIVM, NL)
15:10 - 15:30 Coffee break

Session 3: Urban Wildlife
15:30 - 15:50 Urban red foxes (Vulpes vulpes) in the UK: Ecology and Disease Implications (Bryony Tolhurst, University of Brighton, UK)
15:50 - 16:10 Urban greening and rats - the relation between urban greenspace, zoonotic pathogen prevalence and richness in rats (Marieke De Cock, RIVM, NL)
16.10 - 16.30 Rose-ringed parakeets (Psittacula krameri) in the city (Diederik Strubbe, UGent, Be)

Closing remarks, Poster awards & Drinks

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Sponsor: INBO

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- Population modelling
- New methods development

Invasive species

- Monitoring, surveillance and open data
- Risk management and management review
- Impact assessment and risk analysis

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The Graduate School for Production Ecology & Resource Conservation (PE&RC) is a national collaborative research and postgraduate training institute. Members of PE&RC are academic staff, postdocs and PhD candidates of Wageningen University, Utrecht University, University of Amsterdam, Vrije Universiteit Amsterdam, Radboud University, Naturalis Biodiversity Center, and the Netherlands Institute of Ecology.

Central focus of the collaboration is the PhD programme that is embedded in a coherent and productive research environment that aims to perform frontier academic research of the highest quality.

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Oral presentations

Losing the upper hand: Establishment of highly pathogenic avian influenza in wildlife

Thijs Kuiken, Department of Viroscience, Erasmus University Medical Centre, Rotterdam, The Netherlands.

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Highly pathogenic avian influenza (HPAI) typically emerges in commercial poultry farms by conversion of an innocuous wild-type virus—aptly called low pathogenic avian influenza virus—into one that causes high mortality in poultry. The current H5N1 HPAI virus—clade 2.3.4.4b of the A/Goose/Guangdong/1/96 lineage—originated in a commercial goose farm in China in 1996 and spread across the rapidly growing poultry populations in Asia, substantially spilling over into wild birds in 2005. The virus caused numerous wild bird outbreaks, typically during autumn and winter, but has persisted year-round in wild birds in Europe since 2021. This year, it has spread quickly to breeding seabirds in Europe, North America, and Africa. For many of these long-lived species, already threatened by loss of habitat and climate change, the resulting mortality will have a large impact on their populations. Short-term recommendations include accurate monitoring of the virus and associated mortality in wild birds, and, where appropriate, coordinated removal of infected wild bird carcasses to limit virus spread. Long-term recommendations include enhanced protection of seabird and waterbird sites, vaccination of poultry against HPAI, reduction of poultry farm size and density, and avoidance of waterbird-rich areas as a location for poultry farms. The ongoing global spread of HPAI H5 viruses stresses the importance of international cooperation to better understand the global epidemiology of avian influenza, and is a call to re-assess the poultry sector in a way that embraces the One Health perspective: to sustainably balance and optimize the health of people, animals and ecosystems.

Short BIO

Thijs Kuiken is Professor of Comparative Pathology at the Department of Viroscience, Erasmus MC, in Rotterdam. He graduated as a veterinarian at Utrecht University in 1988, obtained his Ph.D. in 1998 from the University of Saskatchewan on Newcastle disease virus in cormorants, and qualified as a Diplomate of the American College of Veterinary Pathologists in 2002. Achievements of his group include an improved understanding of bat-acquired rabies and confirmation that migratory birds can play a major role in the global spread of avian influenza viruses. His group's current focus is the pathogenesis of virus-associated pneumonia and encephalitis, comparison of viral infections between bats and people, identification of underlying factors for viruses to cross the species barrier from wildlife reservoirs to humans, and assessment of response options to implement transformative changes in society and so prevent the emergence of future viral epidemics.

Sars-CoV-2 transmission to the wild fauna

Steven Van Gucht, Head of Viral Diseases, Sciensano, Brussels, Belgium

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Almost 3 years into the COVID-19 pandemic, the world still faces many uncertainties in terms of future epidemiologic evolution and management. Although SARS-CoV-2 can be considered a typical textbook respiratory virus, this relatively simple virus has surprised both science and the world on many occasions. The past pandemic years have left us with unprecedented new insights in virus evolution, viral disease, vaccinology and sociology.

Many outstanding issues still remain unanswered and will determine the course of this and future pandemics. It's is presumed that the virus originates from bats and an unknown intermediate mammal host led to introduction in humans. The specific drivers and transmission chains that led to the pandemic are still unknown.

In this talk, I will give an overview of the animal species that have already been infected by humans and which new animal reservoirs have been or have the potential to become established. I will discuss whether reverse zoonosis poses a problem for animal and human health and whether a "one health" approach can diminish the likelihood of new epi-/pandemics.

Short BIO

Steven Van Gucht is head of the Laboratory of Viral Diseases of the Belgian health institute Sciensano in Brussels. Since January 2020, he has also been deeply involved in managing the COVID-19 pandemic as an inter-federal spokesperson for the Crisis Center and as a government advisor on numerous scientific councils, including Celeval, GEMS and the recently formed Scientific Strategic Council. He is trained as a veterinarian, has a PhD in virology and is appointed as guest professor at Ghent University since 2014.

The role of wildlife and wildlife surveillance in public health response towards arboviruses

Reina S Sikkema, Nnomzie Atama, Maarten Schrama , Tijs van den Berg , Natasja van Nijen , Emmanuelle Munger, Louie Krol, Jordy G van der Beek, Rody Blom, Irina Chestakova, Anne van der Linden, Marjan Boter, Tjomme van Mastrigt, Richard Molenkamp, Sander JM Koenraadt, Judith MA van den Brand, Bas B Oude Munnink, Marion PG Koopmans, Henk van der Jeugd

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Extensive surveillance of mosquitoes, dead and live birds was set up in 2016 to monitor the introduction and spread of a selection of high-risk arboviruses in the Netherlands. The presence of Usutu virus (USUV) infections was confirmed first in 2016, and genomic sequencing provided evidence for continued enzootic presence of USUV in subsequent years. West Nile virus (WNV) was first detected in 2020, in wild birds as well as mosquitoes. This led to the implementation of blood donor screening in regions at-risk as well as retrospective screening of human patients with unexplained encephalitis, resulting in the detection of multiple human cases.

To further understand the drivers of arbovirus emergence and spread in the Netherlands, additional studies have been implemented to further improve the surveillance system and gain additional knowledge on reservoir hosts, impact and virus ecology.

Short BIO

Reina Sikkema is a veterinarian and researcher at the Virology department of the ErasmusMC in Rotterdam. Currently she is leading the research group on One Health Virology that focuses on laboratory capacity, risk based surveillance and prediction and ecology of emerging diseases, from a One Health perspective. Reina is interested in unravelling the drivers and risk factors of zoonotic disease emergence and spread, by setting combining local data from ecology, sociology, economics and other disciplines combined with the development of advanced diagnostics, to study the ecology of emerging diseases on the human-animal interface. She has set-up and coordinated studies on the human-animal interface in several countries, such as China, Qatar and the Netherlands. These include studies to detect emergence and spread of arboviral diseases of public health relevance, with specific focus on bird ecology and bird reservoirs. As such she is also a member of the West Nile Virus national response team. She also works as a researcher at NIOO- KNAW. Additionally, she is board member of DSWH.

African Swine Fever - management

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In September 2018, African swine fever (ASF) was first detected in two wild boars of the South-East of Belgium (Linden et al 2019). An anthropogenic introduction is likely, as the nearest ASF outbreak was located as far as 1.000 km.

To eradicate the virus, four management measures have been implemented such as complete standstill of any activity in the infected forest, organized searching and removal of the carcasses, fencing and depopulating wild boars within the infected zone and in the white zone. The measures were performed under high biosecurity rules, and their efficacy was measured by testing all wild boars found dead or culled.

The peak of the epidemic was obtained in February 2019 and the last evidence of circulating virus was detected in August 2019. The infected area increased during the crisis, and reached 598 km²; however, the management zone encompassed 1106 km². From September 2018 till March 2021, 7.077 wild boars have been removed from the population, within them 5.338 animals have been qPCR-tested with 833 wild boars notified ASF-positive.
The ASF-free status has been recovered from EC in November 2020 and from OIE in December 2020. The success of the eradication is probably due to several elements: a single focal introduction, a close collaboration of every stakeholder, an early reaction using combined measures adapted to evolving situation. In 2022, active surveillance is still running in the former ASF management zone and passive surveillance in all Wallonia.

Short BIO
Valérie works as a veterinary epidemiologist, at the Department of Studies of the Natural and Agricultural Environment of the Public Service of Wallonia (SPW-DEMNA) as a specialist in the management, conservation and protection of the environment. Her tasks include contributing to wildlife health monitoring and management, and research into wildlife population dynamics, for example through camera traps and telemetry.

She obtained her PhD in veterinary sciences at University College Dublin, Ireland, for a thesis on the epidemiology of the parasite Cryptosporidium spp in cattle. She worked for several years in the field of animal and public health research, including as a Research Officer in the Central Veterinary Laboratory of the Irish Department of Agriculture and as an epidemiologist at the Institute of Tropical Medicine in Antwerp, Belgium, and at Sciensano, the Belgian institute of health, where she contributed to the monitoring of bee mortalities, and to the European OneHealth-EJP project.

Bat or Bad Coronaviruses?

Lineke Begeman, Erasmus MC, Zoogdiervereniging, Wageningen Bioveterinary Research Centre, Nederlandse Voedsel en Waren autoriteit, Rijkinstituut voor Volksgezondheid en Milieu, Universiteit Utrecht, Wageningen Universiteit, Naturalis Biodiversity Center

Zoonoses in the night consortium

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In the past and currently novel coronavirus diseases have emerged in people and domestic animals. Bats have been identified as original hosts of the ancestor viruses for several of these coronaviruses. The Order of Chiroptera (bats) comprise approximately 20% of all mammals, and the occurrence of zoonotic viruses has been estimated to be proportional to the number of species in this Order. Seventeen species of bats occur in the Netherlands and these have not been linked to coronavirus disease outbreaks.

We aimed to learn more about coronaviruses in the Netherlands and their zoonotic potential. We aimed to learn what coronaviruses occur in bats in the Netherlands, how coronavirus prevalence varies over time, and what the tropism is of the virus in bat hosts. This study was part of the 'Zoonoses in the night' consortium and was performed with the help of many volunteers.

Bat faeces sampled throughout the Netherlands were tested for coronavirus RNA presence. Prevalence over time of a coronavirus was investigated in one city in Common Pipistrelles (*Pipistrellus pipistrellus*). Maternity colonies were sampled at formation of the colony in spring, when pups were expected to lose their maternal immunity in June and July, and at formation of the winter hibernation colony early autumn. Bat coronavirus tropism was investigated in naturally infected Nathusius' Pipistrelle's (*Pipistrellus nathusius*) tissues, of bats found dead. Results will be presented and discussed.

Short BIO

Zoonoses in the night is a ZonMw funded project, running from spring 2017 up to summer of 2022, aiming to study bat viruses in the Netherlands. It was a true One Health collaboration of many eight different Dutch institutes. Lineke Begeman was involved as the main researcher. Lineke is a veterinary pathologist, who focused her work on diseases of free-ranging animals. She is currently a PhD candidate at the Viroscience department of Erasmus Medical Centre.

Marine mammal strandings research

Lonneke L. IJsseldijk, Marja J.L. Kik & Andrea Gröne

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Marine mammals are difficult to study at sea, but strandings provide unique and cost-effective opportunities for surveillance purposes. In the southern North Sea, stranding frequency of harbour porpoises (Phocoena phocoena) increased since the 90's and has been particularly high since 2005. Therefore and due to the statutory requirements of international legislation, a post-mortem program was initiated and necropsies have been conducted at Utrecht University since 2008. The aims of the program were to monitor causes of death (CoD), specifically those of anthropogenic origin, and to determine health- and nutritional status of stranded individuals. The largest anthropogenic category was bycatch (17%), with mainly juveniles affected. Other, infrequently diagnosed anthropogenic CoD were trauma (4%), largely most likely due to ship collision, and marine debris ingestion and entanglement (0.3%). Besides, trauma due to grey seal (Halichoerus grypus) attacks was a frequently assigned CoD category (24%). However, the category of infectious diseases is by far the largest (32%), affecting mainly adults. A range of infectious agents, including viruses, have been determined, but the lack of routine screening hampers the assessment of a prevalence for most. Globally, reported infectious disease outbreaks in marine mammals have been rising and there therefore is a pressing need to expand the monitoring efforts to pathogen screening. This would be an important way to investigate both the spread of zoonoses, and the effects of threats like noise and chemical pollution, that do not always leave distinct lesions but rather have indirect effects on their immune system, behaviour, health or reproduction.

Short BIO

Lonneke is a biologist who works as Assistant Professor at the Faculty of Veterinary Medicine of Utrecht University in the Netherlands. She is the project manager of the Dutch Stranding Research program on marine mammals. Lonneke is a member of the Advisory Commission of ASCOBANS and jointly leads the work on standardization of post-mortem protocols throughout Europe. She is also a member of the International Whaling Commissions Expert Panel on Strandings and the Small Cetacean Group of the IUCN. She holds an MSc in Environmental Biology and a PhD on porpoise health. Her research interests intersect the fields of cetacean biology, ecology and pathology.

Wolves returning to the Low Countries: a closer look at the Hechtel-Eksel pack

Jan Gouwy, Joachim Mergeay, Timo Van Der Veken, Koen Van Den Berge, Reasearch Institue for Nature and Forest (INBO), Belgium

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Despite some public awareness campaigns, the arrival and settlement of wolves in Flanders (Northern Belgium) in 2018 came as a surprise to most people. After all, the species had been absent for over 200 years and it was a common belief that wolves lived in vast stretches of wilderness in the far corners of Europe. Like everywhere else in Europe where wolves are making a comeback, many people are struggling to believe that wolves arrived without human intervention. With wolf ecology in mind, looking back in time and space on a continental scale provides answers tot his spectacular comeback.

Nowadays, GPS transmitters and genetics provide us with detailed information about wolf movements across Europe. Monitoring with camera traps, tracking and genetic sampling provides us information about the home range size and terrain use of the Hechtel-Eksel pack. Analysis of scats collected in 2018-2021 provided insight into the diet of these wolves settled in a highly fragmented landscape dominated by human infrastructure, scattered rural habitations and ribbon development, but with large military terrains as safe refuge sites. Looking at the future, human re-adaptation to the presence of this large predator will be a necessity, as more wolves will arrive and try to settle in our regions year after year.

Short BIO

Jan Gouwy works as a research assistant at the Research Institute for Nature and Forest (INBO) of the Flemish Government since 2008. He is part of the Wildlife Management and Invasive Species team and has been working on numerous projects on distribution, ecology and management of carnivore species. Between 2012 and 2020 he also collaborated intensely with Prof. Vadim Sidorovich on research on wolf and lynx ecology in the forests of Belarus. Since their settlement, Jan has been monitoring the wolves in Flanders intensively.

Raccoons: an invasive alien species with public health significance

Miriam Maas[1], Rea Tatem-Dokter[1], Mike Heddergott[2], Vinciane Schockert[3], Valérie de Waele[3], Alain C. Frantz[2]

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The geographic range of the zoonotic raccoon roundworm (Baylisascaris procyonis) is expanding together with the range of its host, the raccoon (Procyon lotor). This creates a new public health risk in parts of Europe where this parasite was previously absent. In the Netherlands, a raccoon population is becoming established and incidental findings of B. procyonis have been reported. In Wallonia, Belgium, the raccoon population has reached an estimated 50.000-75.000 individuals.

To assess the risk to public health, the prevalence of B. procyonis was determined in the province of Limburg, and in the region of southern Belgium. Furthermore, genetic methods were employed to assess invasion pathways of both the raccoon and B. procyonis to aid in the development of control measures.
Macroscopic analysis of intestinal content and testing of faecal samples were performed to detect B. procyonis adults and eggs. The population genetics of both B. procyonis and its raccoon host were analysed using samples from central and northwestern Europe.
B. procyonis was found in 14/23 (61%, 95% CI: 41%–78%) raccoons from Limburg, but was not detected in 50 Belgian raccoons. Genetic analyses showed that the majority of the Dutch raccoons and their roundworms were introduced through ex-captive individuals.

As long as free-living raccoon populations originate from captivity, population control methods may be pursued. However, natural dispersal from the border regions will complicate prolonged population control. To reduce the public health risk posed by B. procyonis, public education to increase awareness and adapt behaviour towards raccoons is key.

Short BIO
Miriam Maas works as researcher for the Dutch National Institute for Public Health and the Environment. Her work concentrates on wildlife-borne zoonoses, with a focus on zoonoses related to wild rodents and invasive mammal species. She has a special interest in urban ecology and the challenges of greening of cities.
She graduated from Veterinary Medicine at the University of Utrecht in 2010. With an interest in wildlife and infectious diseases, she continued with a PhD on Tuberculosis in African lions. After this PhD, she started as a researcher at the Centre of Infectious Disease control of the Dutch National Institute for Public Health and the Environment.

Urban red foxes (Vulpes vulpes) in the UK: Ecology and Disease Implications

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Red foxes (Vulpes vulpes) are common in UK urban ecosystems and generally occur at higher densities here than in rural areas. In studied cities (e.g., Bristol, Oxford, Brighton) they are highly territorial and favour private gardens. Our work investigates fox densities, movement ecology, health, and welfare, within a context of enabling human-wildlife coexistence, including disease management.

In the UK people are generally tolerant of urban foxes (but attitudes can be polarised) and no significant zoonoses have been detected. This contrasts with fox populations elsewhere in Europe/globally, where foxes are important hosts of rabies and echinococcosis. However, urban foxes in the UK are putative sylvatic reservoirs of pathogens of veterinary concern, including the nematode Angiostrongylus vasorum (av) and sarcoptic mange (Sarcoptes scabeii). Further, their relative role as hosts of the zoonotic Toxocara canis is largely unexplored.

Using citizen science methods, we found that urban fox populations are increasing throughout the UK and expanding their distribution northwards. We also detected a general absence of mange foci, i.e., the disease is endemic and widespread. Brighton foxes favour large, well-connected suburban gardens, and management of density dependent infectious diseases should focus on these environments. Disease control for av must consider the behaviour of terrestrial gastropod molluscs as their occurrence drives canine infection risk. Lastly, fox diet appears to be more carbon-based and contain more fat in urban versus rural environments, consistent with widespread anthropogenic feeding in cities.

The research was conducted in collaboration with Nottingham Trent University (Dawn Scott, Simon Tollington, Jono Fletcher) Queen's University Belfast (Eric Morgan), Ruth Cox (Animal and Plant Health Agency), and Rowenna Baker and Francesca Cagnacci (Edmund Mach Foundation).

Short BIO

Dr Bryony Tolhurst is a Principal Lecturer in ecology and conservation at the University of Brighton, UK. She is predominantly a mammal behavioural ecologist in the context of human-wildlife conflict, whose ultimate research goal is to inform and enable human-wildlife coexistence. Her current projects include studies of movement ecology and population dynamics of urban mammals in the UK, in the context of supplementary feeding by humans, and infectious disease transmission between wild carnivores and pets. In particular she is interested in pathogens of veterinary importance including Angiostrongylus vasorum and Sarcoptes scabieii. In addition, she works on resolving conflict due to depredation of livestock by leopards and developing tools to estimate population size and habitat selection by pangolins, both in Kenya. She is keen to collaborate on any aspect of wildlife management relating to disease or other sources of conflict, in the UK, Europe, and beyond.

Urban greening and rats The relation between urban greenspace, zoonotic pathogen prevalence and richness in wild rats

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Increasing biodiversity is one of the many beneficial effects of urban greening. However, increasing biodiversity could also result in an increase of unwanted or pest species such as wild rats, which are known to be host to a wide range of zoonotic pathogens that can cause severe disease in humans. Therefore, it is important to gain more insight into the effect of urban green on wild rats to minimize the potential negative effects for public health.

In this study we investigated the relation between the amount of urban green and zoonotic pathogen prevalence in wild rats. In addition, we investigated which other factors are related to zoonotic pathogen prevalence and richness. We trapped brown rats in Amsterdam, Rotterdam and Eindhoven, followed by the detection of zoonotic pathogens (18 different bacteria/viruses/parasites) using (q)PCR (and IFA/ELISA). All results were modelled using binomial and poisson GLMMs.

We detected 13/18 tested zoonotic pathogens in these rats, with the highest prevalence detected for *Bartonella* spp. (25%), followed by *Leptospira* spp. (20%) and ESBL/AmpC-producing *E.coli* (12%). *Bartonella* spp., *Leptospira* spp. and *Borrelia* spp. had significantly higher prevalences in rats from urban parks. Pathogen richness had a significant positive relation with both NDVI (measure of greenness) and rat bodyweight. Thus, rats living in greener urban areas and older rats carry significantly more zoonotic pathogens. The observed pathogen prevalences are not alarmingly high with regard to public health, but awareness for risk groups, such as pest controllers, should be improved.

Short BIO

Marieke de Cock is a 4th year PhD student at RIVM and Wageningen University working on the topic: 'The effect of urban greening on zoonotic pathogens transmitted by wild rats'. Her PhD project is part of the One Health European Joint Programme. She studied both her Bachelor and Master in Biology at Wageningen University, with a thesis at the department of Entomology and an internship at RIVM.

Rose-ringed parakeets (*Psittacula krameri*) in the city

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Due to its popularity as a pet bird, ring-necked parakeets (Psittacula krameri) have been able to establish invasive populations worldwide, including in areas with climates significantly colder than the native range of this Afro-Asiatic bird species. Mechanisms contributing to the succes of ring-necked parakeets as an invasive species include their pre-adaptation to human environments across their native range, release from predators across the invasive range, and their broad and flexible foraging behavior that allows them to exploit available food sources. Intraspecific niche variation in cold tolerance combined with ample trade in individuals from across the native range also likely contributes to the success of the species in colder parts of Europe.

We collected environmental and socioeconomic data of parakeet impacts using a systematic evidence search framework. A total of 42% of entries reported damage to agriculture (mainly in native ranges), while within Europe most entries concerned interspecific competition (39%). When using this information for conducting invasive species impact assessments, depending on the way the evidence is used, ring-necked parakeets can cause 'minimal-moderate' to 'moderate-major' overall impacts. I close with discussing how this information can be leveraged to best inform policy-makers and conservations managers, e.g. through the production of policy briefs.

Short BIO

Diederik Strubbe is an ecologist researching processes affecting the invasion success of non- native species. He combines observational, experimental and niche modelling techniques to unravel how species introduced to areas beyond their native distribution ranges cope with new environments, and how such 'invasive species' can impact native communities and alter ecosystem functioning. His research aims at a better understanding of the factors affecting the reliability of forecasts of invasion risk.

Short communications

Zoonotic pathogens linked with hedgehog diphtheric disease

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Hedgehog diphtheric disease (HDD), an ulcerative skin disease with a high fatality rate is an emerging threat to European hedgehogs (*Erinaceus europaeus*). We explored the potential role of a panel of zoonotic pathogens in the presumed multifactorial nature of HDD in 188 hedgehogs from three wildlife rescue centers in Belgium.

As expected, and with a prevalence of 67% in 57 hedgehogs with skin lesions, characteristic of HDD, the occurrence of *Corynebacterium ulcerans* was strongly associated with the disease. Remarkably, with a prevalence of 42% in affected animals, infections with *Borrelia burgdorferi sensu latu* were 3.92 times more likely to be detected in HDD (95% confidence interval: 1.650 – 9.880; p = 0.0024). Overall, 40 hedgehogs tested positive for the *Borrelia burgdorferi sensu latu* complex, including *B. afzelii* (n = 30)*, B. bavariensis* (n = 7) and *B. spielmanii* (n = 7). Other widely occurring pathogens included *Salmonella* (prevalence of 19%, with three PFGE profiles) and *Leptospira* sp. (prevalence of 11%, including *L. interrogans* and *L borgpetersenii*) but these were not associated with occurrence of HDD.

These findings show that hedgehogs in Belgium represent a significant reservoir of multiple zoonotic bacteria, of which toxigenic *C. ulcerans* and *Borrelia* burgdorferi *sensu latu* are associated with widespread hedgehog skin pathology and mortality.

Ticking off the ungulate box – the role of different ungulate species in the ecology of tick-borne pathogens

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Ungulates play a central role in the life cycle of *Ixodes ricinus*, an important vector of tick-borne pathogens in Europe. The composition of ungulate communities is changing across Europe, with species expanding their ranges and increasing in numbers. We identified the role of different ungulate species in the spread of *I. ricinus*-borne pathogens. Pathogens that can cause disease in both humans and livestock.

Through a literature review and field studies, we investigated the relative importance of ungulates in the transmission of the different ecotypes of *Anaplasma phagocytophilum* and genospecies of *Borrelia burgdorferi* s.l.. We quantified tick burdens, relative ungulate densities, vegetation structure and (infected) tick density in the vegetation.

These studies indicated that deer contributed more to the spread of tick-borne pathogens than wild boar, and fallow deer more than the other deer species. We then modelled how changing an ungulate community composition affects the establishment of pathogens, expressed as the R_0. An increase of fallow deer, and co-varying decrease of roe deer, increased the R_0 of the zoonotic *A. phagocytophilum* ecotype 1, while it decreased for the non-zoonotic ecotype 2. The effects on *Borrelia afzelii* and *B. garinii* were smaller.

Depending on the pathogen, different deer species may thus vary in their effect on the circulation of tick-borne pathogens. Therefore, we conclude that the different roles of the ungulate species should be taken into account, both in research and management.

Poster presentations

Prevalence of Fox Tapeworm in Invasive Muskrats in Flanders

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Since 1994, muskrats (*Ondatra zibethicus*) caught in Flanders (or just across the border) have been dissected with the aim of understanding their ecology. Whilst doing so a large number of parasites were observed in the abdomen of the dissected animals, most notably Taenia taeniaformes.

In 2008 a first individual infected with fox tapeworm (*Echinococcus multilocularis*) was found, caught just across the regional border in Wallonia. Hence, from 2009 onwards all muskrats caught in Flanders, Wallonia and France by pest controllers of the Flanders Environment Agency (VMM) were collected and dissected with the aim of understanding the prevalence of this parasite.

Visual examination of the livers of 15.948 muskrats caught between 2008 and 2017 revealed 203 infected animals. Regionally we found 82 infected animals out of 9.425 (0,87%) in Flanders. All of the infected animals were found in municipalities bordering the Flemish-Walloon border.

Although EM infection was expected to spread northward from Wallonia to Flanders, this was not observed in the dissected muskrats. Here we argue that keeping muskrat populations low through extensive culling programs may have aided in stopping this spread. In 2022 we are again examining every muskrat caught in Flanders for the presence of fox tapeworm.

Detection of *Echinococcus multilocularis* prevalence in the red fox (*Vulpes vulpes*) in the Wallonia part of the geophysical region of Hesbaye (Belgium) using real-time PCR.

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Alveolar echinococcosis caused by the metacestode stage of *Echinococcus multilocularis*, is considered as a serious and potentially lethal zoonosis in the Northern Hemisphere's cold or temperate regions. The parasite has a sylvatic life cycle based on predator-prey interactions, mainly between red foxes (*Vulpes vulpes*) and small rodents and has spread across Europe over the last decades.

Therefore, the continued monitoring of animal infection and environmental contamination is a key issue in public health surveillance. Following an active surveillance process done in the Wallonia part of the geophysical region of Hesbaye (low northern alluvial plateau in the eastern Belgium), a collection of 213 red foxes, harvested between 2018 and February 2022, were analyzed by real-time PCR technique (qPCR) to detect *E. multilocularis* DNA released in red fox intestines.

The results highlight an important *E. multilocularis* prevalence of 44,6 % confirming a geographical expansion of the parasite in Belgium in comparison with previously published results.

High mortality in European Hedgehogs associated with ulcerative skin lesions in Wallonia (Belgium): Isolation of potentially zoonotic *Corynebacterium ulcerans*

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Corynebacterium ulcerans is an emerging zoonotic pathogen that has been isolated from hedgehogs. The objectives of this study were (1) to determine the prevalence of this bacterium in two cohorts of hedgehogs and (2) to clarify its zoonotic potential. 218 hedgehogs were necropsied and classified into two cohorts according to the absence (cohort A, control group) or presence (cohort B) of specific skin lesions. Molecular and conventional analyses were performed on samples from both cohorts.

The necropsies revealed a high proportion (64.7%) of individuals with ulcerative skin lesions. The frequency of detection of tox-bearing *Corynebacteria* of the diphtheriae complex was much higher in cohort B (80%) than in the control cohort (11.7%) and the invasive nature of these Corynebacteria is demonstrated. Mass spectrometry analysis confirmed the presence of Corynebacterium ulcerans in several samples and 100% of these strains produced diphtheria toxin in vitro. Without being able to establish a causal link, our results suggest that this *Corynebacterium* is an opportunistic pathogen taking advantage of skin trauma to induce, alone or in synergy, specific skin lesions in hedgehogs. Moreover, the zoonotic risk is real. The fact that toxigenic *Corynebacterium ulcerans* strains were detected in the skin lesions of 75% of the animals (60 out of 80) that were treated/manipulated in the centers should encourage caution.

Using a trait-based approach to assess climate change vulnerability in Dutch mammals

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The shifting climate is expected to become an important driver of species extinction and redistribution. Using a trait-based approach we assessed the vulnerability to climate change of 59 mammalian species native to the Netherlands. To determine whether the current surveillance by the DWHC can detect changes in vulnerable species populations, the results of the assessment were linked to the current number of mammals sampled for general surveillance in the Netherlands.

Species' vulnerability was estimated based on three parameters:
(i) degree of climatic exposure throughout the geographical range of the species;
(ii) the species' lack of potential to persist *in situ* (sensitivity)
(iii) the species' inability avoid, recover, or adjust to the impacts of climate change (low adaptive capacity).

We identified 25% of the mammals to be highly exposed, 24% of the mammals to be highly sensitive, and 14% to have a low adaptive capacity. Two species were highly vulnerable (i.e., highly exposed, highly sensitive, and low adaptive capacity). The comparison with the DWHC general surveillance database revealed that species vulnerable to climate change are relatively poorly represented. By using species-specific trait data in relation to a climate change exposure assessment, we were able to enhance and contextualize our understanding on how a driver is likely to affect a species in a certain area of interest. This can serve as a starting point of guiding current surveillance strategies.

Distemper in Brussels urban foxes

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In 2020, distemper was diagnosed in Brussels urban foxes with neurologic signs or found dead. The high population density of urban foxes with fading territoriality offered ideal circumstances for a rapid dissemination after introduction of the virus.

Selected tissue samples collected during necropsy of ten foxes were examined with immune-histochemistry and PCR. Al immuno-labeled samples proved positive for canine distemper virus (CDV). Both a pan- paramyxovirus-PCR and a pan-morbillivirus PCR were positive in all examined samples. Sequencing the obtained PCR bands allowed to situate the CDV strain within a cluster of viruses found earlier in foxes in Germany.

Relationship of CDV strains with strains from further east, was also found in a distemper outbreak in stone martens in Belgium in 2010. Considering distemper does not occcur in wild carnivores in the UK, applying stricter import politics for dogs, and considering distemper is poorly controled in dogs in eastern Europe, a possible role of the intensive dog traffic from eastern to western continental Europe can be presumed. Systematic phylogenetic screening of CDV strains in wildlife and in domestic dogs is needed to elucidate the role of dog traffic in distemper epidemics in continental Europe.

Falcon: User-friendly software for digital animal and observation registration in wildlife rehabilitation centres

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Animals and observations on these animals can be registered by means of user-friendly software at wildlife rehabilitation centres. The primary aim is to reduce the workload of wildlife rehabilitation centres by simplifying administrative tasks; in addition, the software can help to further professionalise by adding functions that support the employees. A digital system also offers opportunities for efficient collaborations, including between the centres themselves, with veterinarians and with scientific parties.

By registering animals within Falcon, a secondary system can also be set up where the incoming animals and observations lead to an 'early warning system' for outbreaks of (new) animal diseases and other (ecological) signals. By offering wildlife rehabilitation centres the opportunity to participate as a link in the One Health approach, the position of these centres in society can be strengthened and the important work they perform can be underlined.

A broad collaboration is needed to set up this system. Falcon ICT already collaborates with wildlife rehabilitation centres, Van Hall Larenstein University of Applied Sciences, Wageningen University, Ministry of Agriculture, Nature and Food Quality, Stichting DierenLot, Dutch Wildlife Health Centre, RIVM, Vogelbescherming Vlaanderen, seven veterinarians specialized in wildlife and many other partners who have indicated that they wish to participate in an advisory and review panel.

Health effects of patagial wing tags in red kites (*Milvus milvus*) in England

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Patagial wing tags are commonly used for identification of red kites (*Milvus milvus*) for post-release monitoring, as they are easy to apply, affordable, permanent are apparently safe. The red kite was successfully reintroduced in the United Kingdom by the end of the 20th century and post-release health surveillance has been achieved through radio and satellite tracking, monitoring nest sites and pathological investigation of red kites found dead.

This study reports on pathological findings associated with the use of patagial wing tags in three of 142 (2.1%) of wing-tagged red kites examined post-mortem since the beginning of the reintroduction project in 1989. Further surveys of the effects of patagial wing tags on red kites and other birds are advocated and the future use of patagial wing tags in raptors should be carefully monitored.

Studying *Borrelia* infections in great tits by xenodiagnoses

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A crucial factor to predict the persistence and spread of infections in natural systems (and potential spill-over to humans) is the capacity of so-called reservoir hosts to maintain the infection and transmit it to others. This is known to vary greatly between species, but also within species and through time, although this part of the variation is often less well understood. We focus on between- and within- individual variation in infectiousness in a natural population, using a bird-tick-*Borrelia* system as model.

Great tits are among the most important reservoirs of *Borrelia garinii*, one of the main causal agents of Lyme disease. We study how the capacity of birds to transmit these bacteria to feeding ticks varies between individuals, how it varies through the annual cycle, and whether stressful episodes may reactivate infections in birds that previously were not infective. To determine the infectiousness of a bird we make use of xenodiagnosis i.e. allowing pathogen-free ticks to feed on birds and test for successful bird-to-tick transmission. We are doing this in a well-studied population where we can repeatedly test the infectiousness of the same individuals and relate this to their age, sex, condition and other factors. I will present our, yet to be analysed, first results collected in the latest breeding season as well as our future plans for the project.

A case report of an uncommon parasitic infection of *Collyriclum faba* in a female Red-backed shrike (*Lanius collurio*) in Hotton (Belgium)

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During summer 2022, a wild adult female red-backed shrike (*Lanius collurio)* was caught during a scientific capture session in Belgium with a large crusted mass within the skin of the cloacal region. She presented around 10 vesicles about 5mm of diameter. It was non obstructive, but she had a poor body condition. She was transferred in the wildlife rehabilitation center of Hotton (Belgium) for veterinary auscultation. The veterinary decided to bring her at the veterinary faculty of Liège for a surgery. After anesthesia, vesicles were opened, and content was identified as a fluke infection of *Collyriclum faba.* After wound healing and a control antiparasitic treatment she was successfully released.

Presence of Antimicrobial Resistance on Highly Migratory Sharks of Cocos Island: A Pristine and Pelagic Marine Ecosystem

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Antibiotic resistance is a global scale problem in different environments, including untouched and minimally impacted ones, wildlife can act as sentinels of antibiotic resistant microbes present in pristine wild regions far from intense human activity. Cocos Island is an oceanic and protected island in the tropical Pacific of Costa Rica and part of the Cocos-Galapagos-Malpelo migratory pathway characterized for being a hotspot for highly migratory marine species. Sharks are a prominent taxon in Cocos Island arriving from the coastal territories of Central America and South America where they give birth in highly impacted and polluted rivers and estuaries that are surrounded by farmlands and aquaculture establishments where intensive use of antibiotics on livestock take place exposing these sharks to a potential antibiotic resistant microbiome. There are no antibiotic resistance studies in Cocos Island, a pilot sampling for antibiotic resistance was conducted in a tagging expedition capturing Galapagos, black tip, and silvertip sharks. Cloacal and mouth swabs were performed and preserved in Cary-Blair medium until cultured in TCBS Agar, Harlequin E. coli/Coliform Agar and Enterococcosel Agar. The bacterial identification and antibiogram was conducted by the automatized Vitek system 2. *Vibrio alginolyticus* and *V. metschnikovii* presented acquired resistance for Ampicillin, while *Enterococcus faecalis* for Quinunpristin/Dalfopristin, Teicoplanin, Erythromycin and Vancomycin. These preliminary results put migratory species and in this case sharks as potential carriers of resistant microbiomes from impacted regions to pristine environments where migratory routes act as potential gateways although other means of dissemination such as marine currents can not be discarded.

Ixodes ricinus and its pathogens near greenspace infrastructure: spatial sorting explained by local host abundance

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Drivers of tick (*Ixodes ricinus*) density and pathogen prevalence remain a topical knowledge gap, with host abundance and vegetation characteristics as proven drivers at large geographic scales. Recent studies redirect focus to within-greenspace variation, as understanding its drivers can help reduce tick bite risk. In present study, conducted within 10 public greenspaces in Flanders, Belgium, density of nymphs (DON) was consistently higher in the interior of forest stands compared to recreational infrastructures (benches and trails). Ticks were screened for pathogenetic bacteria (*Borrelia burgdorferi* s.l., *Rickettsia*, *Neoehrlichia mikurensis*, *Anaplasma phagocytophilum* and *Borrelia miyamotoi)* and variation in nymphal infection prevalence (NIP) and DON was explored using generalized linear models, including local host abundance (measured by camera traps) and vegetation characteristics as explanatory variables. We observed higher DON when well-developed herb- and canopy-layer vegetation was present. The same was true for higher abundance of small mammals, in addition to consistently Lower DON near infrastructure. Our data suggest an infrastructure effect on local host abundance, which may lead to spatial sorting of (infected) ticks. One example is the higher NIP of *Anaplasma* in forest interior, correlating with higher reservoir host (deer) abundance. However, NIP of different pathogens did not appear to have a single driver, as demonstrated by the genospecies of *Borrelia burgdorferi*: *B. afzelii* NIP correlated with infrastructure and vegetation characteristics, whereas *B. garinii* NIP did so with local abundance of songbirds, its reservoir. Ongoing analyses will focus on quantifying these direct and indirect infrastructure effects by use of structural equation modelling.

Potentially zoonotic viruses detected in wild rodents from Antwerp, Belgium

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We present the preliminary results of a survey of viruses of public health and veterinary importance from wild rodents trapped in the province of Antwerp, Belgium. From October 2020 through April 2022, rodents were captured every autumn and spring in 6 different sites classified as "forest", "urban park" and "zoo" as part of the Biodiversa "Bioroddis" project. Serum and tissue samples were collected from *Myodes glareolus*, *Apodemus sylvaticus*, and *Microtus agrestis* and analysed for the detection of Orthohantavirus, Mammarenavirus, Orthopoxvirus and Coronavirus.

To date, samples were seropositive for Orthopoxvirus (101/516), Orthohantavirus (41/516) and Mammarenavirus (8/516). For SARS-CoV-2, one IFA-positive *A. sylvaticus* was negative by seroneutralisation. The presence of Puumala virus was confirmed by PCR, while 112 of 276 rodents tested were pan-coronavirus PCR positive. Sequencing pointed to the presence of Alpha and Betacoronavirus.

These results demonstrate the presence of all groups of virus studied in the 3 types of landscapes, with an apparent predominance of seropositive rodents in the "forest" followed by the "urban park"; except for the Mammarenavirus that seems to be more abundant in the "urban park" environment and was absent in the "zoo". Regarding rodent species, *M. glareolus* and *A. sylvaticus* were seropositive for all the virus studied, while *M. agrestis* was seropositive for Orthopoxvirus only. *Myodes glareolus* preliminary showed a higher prevalence for all viruses except for Mammarenavirus. Further analyses are warranted to characterize the viruses detected and assess the role of the different host species in their dynamics.

Investigating SARS-CoV-2 spillover to sewer rats, Antwerp, Belgium

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As the SARS-CoV-2 virus became omnipresent among humans with the progressing pandemic, the spillover to other animals has become a great risk. Because of the presence of SARS-CoV-2 virus in human faeces, there is the possibility of interspecies transmission to sewer-hosted rats. Such transmission may lead to the establishment of new animal reservoirs, which may later increase the risk of transmission of SARS-CoV-2, further evolved in rats, to the human population. We sampled Norway rats (Rattus norvegicus) in underground sewer systems in Antwerp in November-December 2020 (N=39), April-May 2021 (N=50) and in February 2022 (N=27, plus 23 faecal droppings). Two faecal samples collected in February 2022 from the same site each tested positive for SARS-CoV-2 with high Ct values in one of two qPCR repeats, but the ARTIC protocol failed to obtain sufficient amplicons for successful sequencing. The risk of human-to-wildlife spillover remains, and it is crucial that wildlife population continue to be monitored for SARS-CoV-2.

Evaluating the risk of human-to-wildlife transmission of SARS-CoV-2 through receptor binding modelling

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The causative agent of the COVID-19 pandemic, SARS-CoV-2 is capable of infecting many different mammal species. As a significant proportion of people worldwide are infected with SARS-CoV-2, there is a non-negligible risk of humans spreading SARS-CoV-2 to wildlife, in particular mammals. The susceptibility for SARS-CoV-2 varies among mammalian taxa, in part caused by genetic differences in the ACE2 gene that encodes the cell surface receptor for viral cell entry. We sampled archived specimens of 25 West-European mammal species and used a series of hemi-nested RT-PCRs appropriate for fragmented mRNA to amplify and sequence their ACE2 coding region. Together with publicly available ACE2 sequence data, we evaluate the binding capacity of wild-type SARS-CoV-2, as well as newer variants, to ACE2 receptors of species across the mammalian phylogeny. The ACE2 receptors of most species are predicted to bind well to the different SARS-CoV-2 variants' receptor binding domain, with similar, slightly worse or better binding capabilities than human ACE2. We discuss the shortcomings of in silico receptor binding analyses to predict virus infection dynamics, though overall we confirm that a large proportion of mammal species are susceptible to SARS-CoV-2.

Coronaviruses in bats in Flanders, Belgium

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Coronaviruses are present in several bat and other wildlife species in Europe, but so far no coronaviruses have been detected in bats in Belgium. We non-invasively collected 1826 fecal droppings from 17 church attics in Antwerp and East Flanders provinces, by placing clean paper sheets on the attic floors and collecting droppings the next day. During the swarming season, we furthermore collected swab and excretion samples from 288 live bats caught over four sessions. DNA/RNA was extracted from pools of 8 fecal samples and tested with a pan-coronavirus qPCR (Escutenaire et al., 2007). 65 samples were considered positive, and re-tested with a conventional PCR (Holbrook et al., 2021), though only 14 samples were positive with the latter test. Sanger sequenced RdRp sequences revealed the presence of three distinct coronaviruses: a Merbecovirus strain (betacoronavirus) in 10 *Plecotus auritus* samples, and two distinct alphacoronavirus strains, in respectively 3 samples of *Myotis mystacinus* and 1 sample of *Myotis daubentonii*. The alphacoronavirus strains are closely related to similar strains detected previously in *Myotis* species across Europe, while the betacoronavirus strain clustered with both a known strain from *P. auritus* from Italy and a strain from *Rhinolophus ferrumequinum* from South Korea. Considering the relatively low prevalence, our high sample size acquired through efficient fecal dropping sampling was likely crucial for sufficient coronavirus detection power.

Bacteria of public health concern in fecal samples of Kuhl's pipistrelle bats in connection with environmental degradation of Mediterranean ecosystems

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The increasing emergence of infectious diseases, including zoonotic and animal pathogens poses a serious threat to human and animal health, and entails a significant economic burden worldwide. In a One Health context, a multidisciplinary approach on the relationship between anthropogenically-derived ecosystem degradation and pathogen spillover risk has become paramount to prevent future pandemic events. Bats are well-known hosts of a wide range of zoonotic pathogens. As many species of bats are highly adapted to anthropogenically modified ecosystems, unique attention has been placed on the spillover risk of bat-borne pathogens onto livestock and human populations. Particularly, previous studies have identified bacterial pathogens within the fecal microbiome of bats. The aim of this project was to study the link between the presence of zoonotic and animal bacteria in bat fecal samples and environmentally degraded ecosystems. Fecal samples (n=31) were collected during summer 2021 directly from Kuhl's pipistrelle bats (*Pipistrellus kuhlii)* captured in the following Mediterranean ecosystems: old-growth forest (n=8), extensive agriculture landscape (n=6), immature and secondary forest (n=8), and urban and intensive agriculture landscape (n=9). DNA from samples were sequenced using MinION Nanopore Oxford Technology. The metagenomic analysis revealed the presence of bacterial species encompassing both zoonotic and animal pathogens in different proportions depending on the ecosystem surveyed. However, undisturbed scenarios presented a higher alpha diversity and richness of pathogenic bacteria. Therefore, anthropogenic pressure did not influence the presence of pathogenic bacteria in Kuhl's pipistrelle bats in NE Spain.

Comparison of trap-bias and health outcomes between Sherman and Heslinga live-traps in Wisconsin, United States

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Small rodent trapping is a common practice in wildlife, forest and ecological research and education. Since their establishment in the 1960s, Institutional Animal Care and Use Committees have greatly improved handling and sampling procedures to better protect small mammals captured during field studies. However, trapping can still be considered sub-optimal. The objective of this study was to compare 1) rodent health and 2) capture biases for two live-trap types: the Sherman live-trap and the Heslinga live-trap. We hypothesized that the elevated nesting chamber and gravity-fed door of the Heslinga trap would improve animal health indicators (alertness, turgor, condition of fur, injuries) and survival compared to the conventional Sherman trap. Conversely, the larger entrance of the Sherman trap would allow for the capture of more rodent species (richness). In a paired study design, small rodents were trapped from July to September 2019 in a mixed forest in Northcentral Wisconsin, United States. Heslinga traps were more likely to capture shrews (*Sorex* spp.) compared to Sherman traps (15 shrews in 727 trap nights versus 1 shrew in 731 trap nights). There was no significant difference in *Peromyscus* spp. captures. Failed trap events were caused by triggered doors without a small rodent capture in Heslinga traps and insensitive / stuck treadles in Sherman traps. Most captured animals were active, dry and well-hydrated. We showed the importance of utilizing different trap types to assess rodent communities and explored a quick health scoring system that can be utilized to evaluate and adjust trap conditions to improve small rodent trap protocols.

Monkeypox viruses circulate in distantly-related small mammal species in the Democratic Republic of the Congo

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Human monkeypox is a zoonotic disease caused by monkeypox virus, which naturally occurs in Africa where two genetic clades have been discerned: a West African and a Congo Basin clade. The increasing incidence for both strains in endemic areas and outbreaks outside of this region highlight the need for a better understanding of the eco-epidemiological drivers of the disease. However, the presumptive animal source of primary human infections remains unidentified and the virus' natural reservoir cryptic.

Since 2010 we have been monitoring the biodiversity of small mammals and their pathogens in several areas in the Ituri and Tshopo provinces of the Democratic Republic of Congo (DRC). A subset (n=256) of samples, including tissues collected from rodents (n=97), shrews (n=93) and bats (n=66) over a period of six years, was tested for the presence of MPXV DNA using two PCR assays targeting different viral genes and positives were confirmed by Sanger sequencing.

Tissues from three rodent species (*Funisciurus bayonii*, *Stochomys longicaudatus*, *Cricetomys* sp. 2 sensu) and one shrew (*Crocidura littoralis*) contained MPXV DNA. By applying in-solution hybridization capture and high-throughput sequencing, we successfully retrieved one complete MPXV genomes from *F. anerythrus* and *C. littoralis*, and one partial genome (59%) from *F. bayonii* (has to be confirmed). Bayesian phylogenetic analyses revealed that the MPXVs found in the squirrel and shrew are closely related to each other and fall within the diversity of MPVX strains found in humans in Central Africa. Therefore, MPXV appears to naturally circulate in multiple, distantly-related rodent species from at least three different families (Sciuridae, Muridae and Nesomyidae), as well as in shrews (order Eulipotyphla). While some of these detection events may reflect dead-end infections, they are compatible with the hypothesis that MPXV has a broad host range and possibly a complex multi-host ecology.

African Swine Fever in Wild boars in Belgium : Story of a successful eradication

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In September 2018, ASF was detected on wild boars in the south of Belgium. Zoning was immediately applied and strong measures were implemented in both domestic and wild *Suidae*. Thanks to good preparedness and collaboration, Belgium was successful to eradicate ASF in wildlife in one year and domestic pig remained officially ASF free. Belgium regained its "all suidae" free status 2 years after the arrival of the disease (one year after eradication, according to the WOAH (ex OIE) code).

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