European Journal of Wildlife Research (2026) 72:4
https://doi.org/10.1007/s10344-025-02008-0

REVIEW

Pathogens in the garden dormouse *Eliomys quercinus*

Sarah P. Stubbe[1] · Eva Marie Kramer[1] · Sven Büchner[1,2] · Christine Jelinek[1,3] · Calvin Mehl[3,4] · René Ryll[3] · Elisa Heuser[3] · Dania Richter[5] · Donata Hoffmann[3] · Emilija Vasiliūnaitė[6] · Christopher B. Buck[7] · Indrė Kučinskaitė-Kodzė[6] · Alma Gedvilaitė[6] · Patricia König[3] · Viola C. Haring[3] · Vanessa Schulze[3] · Silva Holtfreter[8] · Christian Kohler[9] · Tobias Eisenberg[10] · Marie Christin Apfel[11] · Stephan Drewes[3] · Kathrin Jeske[3] · Cristian Raileanu[3,12] · Holger Meinig[1] · Anna Obiegala[13] · Martin Pfeffer[13] · Dina Raafat[8,14] · Dietrich Pöhle[15] · Claudia Ulber[15] · Cornelia Silaghi[3] · Rainer G. Ulrich[3,4] · Michael Lierz[1] · Johannes Lang[1]

Received: 25 April 2025 / Revised: 27 August 2025 / Accepted: 26 September 2025

Abstract

Wild rodents are important reservoirs and vectors of various pathogens, and play a crucial role in the spread of zoonotic pathogens. The garden dormouse (*Eliomys quercinus*), an arboreal nocturnal rodent species native to Europe, has declined throughout much of its natural range in recent decades. The reason for this ongoing decline is not yet fully understood, but infectious diseases may play a role. This study aimed to review the diversity of pathogens associated with the garden dormouse. For this purpose, a comprehensive review of the existing literature on garden dormouse-associated viruses, bacteria and protozoa was conducted. In parallel, we analysed samples from 294 garden dormice, that were found dead in Germany, for rodent-associated and zoonotic pathogens. The scientific literature currently, comprising 53 references, covers 73 years and primarily addresses *Borrelia* spp. and *Eimeria myoxi*. In the literature, a total of eight pathogens have been detected in garden dormice. In our own investigations, we were able to detect four different pathogens as well as antibodies against hepatitis E virus. The most prevalent pathogen found in our study was *Staphylococcus aureus* (29%, $n=58$). *Borrelia spielmanii* and *B. afzelii* were found in 5.6% of garden dormice ($n=143$) and 22% of the ticks attached to garden dormice ($n=32$). This study reports the first documentation of *Leptospira* spp. in garden dormice, with *L. borgpetersenii*, serogroup Sejroe, sequence type 197 detected in 2 of 176 animals. Beside these zoonotic pathogens metagenomic sequencing of selected samples revealed representatives of multiple DNA-virus families, including *Parvoviridae* and *Polyomaviridae*, most likely without zoonotic potential. There is currently no evidence, either from the literature or from our own investigations, that pathogens play a significant role in the decline of the garden dormouse in Germany.

Keywords Viruses · Bacteria · Protozoa · Zoonosis · *Borrelia* spp. · Metagenomic sequencing

Introduction

The garden dormouse (*Eliomys quercinus*), an arboreal rodent species native to Europe, occurring in the western Iberian Peninsula, Italy, France and on some Mediterranean islands, extending further to central and eastern Europe and the Urals (Storch 1978; Bertolino et al. 2008), has disappeared from a large part of its geographic range in recent decades (Bertolino 2017). Consequently, it is listed as vulnerable by the International Union for Conservation of Nature (IUCN) (Bertolino et al. 2024). Garden dormice commonly inhabit broad-leaved, mixed, or coniferous forests, but can also be found in high-altitude shrubs and rocky slopes (Büchner et al. 2024). They make use of rocky environments with tree or shrub cover (Bertolino et al. 2005) and can be found in these habitats from sea level to the upper limit of the arboreal vegetation (2,000–2,200 m) (Bertolino et al. 2008). Garden dormice are also synanthropic, in some

---

Sarah P. Stubbe and Eva Marie Kramer contributed equally to this work and share first authorship.

Extended author information available on the last page of the article regions occupying gardens, orchards, vineyards and even houses within human settlements (Gil-Delgado et al. 2010; Büchner et al. 2018).

The decline in garden dormouse populations appears to be the result of multiple, interacting factors. Habitat loss and fragmentation, reduced food availability, and exposure to environmental toxins such as rodenticides have been identified as primary drivers (Büchner et al. 2024; Famira-Parcsetich et al. 2024). However, the role of infectious diseases is yet to be established.

Wild rodents are natural reservoirs for a diverse array of viruses, bacteria, fungi, and parasites. While many of these pathogens persist asymptomatically in their reservoir hosts, they can cause severe or even fatal disease in other species, including humans (Meerburg et al. 2009; Nakamura et al. 2013; Yarto-Jaramillo 2015; Kirilov et al. 2022). Globally, approximately one-third of infectious agents detected in rodents – including viruses, bacteria, and protozoa – are capable of infecting humans (Han et al. 2015). Because garden dormice, similar to house mice (*Mus musculus*, *M. domesticus*) and rats (*Rattus* spp.), may occur in close proximity to human dwellings, the potential for zoonotic transmission – particulary via athropod vectors – warrants detailed investigation.

Vector-borne zoonotic pathogens

Among rodent-associated vector-borne zoonotic bacteria, the *Borrelia burgdorferi* sensu lato complex is particulary noteworthy. These spirochetes, which cause Lyme disease – the most prevalent tick-borne disease in humans in the Northern Hemisphere (Matuschka and Spielmann 1986) – are transmitted by *Ixodes* ticks. The vectors acquire the infection during larval feeding on infected rodents and subsequently transmit the bacteria to new hosts during the blood meal as nymphal stage (Steere AC 1989; Donahue et al. 1987; Lane and Loye 1991). Distinct *Borrelia* genospecies differ in their host associations: *B. afzelii* is maintained mainly by mice (*Apodemus* spp.) and voles (*Clethrionomys* spp.) (Wolcott et al. 2021), whereas *B. spielmanii* has been closely linked to the garden dormouse (Richter et al. 2004, 2006).

Rodents also serve as reservoirs for other tick-borne pathogens, including tick-borne encephalitis virus (*Flaviviridae*), and intracellular bacteria of the order Rickettsiales, such as *Anaplasma* spp., *Ehrlichia* spp. and *Rickettsia* spp. Additionally, protozoan parasites such as *Babesia* spp. and *Theileria* spp., which are of veterinary relevance, have been documented in rodent hosts (Meerburg et al. 2009; Kirilov et al. 2022).

Non vector-borne zoonotic pathogens

Beyond vector transmission, rodents can carry numerous viruses and bacteria that are directly transmissible to humans. Hantaviruses (*Hantaviridae*) are a prominent example, with species from the families *Muridae* and *Cricetidae* serving as reservoirs. In Europe, Puumala virus (PUUV) is the most commonly detected zoonotic rodent-borne hantavirus, though symptoms in humans are typically mild to moderate. However, hantavirus species such as Seoul virus (SEOV) and Dobrava-Belgrade virus (DOBV), which may cause more severe symptoms, are also present (Klempa et al. 2006).

Rodents and shrews in Europe are also known to transmit encephalitis-causing viruses such as bornaviruses and lymphocytic choriomeningitis virus (LCMV).

The variegated squirrel bornavirus 1 (VSBV-1) is associated with exotic squirrel species, while Borna disease virus 1 (BoDV-1) is maintained in bicolored white-toothed shrews (*Crocidura leucodon*) (Dürrwald et al. 2014; Hoffmann et al. 2015; Schlottau et al. 2017). In humans and other mammals, BoDV-1 infections can cause fatal, immune-mediated non-suppurative encephalitis with neurological deficits (Richt et al. 2001; Rubbenstroth et al. 2019; Schulze et al. 2020). Similarly, arenaviruses (*Arenaviridae*) can cause encephalitis in humans and are transmitted primarily by rodents of the families *Muridae* and *Cricetidae*. The lymphocytic choriomeningitis virus, the only arenavirus with a global distribution, is hosted mainly by the house mouse but has also been detected in wood mice (*Apodemus sylvaticus*) from Germany (Mehl et al. 2024) and Spain (Ledesma et al. 2009) and pet Syrian golden hamsters (*Mesocricetus auratus*) (Ackermann et al. 1972). Human infections occur through direct contact with rodents or their excreta and may cause aseptic meningoencephalitis or congenital malformations of the central nervous system (CNS) and eyes of embryos (Ackermann et al. 1972, 1975; Jay et al. 2005).

Other zoonotic rodent-borne viruses from Germany include hepeviruses, such as rat hepatitis E virus (ratHEV) (Johne et al. 2010), which may cause acute or persistent hepatitis in humans (Andonov et al. 2019) and orthopoxviruses such as cowpox virus (CPXV) or monkeypox virus (MPV) (Ntumvi et al. 2018; Meseko et al. 2023; Jo et al. 2024).

Among bacteria zoonoses, *Streptobacillus moniliformis*, the causative agent of rat bite fever, is noteworthy. This pathogen is transmitted directly via bites or indirectly through contaminated food or water, leading to fever, arthritis, and a maculopapular, petechial or pustular rush, and occasionally to life-threatening complications (Kondruweit et al. 2007; Eisenberg et al. 2017).

In Europe, the European brown hare (*Lepus europaeus*) is the main reservoir host for *Francisella tularensis*, the causative agent of tularemia, but *F. tularensis* has been detected also in voles of different species (Kaysser et al. 2008; Runge et al. 2011; Jeske et al. 2019).

Rodents also serve as important reservoirs for pathogenic *Leptospira* spp., spirochete bacteria that cause leptospirosis – one of the most widespread zoonotic diseases worldwide. Symptoms range from mild (headaches, chills) to severe forms such as Weil's disease or pulmonary involvement (Karesh et al. 2012; Hamond et al. 2023).

Rodent specific and wildlife-relevant pathogens

Not all rodent-associated pathogens are zoonotic. Some are host-specific commensals or affect other wildlife species, potentially influencing population dynamics. A good example is the decline of the European red squirrel (*Sciurus vulgaris*) in Great Britain, which was driven largely by the introduction of invasive Eastern grey squirrels (*Sciurus carolinensis*) carrying squirrelpox virus (SPPV). While grey squirrels remain unaffected, the virus is lethal to red squirrels (Rushton et al. 2006; Lurz et al. 2025). The effects of this introduced pathogen is exacerbated by anthropgenic influences, such as deforestation, habitat degradation, and resource competition. In addition, British red squirrels are threatened by *Staphylococcus aureu*s, which can cause fatal exsudative dermatitis (Simpson et al. 2013). In these cases, rats (*Rattus norvegicus*, *Rattus rattus*) and moles (*Talpa europaea*) are considered reservoir hosts. Rodents may also carry host-specific viruses – such as herpesviruses and polyomaviruses – that do not infect other mammalian species but may still impact rodent health (Ehlers et al. 2007, 2019). Likewise, certain animal pathogens, such as rustrela virus (Bennett et al. 2020), can be transmitted from rodents to larger mammals, where they may cause diesease in susceptible hosts.

This study aims to (i) provide a comprehensive literature review of known bacterial, viral, and protozoan pathogens in *E. quercinus*, and (ii) present original pathogen screening results from incidental collected samples from dead garden dormice found in Germany, to assess whether pathogens may be contributing to the species' decline, and additionally whether *E. quercinus* poses a zoonotic risk, given that they often inhabit areas in close proximity to humans. This pathogen screening was based on pathogen-specific and non-targeted metagenomic analyses, and existing sequence read archive (SRA) evaluation.

Materials and methods

Literature review

Relevant papers were searched and selected in January 2025 using the international online databases: PubMed and Web of Science. The searches covered the scientific literature published up to, and including, December 2024 with no time or language limits. To find studies on garden dormice, the following search strings were used: (Viruses OR Bacteria OR Protozoa OR Disease OR Pathogen) AND (Garden dormouse OR *Eliomys quercinus* OR *Eliomys* OR Gliridae). The workflow followed the PRISMA guidelines (Page et al. 2021).

Sample collection and pathogen screening

Carcasses of 294 garden dormice found dead in Germany between 2015 and 2021 (Fig. 1), were subjected to post-mortem examination (Famira-Parcsetich et al. 2024), during which, samples were taken for further analysis. The number of samples submitted for testing for various pathogens, including various bacteria and viruses, varied due to a number of factors, including the sometimes poor quality of the sample material, resulting from decomposition. For example, samples were not used if the organs had become desiccated or severely autolytic due to prolonged exposure to the elements, whereas samples were used even after a prolonged period of freezing (Nippert et al. 2023). Other factors included differing funding sources and the time at which the samples were analysed during the course of the project. We engaged in numerous collaborative endeavours with diverse research laboratories, coordinated by the network "Rodent-borne pathogens" (Ulrich et al. 2009, 2025 in press).

Depending on the tissue tropism of each pathogen, relevant tissues were homogenized and nucleic acids were extracted. Detection of pathogens or their nucleic acids, or reactive antibodies was performed according to previously established protocols. Detailed information including examined pathogens, methods and references can be found in Table 1.

Metagenomic sequencing

A subset of obtained kidney samples ($n=73$) was subjected to metagenomic next-generation sequencing (NGS). For this purpose, DNA was extracted from kidney tissue and amplified

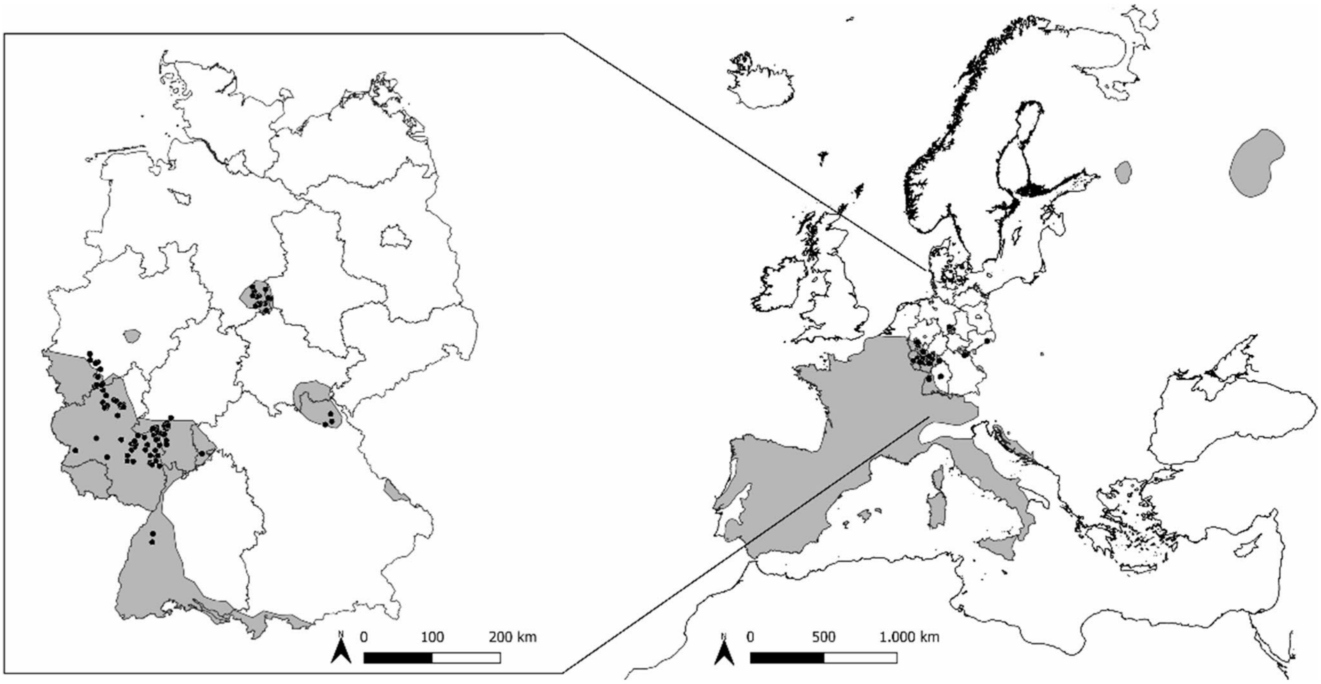

Fig. 1 Distribution range of garden dormice in Europe, and Germany in particular (grey, IUCN 2023). Origin of the specimens examined in this study (black dots). ©EEA 2022 and ©GeoBasis-DE/BKG 2021

via strand displacement amplification (SDA) with EquiPhi29 DNA polymerase as described previously (Vasiliūnaitė et al. 2024). Seven such DNA samples were used directly for sequencing library preparation. Another 66 samples were randomly combined into three pools for sequencing (details available at Online Resource 1). Sequencing libraries were prepared with Nextera XT library preparation kit (Illumina Inc., San Diego, CA, USA) and sequenced using a NovaSeq Xplus 10B machine with 2 × 150 bp (bp) paired-end reads at the Sequencing Facility of Center for Cancer Research, National Cancer Institute, (Frederick, MD, USA). Additionally, 161 garden dormouse associated Sequence Read Archive (SRA) datasets available online before 2025-02−01 were downloaded and analyzed in parallel (list of SRA datasets available at Online Resource 2). Obtained sequencing reads from both our study and the publicly available SRAs were trimmed with fastp tool (v0.24.0) (Chen 2023). Sequences were assembled de novo with megahit (v1.2.9.) (Liu et al. 2023), and viral sequences longer than 300 nucleotides (nt) were annotated with Cenote-taker3 (v3.3.2) (Tisza et al. 2021). Additionally, MetaPhlAn 4.0.3 (database vJun23) (Blanco-Míguez et al. 2023) analysis was performed with standard parameters to determine the presence of bacterial pathogens.

The computational resources of the National Institutes of Health high-performance computing cluster Biowulf were utilized. Sequencing reads were uploaded at the National Center for Biotechnology Information (NCBI) under BioProject accession number PRJNA1241767.

Furthermore, samples were analysed for the presence of polyomaviruses. The results of these analyses have been previously published and appear in the literature review (Vasiliūnaitė et al. 2024).

Results

Literature review

The literature search yielded a total of 53 publications, covering a 73-year period (1951–2024), and describes the detection of eight different pathogens in garden dormice (Table 2). Prior to 2010, fewer than one manuscript was published per year, but since 2011 an increase was observed. In the current decade, an average of 3.25 manuscripts were published per year (Fig. 2). However, 40 of the 53 publications were excluded from the analysis because, on closer inspection, they did not meet the search criteria (Fig. 3). Two of the literature sources do not address pathogens or the garden dormouse. Four of the sources address the garden dormouse, but do not discuss pathogens. Pathogens in other species, such as the edible dormouse (*Glis glis*), are discussed in 23 publications. Eleven of the papers focus on endoparasites such as nematodes or cestodes that do not align with the aims of this study (Fig. 3).

Of the remaining 13 publications (Table 2), three manuscripts were published in the 1950 s and 1970 s and focus on

Table 1 Analysis of garden dormouse samples for 16 pathogens, including sample material, sample size, detection method and respective references and results of the examinations with information on the number of positive samples (and precise pathogen differentiation) and the resulting prevalences. Responsible laboratories are indicated as footnotes

Pathogen	Sample Material	Sample Size	Method Type	Reference	Positive Samples	Prevalence (%)	95% Confidence Interval
RNA – Viruses							
pan-hantavirus[1]	Lung	19	RT – PCR, L segment	Klempa et al. (2006)	0	0	
Puumala virus and related[1]	Lung	19	RT-PCR, S segment	Schmidt et al. (2016)	0	0	
Borna disease-virus-1[1]	Brain	60	RT - qPCR	Schulze et al. (2020)	0	0	
Arenaviruses[1]	Kidney	176	RT - PCR	Vieth et al. (2007)	0	0	
Hepatitis E-Virus[1]	Liver	19	RT - PCR	Ryll et al. (2017)	0	0	
SARS-CoV-2[2]	Throat Swab	23	RT - PCR	Corman et al. (2020)	0	0	
DNA – Viruses							
Herpesviruses[1]	Spleen	64	PCR	Chmielewicz et al. (2001)	0	0	
Orthopoxviruses[1]	Nasal septum	70	qPCR	Scaramozzino et al. (2007)	0	0	
Bacteria							
Streptobacillus moniliformis[3]	Throat swab	28	qPCR	Fawzy et al. (2022)	0	0	
Leptospira spp.[4]	Kidney	176	qPCR MLST	Stoddard et al. (2009) Victoria et al. (2008) Boonslip et al. (2013)	2 (*Leptospira borgpetersenii*, serogroup Sejroe, sequence type 197)	1.1	0–3%
Borrelia spp.[5]	Skin	143	Nested-PCR	Richter and Matuschka (2006)	8 (*Borrelia spielmanii* (7/8), *Borrelia afzelii* (1/8)	5.6	9–18%
Borrelia spp.[5]	Ticks	32	Nested-PCR	Richter and Matuschka (2006)	7 (*Borrelia spielmanii*)	22	7–36%
Anaplasma/*Ehrlichia* spp.[1]	Spleen	18	PCR	Parola et al. (2000)	0	0	
Rickettsia spp.[1]	Spleen	18	PCR	Regnery et al. (1991)	0	0	
Staphylococcus aureus[6]	Nose	58	Selective media, agglutination test, PCR	Mrochen et al. (2018)	17	29	17–41%
Protozoa							
Babesia spp.[1]	Spleen	18	PCR	Hilpertshauser et al. (2006)	0	0	
Serology							
Anti-HEV antibodies[7]	Chest cavity fluid	68	Indirect-IgG- ELISA	Simanavicius et al. (2018)	1 (IgG to rat HEV CP(112–608) and IgG to HEV GT3 CP (1–660))	1	0–4%

[1] Friedrich-Loeffler-Institut, Federal Research Institute for Animal Health, 17,493 Greifswald – Insel Riems, Germany; [2] Clinic for Birds, Reptiles, Amphibians and Fish, Justus-Liebig-University Giessen, 35,392 Giessen, Germany; [3] Hessian State Laboratory, 35,392 Giessen, Germany; [4]Institute of Animal Hygiene and Veterinary Public Health, Veterinary Faculty, Leipzig University [5] Institute of Geoecology, Landscape Ecology and Environmental Systems Analysis, Technische Universität Braunschweig, 38,106 Braunschweig, Germany; [6] Institute of Immunology, University Medicine Greifswald, 17,475 Greifswald, Germany; [7] Institute of Biotechnology, Life Sciences Center, Vilnius University, 01513 Vilnius, Lithuania

CP capsid protein, *GT3* genotype 3, *HEV* hepatitis E virus, *IgG* immunoglobulin G, *ratHEV* rat hepatitis E virus, *SARS-CoV-2* severe acute respiratory syndrome coronavirus 2, *MLST* Multi locus sequence typing

viruses, bacteria and protozoa in garden dormice, including tick-borne pathogens, such as *Rickettsia prowazeki* (Perez Gallardo et al. 1951) and *Coxiella burnetii* (Perez Gallardo et al. 1952). A further increase in the number of publications on tick-borne bacteria in garden dormice was observed between 1999 and 2011, particularly with regard to *Borrelia* spp. in France and Germany (Matuschka et al. 1999; Richter et al. 2004, 2011). From 2005 onwards, several publications on protozoa emerged (Bertolino and Canestri-Trotti 2005; Kvičerová et al. 2011; Azami-Conesa et al. 2023;

Table 2 Results of the literature search for bacteria, viruses and protozoa in garden dormice. Pathogens analysed in publications and determined prevalences

Pathogen	Reference	Country	Prevalence (cohort size)	95% Confidence Interval
RNA-Viruses				
Borna disease virus	Fischer et al. (2018a)	Germany	0% (*n*=156)	
DNA-Viruses				
Polyomavirus	Vasiliūnaitė et al. (2024)	Germany	3% (*n*=74)	0–6%
Anti-polyomavirus antibodies	Vasiliūnaitė et al. (2024)	Germany	17% (*n*=69)	8–26%
Bacteria				
Enterococcus feacium	Silva et al. (2012)	Portugal	97% (*n*=33)	91–100%
Enterococcus faecalis	Silva et al. (2012)	Portugal	3% (*n*=33)	0–8%
Spirochetal infection	Matuschka et al. (1999)	France	91% (*n*=60)	85–99%
Borrelia afzelii	Richter et al. (2004)	France	31% (*n*=35)	16–47%
Borrelia spielmanii	Richter et al. (2004)	France	80% (*n*=35)	67–93%
	Richter et al. (2011)	Germany	[1]	
Staphylococcus aureus	Gómez et al. (2014)	Spain	0% (*n*=1)	
Coxiella burnetii	Perez Gallardo et al. (1952)	Spain	-[1]	
Rickettsia spp.	Perez Gallardo et al. (1951)	Spain	-[1]	
Protozoa				
Eimeria sp.	Fischer et al. (2018a)	Germany	2% (*n*=57)	0–5%
Eimeria myoxi	Cuoso-Pérez et al. (2023)	Spain	57% (*n*=28)	39–75%
	Kvičerová et al. (2011)	Czech Republic	85% (*n*=54)	76–95%
	Bertolino et al. (2005)	Italy	64.7% (*n*=17 in 2000) and 54.6% (*n*=11 in 2002)	42–87% and 25–84%
Eimeria melanuri	Bertolino et al. (2005)	Italy	82.4% (*n*=17 in 2000) and 36.4% (*n*=11 in 2002)	64–100% and 8–65%
Leishmania infantum	Azami-Conesa et al. (2023)	Spain	0% (*n*=1)	

[1] These publications are based on experimental infection trials, no prevalences are given.

Couso-Pérez et al. 2023), and from the 2010s on, single publications on pathogens such as *Enterococcus* sp. (Silva et al. 2012), *Staphylococcus aureus* (Gómez et al. 2014) and polyomaviruses (Vasiliūnaitė et al. 2024) were published (Table 2).

Specific pathogen screening

In our own investigations, we were able to detect four different pathogens as well as antibodies against hepatitis E virus (HEV). *Leptospira* spp. DNA was found in two of 176 (1.1%, 95% CI 0–3%) kidney tissue samples. These were further identified by multi locus sequence typing (MLST) as *Leptospira borgpetersenii*, serogroup Sejroe, sequence type (ST) 197 (Table 1). The positive samples came from one animal in Rhineland-Palatinate (death 2019) and one animal in North Rhine-Westphalia (death 2021). In addition, DNA of *Borrelia burgdorferi* s.l. was detected in eight of 143 (5.6%, 95% CI 9–18%) skin samples. We detected *Borrelia spielmanii* in seven of the eight positive samples, and *Borrelia afzelii* in one sample. In seven of 149 ticks, from 32 different animals, we detected *B. spielmanii* DNA. Of the seven animals in which *B. spielmanii* was detected, three were found to be carrying ticks that also tested positive for this bacterial DNA. In one out of 68 (1%, 95% CI 0–4%) chest cavity fluid samples, antibodies against HEV (IgG to rat HEV CP (112–608) and IgG to HEV GT3 CP (1–660)) were detected. The highest prevalence was found for *Staphylococcus aureus* at 29% (95% CI 17–41%), with 17 out of 58 nose samples testing positive (Table 1). Of these 7/17 (41%) belonged to the lineage clonal complex (CC) 121/CC1956. Moreover, we isolated several CC188 (*n*=3), CC49 (*n*=2), CC15 (*n*=2) strains, as well as single isolates belonging to CC5, CC7, CC121, CC130 and CC133. All isolates were methicillin susceptible *S. aureus* (MSSA), with singular isolates showing resistances to penicillin, ciprofloxacin, erythromycin and others (Table 3).

Metagenomic sequencing

MetaPhlAn analysis of metagenomic sequencing data from garden dormouse kidney-derived DNA extracts (*n*=73) and publicly available SRA datasets obtained from different garden dormouse tissues (feces, gut, liver, muscle, hypothalamus, other unidentified tissue, *n*=161) revealed a diverse range of bacterial pathogens (Fig. 4, Online Resource 3 and 4). The highest diversity of the species identified was observed in fecal samples (30 species). Detection of *Enterococcus faecium* and *E. faecalis* in fecal samples was consistent with previously reported findings, however other *Enterococcus* and other species not previously reported in garden dormouse were also identified (Table 2;

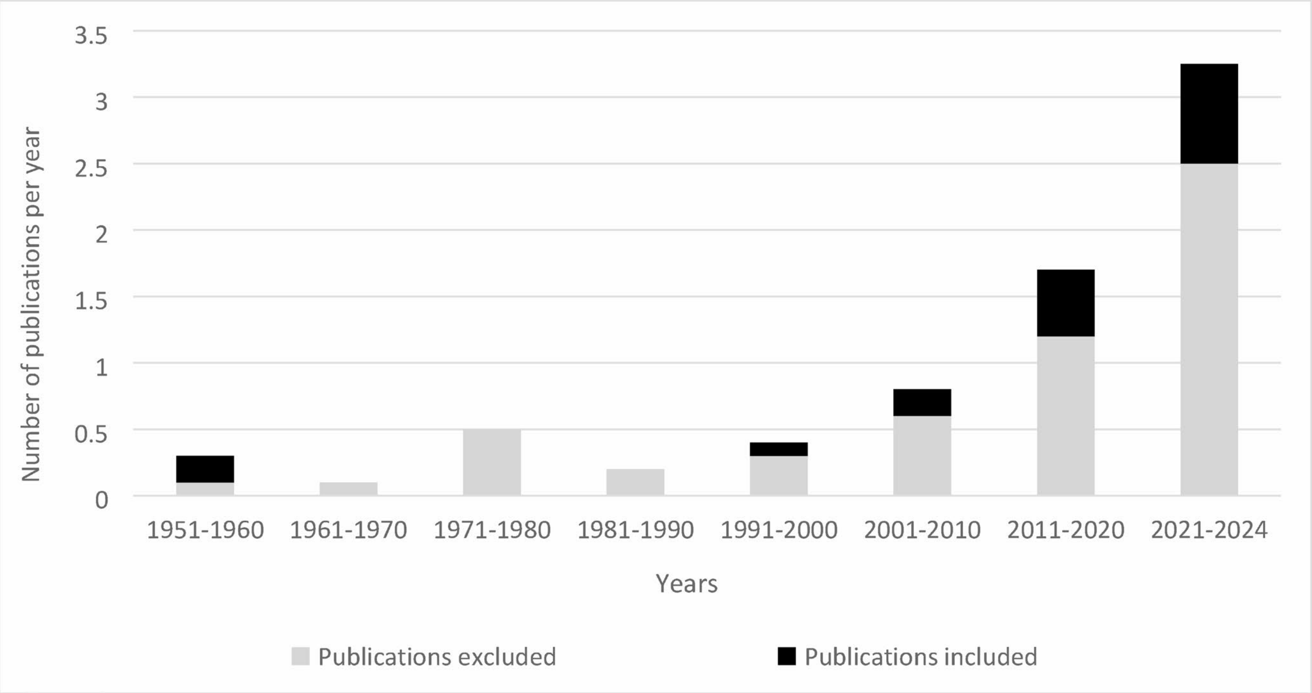

Fig. 2 Results of the literature search are presented as the number of publications per year, within a defined time period. The results are presented in their entirety, with those dealing with the topics of interest (viruses, bacteria, protozoa in garden dormice) in black, and those which were excluded in light grey

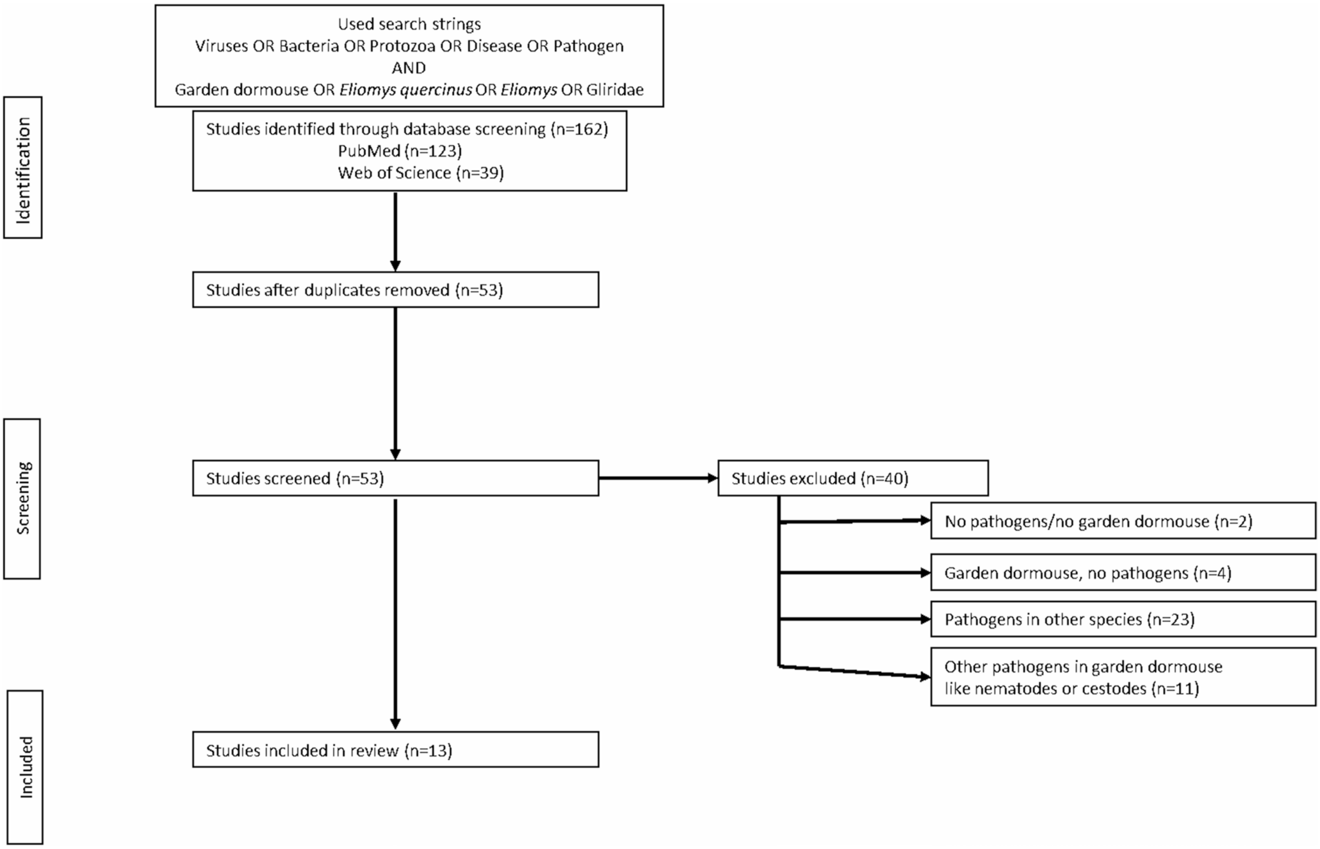

Fig. 3 Overview of the search strategy for viruses, bacteria, and protozoa in garden dormice and the results of the literature research, PRISMA flowchart adapted from Page et al. (2021)

Table 3 Virulence gene and resistance patterns of *Staphylococcus aureus* isolates from garden dormice

Sample ID	spa type	spa repeats	MLST	deduced CC	*gyr*	*mecA*	*mecC*	*mecU*	*luk-PV*	*sak*	*chp*	*scn*	*sa3int*	Cefoxitin-Screen	Benzylpenicillin	Oxacillin	Oxacillin+Cefazolin	Gentamicin
KS19/0211	t105	26–23-17–34-17–20-17–17-16	-	CC5	+	-	-	-	-	+	+	+	+	-	S	S	S	S
KS19/0196	t091	07–23-21–17-34–12-23–02-12–23	-	CC7	+	-	-	-	-	-	+	+	+	-	S	S	S	S
KS19/1334	t084	07–23-12–34-34–12-12–23-02–12-23	-	CC15	+	-	-	-	-	-	-	-	-	-	S	S	S	S
KS19/1351	t084	07–23-12–34-34–12-12–23-02–12-23	-	CC15	+	-	-	-	-	+	+	+	+	-	S	S	S	S
KS19/1310	t208	04–20-17–17-31–31-24–17-17–17-17–25	-	CC49	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/0204	t13540	14–44-34–17	ST9472	CC121/1956	+	-	-	-	-	-	-	-	-	-	S	S	S	S
KS19/0213	t3750	04–20-25–23-24–17	ST2328	CC121/1956	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/1302	t3750	04–20-25–23-24–17	-	CC121/1956	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/1303	t3750	04–20-25–23-24–17	-	CC121/1956	+	-	-	-	-	-	-	-	-	-	R	S	S	S
KS19/1305	t11686	14–44-34–50-17	ST1956	CC121/1956	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/1308	t524	04–17	ST2328	CC121/1956	+	-	-	-	-	-	-	-	-	-	S	S	S	S

Table 3 (continued)

Sample ID	spa type	spa repeats	MLST	deduced CC	*gyr*	*mecA*	*mecC*	*mecU*	*luk-PV*	*sak*	*chp*	*scn*	*sa3int*	Cefoxitin-Screen	Benzylpenicillin	Oxacillin	Oxacillin + Cefazolin	Gentamicin
KS19/1318	t3750	03–16-21–17-23–13-17–17	-	CC121/1956	+	-	-	-	-	+	-	+	+	-	S	S	S	S
KS19/0195	t3568	04–39-17	ST130	CC130	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/1321	t7355	03–16-21–17-23–13-17–17	ST133	CC133	+	-	-	-	-	-	-	-	+	-	S	S	S	S
KS19/1312	t189	07–23-12–21-17–34	-	CC188	+	-	-	-	-	+	-	+	+	-	R	S	S	S
KS19/1317	t189	07–23-12–21-17–34	-	CC188	+	-	-	-	-	+	-	+	+	-	S	S	S	S
KS19/1320	t189	07–23-12–21-17–34	-	CC188	+	-	-	-	-	+	-	+	+	-	S	S	S	S

Sample ID	Gentamicin + Ciprofloxacin	Levofloxacin	Levofloxacin + Moxifloxacin	inducable clindamycin resistence	Erythromycin	Clindamycin	Linezolid	Daptomycin	Teicoplanin	Vancomycin	Tetracyclin	Tigecycline	Fosfomycin	Fusidinsäure	Mupirocin	Rifampicin	Trimethoprim/ Sulfamethoxazol
KS19/0211	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/0196	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1334	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1351	I	I	S	+	R	*R	S	S	S	S	S	S	S	S	S	S	S
KS19/1310	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/0204	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/0213	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1302	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1303	R	I	ND	-	S	S	S	S	S	S	R	S	S	R	S	S	S
KS19/1305	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1308	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1318	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/0195	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1321	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1312	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1317	R	I	ND	-	S	S	S	S	S	S	S	S	S	S	S	S	S
KS19/1320	I	I	S	-	S	S	S	S	S	S	S	S	S	S	S	S	S

MLST Multi locus sequence typing, *CC* clonal complex, *gyr* gyrase, *mec* methicillin, *luk* leukocidine, *sak* staphylokinase, *chp* chemotaxis inhibitory protein of S. aureus, *scn* staphylococcal complement inhibitor, *sa3int* S. aureus integrase 3, *S* sensitive, *R* resistant, **R* AEC modified resistant, *ND* not determined.

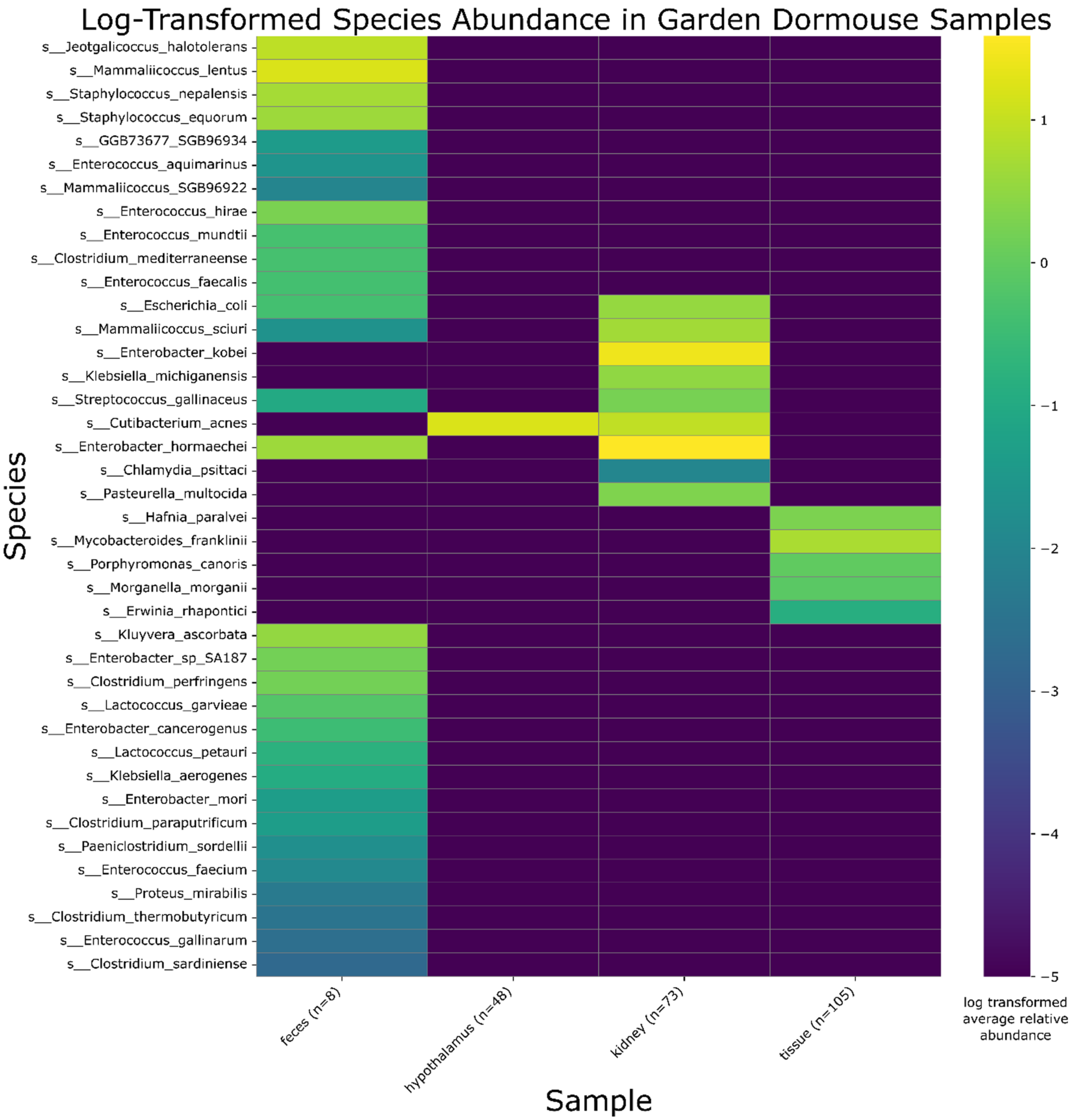

Fig. 4 Log-transformed heatmap of microbial species abundance across garden dormouse samples. The species were profiled using MetaPhlAn4 (Blanco-Míguez et al. 2023). The analysis included garden dormouse kidney samples sequenced in this study and the garden dormouse sequence read archive (SRA) datasets, and abundance values are expressed as log-transformed relative abundances. Warmer colors (e.g. yellow) indicate higher log-abundance values, while colder colors (e.g. blue) indicate lower or absent microbial presence in that tissue. MetaPhlAn4 screen results were combined by sequenced tissue type (feces; hypothalamus; kidney; gut, liver, muscle, and other unidentified tissue), and average relative abundance was determined for each tissue type for each microbial species detected

Fig. 4). *Cutibacterium acnes* was the only bacterial pathogen detected in the hypothalamus samples; however, this species has been previously reported as a contaminant in certain laboratory reagents and kits (Liu et al. 2022). In addition *Chlamydia psittaci*, *Pasteurella multocida*, *Enterobacter hormaechei* and *E. kobei*, which are known opportunistic agents in animals (Seriki et al. 2025; Smallman et al. 2024; Wang et al. 2024), were detected in kidney derived samples. In other tissue samples, opportunistic and environmental bacteria such as *Hafnia paralvei*, *Mycobacteroides franklinii*, *Porphyromonas canoris*, *Morganella morganii*, and *Erwinia rhapontici* were detected at low abundance. Investigation for viral sequences, with Cenote-Taker3, identified 129 viral contigs of at least 300 nt in length in 54 of the sequenced samples (, revealing the presence of viruses of multiple DNA-virus families, including *Parvoviridae*, *Adenoviridae*, *Circoviridae*, *Polyomaviridae*, *Anelloviridae* and *Genomoviridae* (Online Resource 5). Parvovirus-related sequences belonging to diverse representatives of the family *Parvoviridae* were present in five out of ten kidney sequencing libraries prepared, and in at least four analyses of SRA datasets. Complete genome sequences of 13 circular viruses were assembled (12 without perviously identified polyomavirus, Table 4, Online Resource 6). Assembled viral sequences had very low to no similarity to each other on the nucleotide sequence level, however, some resembled previously identified sequences. For example, a circular gemykrogvirus genome (*Genomoviridae*) extracted from a pooled kidney sample of garden dormice, showed almost 99% identity to the sequence LK931484.1, previously identified in a sample of healthy bovine blood. The near-identical dormouse-derived gemykrogvirus sequence to one reported from bovine blood likely reflects the common environmental source of genomviruses, which are commonly detected in diverse vertebrate and non-vertebrate samples (Kazlauskas et al. 2019). In contrast, multiple genomovirus-related sequences were recovered from pooled kidney samples, highlighting diverse circular single stranded (ss) DNA viruses in the dormouse-associated virome.

Discussion

As part of this study, we conducted an extensive literature review, which shows that prior to 2010, the number of publications concerning pathogens of garden dormice was minimal, with even fewer addressing the bacteria, viruses and protozoa that are present in these animals. This low level of research interest in pathogens in garden dormice is in line with the overall decline in research and publications on garden dormice in general between 2000 and 2017 compared to the period 1950 to 1999, with an apparent increase only in 2017 (Lang et al. 2022). With regard to publications on pathogens in garden dormice, the annual publications increased since 2011. This may be because emerging zoonotic diseases have become a focal point in research, with

Table 4 Complete viral genomes recovered from garden dormouse kidney samples or sample pools. Summary of complete viral genomes identified using Cenote-Taker3 and screened with NCBI BLAST. Sequences were classified into viral families using top NCBI BLAST results, with percent identity and accession numbers shown. Genomes were considered complete based on full-length alignment to reference genomes and the presence of terminal repeats (DTRs)

GenBank accession	Length, nucleotides	Virus family	NCBI blast	Description	Query Cover	%Identity	Acc. Length	Accession
PV685787	1901	*Circoviridae*	blastn	MAG: ssDNA virus sp. isolate 164Circo-2, complete genome	64%	96.76%	1898	OM892393.1
PV685788	2146	*Genomoviridae*	blastn	MAG: *Genomoviridae* sp. isolate ctdb80, complete genome	52%	92.07%	2153	NC_076323.1
PV685792	2202	*Genomoviridae*	blastn	Chicken genomovirus mg4_1196, complete genome	100%	79.91%	2191	MN379606.1
PV685789	2158	*Genomoviridae*	blastn	MAG: Genomoviridae sp. isolate *Genomoviridae*Dogfe418C1 genomic sequence	97%	91.56%	2156	OQ198078.1
PV685791	2125	*Genomoviridae*	blastn	Sorex coronatus feces associated gemycircularvirus 11, complete genome	98%	91.01%	2126	PQ576940.1
PV685794	2204	*Genomoviridae*	blastn	Red panda feces-associated gemycircularvirus isolate AliP03geno09-2015 genomic sequence	57%	91.18%	2205	MZ556140.1
PV685796	2034	N/A[1]	blastn	Dulem virus 22 isolate Duke43_SS_313, complete genome	91%	93.40%	2046	PP498712.1
PV685795	2254	*Genomoviridae*	blastn	MAG: *Genomoviridae* sp. isolate 6537_278, complete genome	47%	73.75%	2191	MT309841.1
PV685790	2881	*Circoviridae*	blastx	MAG: hypothetical protein [*Cirlivirales* sp.]	35%	57.18%	342	XOF03152.1
PV685797	2191	*Genomoviridae*	blastn	MAG: *Genomoviridae* sp. isolate 210Gen-2, complete genome	17%	77.25%	2196	OM892312.1
PV685793	2121	*Genomoviridae*	blastn	HCBI9.212 virus complete sequence	99%	98.72%	2121	LK931484.1
PV685798	2748	N/A[1]	blastx	-	23%	56.94%	234	XOE94280.1

N/A not available, *MAG* Metagenome-Assembled Genome rodents being identified as reservoirs of many zoonotic pathogens (Karesh et al. 2012; Wu et al. 2018). Additional drivers, such as climate change and its associated alteration of the distribution of arthropods and arthropod-borne pathogens may influence the presence of pathogens in rodents (Caminade et al. 2019). Another aspect that may explain the increase in research on pathogens in garden dormice is the development and improvement of diagnostic methods (Liu et al. 2023). A novel polyomavirus detected in garden dormice by Vasiliūnaitė et al. (2024) serves as a notable illustration. Another factor might be the establishment and ivolvement of the network “Rodent-borne pathogens” (Ulrich et al. 2025 in press).

The samples analysed in this study were collected as part of an extensive research project carried out in Germany over a period of six years (Büchner et al. 2024). A major focus of this project was to investigate the causes of the decline of the garden dormouse in Germany. It is likely that this extensive project has helped to bring the garden dormouse back into the focus of research, resulting in a significant increase in annual publications since 2021. Because some of these publications also come from other European countries, such as Spain (Azami-Conesa et al. 2023; Couso-Pérez et al. 2023), it may be assumed that such extensive research initiatives in one country have also led to an increase in research on the garden dormouse in other countries. Furthermore, species are brought to public interest and the attention of financial supporters only in cases where they are listed as endangered or where negative population trends are observed. This in turn leads to increased research and, consequently, more publications (Jarić et al. 2017; Davies et al. 2018).

While numerous studies on endoparasites were identified in the literature (Makarikov 2017; Mas-Coma et al. 1977a, (1977b), (1982); Miquel et al. 1996), they were excluded from this review due to our selection criteria. Since these, like ectoparasites, were neglected in our own investigations as well, this represents a major limitation in our study. Notably, cestodes of the family *Hymenolepididae* have been reported in garden dormice but appear to have no impact on garden dormouse health (Makarikov and Georgiev 2020).

Vector-borne pathogens

In the past, a number of studies have focused on vector-borne pathogens such as *Rickettsia prowazeki* (Perez Gallardo et al. 1951), *Coxiella burnetii* (Perez Gallardo et al. 1952) and *Borrelia* spp. (Matuschka et al. 1999; Richter et al. 2004, 2011) in garden dormice. Even in our own investigations, representatives of *Borrelia* spp. were detected. Although *B. afzelii* has been detected in a related host, the edible dormouse (Fietz et al. 2014), we mainly detected *B. spielmanii* with only one instance of *B. afzelii* in our samples. This confirms the role of the garden dormouse as the main reservoir host of *B. spielmanii*, as persistent infectivity of *B. spielmanii* in garden dormice for ticks has been experimentally demonstrated (Richter et al. 2011) and observed in the field (Richter et al. 2004 and manuscript in preparation).

Non-vector-borne pathogens

Of particular zoonotic relevance, here, is the first detection of *L. borgpetersenii* (serogroup Sejroe, ST 197) in the garden dormouse. This species has previously been found in the yellow-necked mouse (*Apodemus flavicollis*) and bank vole (*Myodes glareolus*) (Fischer et al. 2018b). Both species are widespread in Europe and Germany and, like the garden dormouse, inhabit broadleaf and mixed forests, as well as structurally rich gardens and hedges. It is therefore possible that the *Leptospira* were aquired from an environment contaminated by these two rodent species. The transmission of pathogens from other rodents to garden dormice must always be considered. This is illustrated by outbreaks of *Yersinia pseudotuberculosis* infections, and associated deaths, in two enclosure populations of garden dormice in 1991 (Meinig unpublished data) and in 2023 (Pöhle and Ulber unpublished data). In both cases, it was subsequently shown that the bacterium had been introduced by house mice, leading to fatal diseases in the affected animals.

The absence of hantavirus detection in garden dormice, in contrast to findings in edible dormice (Stanojevic et al. 2015), may reflect several contributing factors. Firstly, hantaviruses show a high level of host specificity and spillover infections are detected only very rarely (Schlegel et al. 2014), suggesting that the garden dormouse may not serve as a natural reservoir in the way the edible dormouse does (Plyusnin et al. 2014). Additionally, the transmission and maintenance of a hantavirus within rodent host populations require a minimum host density, which may not be present for the garden dormouse, and certain demographic structures; below these thresholds, viral persistence may fail (Tian et al. 2019).

Like the edible dormouse (Ehlers et al. 2019), the garden dormouse has been shown to harbour an associated polyomavirus (Vasiliūnaitė et al. 2024), however respective viruses belong to different genera of the family *Polyomaviridae*. Both garden dormice in which the polyomavirus was detected showed signs of hepatic changes and a whitish substance was identified in the abdominal cavity of one of the two animals. In this animal, an infectious disease had been suspected as the cause of death (Vasiliūnaitė et al. 2024). However, none of the other tested pathogens were detected in these animals. Antibodies against the new polyomavirus were not detected in either of the two animals, whereas antibodies were found in samples of 12 other garden dormice (Vasiliūnaitė et al. 2024). Although viral DNA and antibodies were detected in different individuals, phylogenetic analysis supports garden dormice as the natural host rather than incidental environmental exposure. The absence of antibodies in DNA-positive animals may reflect an acute infection prior to seroconversion or possible persistence in renal tissue, although the kidney has not yet been confirmed as a reservoir for this virus (Vasiliūnaitė et al. 2024).

Rodent-specific and wildlife-relevant pathogens

Staphylococcus aureus was detected at a high prevalence (29%) in the garden dormouse samples. *Staphylococcus aureus* is an opportunistic pathogen in many small mammals, including mice, shrews, voles, rats and squirrels (Mrochen et al. 2018; Raafat et al. 2020; Yebra et al. 2024). The predominant *S. aureus* lineages that we detected in the garden dormice are also common in other wild small mammals. For instance, CC121/CC1956 is common in mice, shrews and voles (Mrochen et al. 2018), and CC49 is the dominant lineage in wild small rodents (voles and mice), but rare in humans. CC188 is common in laboratory rats and other rodents, but rare in humans. This suggests that certain rodent-adapted *S. aureus* lineages are circulating among different small mammal species, with some overlap between the species. The absence of typical human or livestock CCs, such as CC398-MRSA, in this wild rodent *S. aureus* population, as well as the lack of antibiotic resistances, suggest limited interaction of the garden dormouse population with the human or livestock *S. aureus* population. The lack of typical signs of *S. aureus* infections (i.e. purulent skin infections, abscesses) in the analysed garden dormice, and the high genetic diversity of the *S. aureus* isolates, suggest a commensal relationship rather than active infection, unlike in British red squirrels (Simpson et al. 2013).

Metagenomic sequencing

MetPhlAn analysis revealed a variety of bacterial pathogens. Some of the pathogens were reported in previous studies, such as *Enterococcus feacium* and *E. faecalis*, in garden dormouse feces (Silva et al. 2012), however, to our knowledge, the majority were identified here for the first time. Several of these species, like *Chlamydia psittaci*, *Pasteurella multocida* and *E. hormaechei*, are recognized zoonotic pathogens, and their detection in dormouse kidneys, a normally sterile site, could be relevant. The presence of *P. multocida* may also be attributable to contact with domestic cats, as some of the garden dormice were bitten or even predated on by domestic cats (Famira-Parcsetich et al. 2024). Furthermore, *E. hormaechei* was detected in garden dormouse feces datasets and in 5 out of 10 kidney sequencing libraries with relatively high abundance. Others (e.g., *C. acnes*, *Mammaliicoccus sciuri*) may represent low-virulence commensals or environmental contaminants. It should be noted that the publicly available SRA datasets and our kidney-derived libraries were generated using different protocols, enrichment strategies, and sequencing approaches (metagenomic, genomic, and transcriptomic), reflecting differing study aims. Therefore, these results are exploratory and require confirmation in dedicated follow-up studies.

Metagenomic sequencing revealed viruses from multiple DNA-virus families, including *Parvoviridae*, *Adenoviridae*, *Circoviridae*, *Polyomaviridae*, *Anelloviridae*, and *Genomoviridae*. With the exception of *Polyomaviridae*, previously reported in garden dormice (Vasiliūnaitė et al. 2024), representatives of all other virus families are reported here in garden dormice for the first time. The majority of viral sequences from this study, particularly those from small circular DNA viruses, were highly divergent from previously published sequences and likely represent novel rodent-associated lineages. Notably, all 12 complete circular genomes assembled here were derived from our kidney libraries that were enriched for circular molecules (both pooled and individual samples); none of the publicly available SRA datasets used such enrichment, which likely explains why substantially more circular DNA viruses were recovered in our dataset. Parvovirus sequences were found in five of ten kidney libraries and several SRA datasets; the longest fragment (3056 nt) closely matched a rat-associated parvovirus (98.57% identity), while others were more divergent, suggesting multiple parvovirus lineages. Because many viral detections originate from pooled samples and sequencing strategies varied widely between datasets, abundance signals are exploratory and cannot confirm systemic infection or individual prevalence. Nonetheless, the consistent detection of diverse circular DNA viruses sequences in kidney tissue raises the possibility of active or persistent infections in dormice, warranting targeted follow-up studies to clarify host range and pathogenic potential.

Zoonotic risk and decline of the garden dormouse

The garden dormouse often inhabits areas in close proximity to human settlements, which could facilitate contact between wildlife, humans, and ectoparasites. According to our findings, to date, the results indicate that – apart from *B. spielmanii* and *B. afzelii* –zoonotic pathogens can only be detected in garden dormice in rare cases. Nevertheless, their frequent association with tick populations, capable of feeding on both garden dormice and humans, underscores a potential indirect public health risk, as infected ticks may be transmitted between wildlife reservoirs and people. Monitoring tick-borne pathogens in these habitats remains important to assess and manage local zoonotic risk. Furthermore, the samples examined exhibited a limited presence of pathogens. This finding suggests that infectious diseases may not be the primary factor contributing to the observed decline in the population of garden dormice under the prevailing conditions. In case that a single pathogen is responsible for the observed decline, a higher detection rate than observed in this study should be assumed.

Limitations

Due to the suboptimal quality of the samples, as the animals examined were already undergoing auto- and heterolysis and had been deep-frozen prior to the examination, which made it difficult to detect minor pathological abnormalities or to carry out histopathological examinations, it was not possible to carry out targeted tests for specific pathogens. Given that all garden dormice were found to be deceased, and the majority of these died as a result of predation, it is likely that deaths due to pathogens are underrepresented, and there is also a bias in the detected prevalences. The presence of negative results and low prevalences necessitates careful interpretation, as the sample sizes were too small in some cases to draw reliable conclusions. Furthermore, due to constrained financial resources and laboratory capacity, pathogens such as fungi or helminths, which could also contribute to the decline of the garden dormouse, were not investigated.

Conclusion

Our investigations suggest that, with exception of *B. spielmanii*, *B. afzelii* and *L. borgpetersenii*, no other pathogens with zoonotic potential were present to any significant extent in the garden dormice investigated from Germany. A more thorough analysis, encorporating NGS of RNA viruses, should be done since there might be even more unknown pathogens infecting garden dormice that were missed so far. The novel polyomavirus, that was detected in a previous study, is a good example. Moreover, further investigation into the viruses detected is recommended, as they may potentially be a contributing factor to the observed decline. The literature review revealed that the garden dormouse, and the pathogens affecting this species, have been understudied in the past. Although this study provides valuable data on infectious agents, pathogens alone are unlikely to explain the decline of *E. quercinus*. However, the increasing number of studies on this topic in recent years has created a growing body of research that may help identify the causes of the garden dormouse's decline or, as in the case of pathogens, rule them out as possible factors. Future research should therefore integrate ecological, environmental, and anthropogenic factors to better understand its population dynamics and conservation needs.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s10344-025-02008-0.

Acknowledgements The authors would like to thank all those who helped with the work in the different laboratories. These include Fawaz Al'Sholui and Sabine Prettin for isolation, genotyping and virulence gene profiling of *Staphylococcus aureus*, and Dörte Kaufmann for technical assistance. Thanks to Teresa Nava for her help in creating the map in Figure 1. Thanks to all the volunteers for their help with the collection of dead garden dormice.

Author contributions S.P.S wrote the main manuscript and did the literarture review. E.M.K. dissected a major part of the animals, sent the organs for examination and collated the results. C.J. dissected some of the animals and organised the first examinations. C.M., R.R., E.H., D.R., D.H., E.V., C.B.B., I.K-K., A.G., P.K., V.C.H., V.S., S.H., C.K., T.E., M-C.A., S.D., K.J., C.R., H.M., A.O., M.P., D.R., D.P., C.U., C.S. worked in the different laboratories and analysed the samples for the various pathogens. S.B., R.G.U., M.L. and J.L. supervised the study.

Funding Open Access funding enabled and organized by Projekt DEAL. This study is part of the project "In Search of the Garden Dormouse" in Germany that was funded by the German Federal Agency for Nature Conservation with resources from the German Federal Ministry for the Environment, Nature Conservation, Nuclear Safety and Consumer Protection.

Data availability No datasets were generated or analysed during the current study.

Declarations

Ethics approval All samples were sourced from deceased animals that were collected as part of the project "In search of the Garden Dormouse". It was not an animal experiment.

Competing interests J.L. and S.B. are editors of the special collection to which this manuscript is submitted. The other authors have no competing interests to declare that are relevant to the content of this article.

References

Ackermann R, Stille W, Blumenthal W, Helm EB, Keller K, Baldus O (1972) Syrische Feldhamster Als Überträger von lymphozytärer choriomeningitis. Dtsch Med Wochenschr 97:1725–1731. https://doi.org/10.1055/s-0028-1107638

Ackermann R, Stammler A, Armbruster B (1975) Isolierung von virus der Lymphozytären choriomeningitis Aus abrasionsmaterial Nach kontakt der Schwangeren Mit einem Syrischen Goldhamster (*Mesocricetus auratus*). Infection 3:47–49. https://doi.org/10.1007/BF01641281

Andonov A, Robbins M, Borlang J, Cao J, Hatchette T, Stueck A, Deschambault Y, Murnaghan K, Varga J, Johnston L (2019) Rat hepatitis E virus linked to severe acute hepatitis in an immunocompetent patient. J Infect Dis 220:951–955

Azami-Conesa I, Pérez-Moreno P, Matas Méndez P, Sansano-Maestre J, González F, Mateo Barrientos M, Gómez-Muñoz MT (2023) Occurrence of *Leishmania infantum* in wild mammals admitted to recovery centers in Spain. Pathogens. https://doi.org/10.3390/pathogens12081048

Bennett AJ, Paskey AC, Ebinger A, Pfaff F, Priemer G, Hoper D, Breithaupt A, Heuser E, Ulrich RG, Kuhn JH, Bishop-Lilly KA, Beer M, Goldberg TL (2020) Relatives of rubella virus in diverse mammals. Nature 586:424–428

Bertolino S (2017) Distribution and status of the declining garden dormouse *Eliomys Quercinus*. Mamm Rev 47:133–147. https://doi.org/10.1111/mam.12087

Bertolino S, Canestri-Trotti G (2005) *Eimeria* species (apicomplexa: eimeriidae) infecting *Eliomys quercinus* in an alpine habitat. J Wildl Dis 41:442–445. https://doi.org/10.7589/0090-3558-41.2.442

Bertolino S, Amori G, Henttonen H, Zagorodnyuk I, Zima J, Juzkaitis R, Meinig H, Krystufek B (2008) *Eliomys quercinus*. The IUCN red list of threatened species. Version 2014.3

Bertolino S, Meinig H, Lang J, Büchner S (2024) Eliomys quercinus. the IUCN red list of threatened species 2024: e.T7618A3139783

Blanco-Míguez A, Beghini F, Cumbo F, McIver LJ, Thompson KN, Zolfo M, Manghi P, Dubois L, Huang KD, Thomas AM, Nickols WA, Piccinno G, Piperni E, Punčochář M, Valles-Colomer M, Tett A, Giordano F, Davies R, Wolf J, Segata N (2023) Extending and improving metagenomic taxonomic profiling with uncharacterized species using metaphlan 4. Nat Biotechnol 41(11):1633–1644. https://doi.org/10.1038/s41587-023-01688-w

Boonsilp S, Thaipadungpanit J, Amornchai P, Wuthiekanun V, Bailey MS, Holden MTG, Zhang C, Jiang X, Koizumi N, Taylor K, Galloway R, Hoffmaster AR, Craig S, Smythe LD, Hartskeerl RA, Day NP, Chantratita N, Feil EJ, Aanensen DM, Spratt BG, Peacock SJ (2013) A single multilocus sequence typing (MLST) scheme for seven pathogenic *Leptospira* species. PLoS Negl Trop Dis (1):e1954. https://doi.org/10.1371/journal.pntd.0001954

Büchner S, Trout R, Adamík P (2018) Conflicts with *Glis glis* and *Eliomys quercinus* in households: a practical guideline for sufferers (Rodentia: Gliridae). Lynx, new series 49:19–26. https://doi.org/10.2478/lynx-2018-0003

Büchner S, Lang J, Meinig HU, Nava TF, Zistl K, von Thaden A, Nowak C, Reiners TE, Brünner H, Langer F, Andersen A, Friedel U, Giermann A, Kasch E, Klocke M, Krug A, Kupfer J, Mölich T, Schmid H, Schreiner J, Steib S, Thiel-Bender C, Moczek N, Fietz J, Nowack C (2024) The garden dormouse as a research and conservation priority in a German large-scale citizen science project. Acta Zool Bulg Suppl 19:1–8

Caminade C, McIntyre KM, Jones AE (2019) Impact of recent and future climate change on vector-borne diseases. Ann N Y Acad Sci 1436:157–173. https://doi.org/10.1111/nyas.13950

Chen S (2023) Ultrafast one-pass FASTQ data preprocessing, quality control, and deduplication using Fastp. IMeta 2:2107. https://doi.org/10.1002/IMT2.107

Chmielewicz B, Goltz M, Ehlers B (2001) Detection and multigenic characterization of a novel gammaherpesvirus in goats. Virus Res 75:87–94. https://doi.org/10.1016/s0168-1702(00)00252-5

Corman VM, Landt O, Kaiser M, Molenkamp R, Meijer A, Chu DK, Bleicker T, Brünink S, Schneider J, Schmidt ML, Mulders DG, Haagmans BL, van der Veer B, van den Brink S, Wijsman L, Goderski G, Romette JL, Ellis J, Zambon M, Peiris M, Goossens H, Reusken C, Koopmans MP, Drosten C (2020) Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR. Euro Surveill 25:2000045. https://doi.org/10.2807/1560-7917.ES.2020.25.3.2000045

Couso-Pérez S, Pardavila X, Carro F, Ares-Mazás E, Gómez-Couso H (2023) First report of *Eimeria myoxi* in the garden dormouse (*Eliomys quercinus* Linnaeus, 1766) from Doñana NaturalArea (Andalusia, SW Spain). Parasitol Int 94:102740. https://doi.org/10.1016/j.parint.2023.102740

Davies T, Cowley A, Bennie J, Leyshon C, Inger R, Carter H, Robinson B, Duffy J, Casalegno S, Lambert G, Gaston K (2018) Popular interest in vertebrates does not reflect extinction risk and is associated with bias in conservation investment. PLoS ONE 13:e0203694. https://doi.org/10.1371/journal.pone.0203694

Donahue JG, Piesman J, Spielman A (1987) Reservoir competence of white-footed mice for Lyme disease spirochetes. Am J Trop Med Hyg 36:92–96. https://doi.org/10.4269/ajtmh.1987.36.92

Dürrwald R, Kolodziejek J, Weissenböck H, Nowotny N (2014) The bicolored white-toothed shrew *Crocidura Leucodon* (HERMANN 1780) is an Indigenous host of mammalian Borna disease virus. PLoS ONE 9:e93659. https://doi.org/10.1371/journal.pone.0093659

Ehlers B, Kuchler J, Yasmum N, Dural G, Voigt S, Schmidt-Chanasit J, Jakel T, Matuschka FR, Richter D, Essbauer S, Hughes DJ, Summers C, Bennett M, Stewart JP, Ulrich RG (2007) Identification of novel rodent herpesviruses, including the first gammaherpesvirus of *Mus musculus*. J Virol 81:8091–8100

Ehlers B, Anoh AE, Ben Salem N, Broll S, Couacy-Hymann E, Fischer D, Gedvilaite A, Ingenhütt N, Liebmann S, Martin M, Mossiun A, Mugisha L, Muyembe-Tamfum JJ, Pauly M, Pérez de Val B, Preugschas H, Richter D, Schubert G, Szentiks CA, Teichmann T, Walter C, Ulrich RG, Wiersma L, Leendertz FH, Calvignac-Spencer S (2019) Novel polyomaviruses in mammals from multiple orders and reassessment of polyomavirus evolution and taxonomy. Viruses 10:930. https://doi.org/10.3390/v11100930

Eisenberg T, Poignant S, Jouan Y, Fawzy A, Nicklas W, Ewers C, Mereghetti L, Guillon A (2017) Acute tetraplegia caused by rat bite fever in snake keeper and transmission of *Streptobacillus moniliformis*. Emerg Infect Dis 23:719–721. https://doi.org/10.3201/eid2304.161987

Famira-Parcsetich EM, Meinig H, von Thaden A, Büchner S, Jelinek C, Lierz M, Lang J (2024) Causes of mortality of endangered garden dormice *Eliomys Quercinus* (Linnaeus, 1766) (Rodentia: Gliridae) from Germany. Acta Zool Bulg Supplement 19:33–41

Fawzy A, Giel A-S, Fenske L, Bach A, Herden C, Engel K, Heuser E, Boelhauve M, Ulrich RG, Vogel K, Schmidt K, Eisenberg T (2022) Development and validation of a triplex real-time qPCR for sensitive detection and quantification of major rat bite fever pathogen *Streptobacillus moniliformis*. J Microbiol Methods 199:106525. https://doi.org/10.1016/j.mimet.2022.106525

Fietz J, Tomiuk J, Matuschka FR, Richter D (2014) Seasonal prevalence of Lyme disease spirochetes in a heterothermic mammal, the edible dormouse (*Glis glis*). J Appl Environ Microbiol 12:3615–3621. https://doi.org/10.1128/AEM.00251-14

Fischer D, Ziegler L, Hail K, Heckmann J, Reiners TE, Bauer C, Lierz M, Lang J (2018a) Clinical examination methods and investigation into the occurrence of endoparasites, Borna disease virus and genetic variability in the garden dormouse, *Eliomys quercinus*. Folia Zool 67:69. https://doi.org/10.25225/fozo.v67.i2.a1.2018

Fischer S, Mayer-Scholl A, Imholt C, Spierling NG, Heuser E, Schmidt S, Reil D, Rosenfeld UM, Jacob J, Nöckler K, Ulrich RG (2018b) *Leptospira* genomospecies and sequence type prevalence in small mammal populations in Germany. Vector-Borne and Zoonotic Diseases 18:188–199. https://doi.org/10.1089/vbz.2017.2140

Gil-Delgado JA, Mira Ó, Viñals A, Gómez J, Banyuls N, Vives-Ferrándiz C (2010) Diet of the garden dormouse (*Eliomys Quercinus* Linnaeus 1766) in orange groves: seasonal variation and use of available resources. Mammalia 74:147–151. https://doi.org/10.1515/mamm.2010.027

Gómez P, González-Barrio D, Benito D, García JT, Viñuela J, Zarazaga M, Ruiz-Fons F, Torres C (2014) Detection of methicillin-resistant *Staphylococcus aureus* (MRSA) carrying the *MecC* gene in wild small mammals in Spain. J Antimicrob Chemother 69:2061–2064. https://doi.org/10.1093/jac/dku100

Hamond C, LeCount K, Browne AS, Anderson T, Stuber T, Hicks J, Camp P, Fernandes LGV, van der Linden H, Goris MGA, Bayles DO, Schlater LK, Nally JE (2023) Concurrent colonization of rodent kidneys with multiple species and serogroups of pathogenic *Leptospira*. Appl Environ Microbiol 89:e0120423. https://doi.org/10.1128/aem.01204-23

Han BA, Schmidt JP, Bowden SE, Drake JM (2015) Rodent reservoirs of future zoonotic diseases. Proc Natl Acad Sci U S A 112:7039–7044. https://doi.org/10.1073/pnas.1501598112

Hilpertshauser H, Deplazes P, Schnyder M, Gern L, Mathis A (2006) *Babesia* spp. identified by PCR in ticks collected from domestic and wild ruminants in Southern Switzerland. Appl Environ Microbiol 72:6503–6507. https://doi.org/10.1128/AEM.00823-06

Hoffmann B, Tappe D, Hoper D, Herden C, Boldt A, Mawrin C, Niederstrasser O, Muller T, Jenckel M, van der Grinten E, Lutter C, Abendroth B, Teifke JP, Cadar D, Schmidt-Chanasit J, Ulrich RG, Beer M (2015) A variegated squirrel Bornavirus associated with fatal human encephalitis. N Engl J Med 373:154–162

Jarić I, Roberts DL, Gessner J, Solow AR, Courchamp F (2017) Science responses to IUCN red listing. PeerJ 5:e4025. https://doi.org/10.7717/peerj.4025

Jay MT, Glaser C, Fulhorst CF (2005) The arenaviruses. J Am Vet Med Assoc 227:904–915. https://doi.org/10.2460/javma.2005.227.904

Jeske K, Tomaso H, Imholt C, Schulz J, Beerli O, Suchomel J, Heroldova M, Jacob J, Staubach C, Ulrich RG (2019) Detection of *Francisella tularensis* in three vole species in central Europe. Transbound Emerg Dis 66:1029–1032. https://doi.org/10.1111/tbed.13078

Jo WK, Anzolini Cassiano MH, de Oliveira-Filho EF, Brünink S, Yansanjav A, Yihune M, Koshkina AI, Lukashev AN, Lavrenchenko LA, Lebedev VS, Olayemi A, Bangura U, Salas-Rojas M, Aguilar-Setién Á, Fichet-Calvet E, Drexler JF (2024) Ancient evolutionary origins of hepatitis E virus in rodents. Proc Natl Acad Sci U S A 121:e2413665121. https://doi.org/10.1073/pnas.2413665121

Johne R, Heckel G, Plenge-Bönig A, Kindler E, Maresch C, Reetz J, Schielke A, Ulrich RG (2010) Novel hepatitis E virus genotype in Norway rats, Germany. Emerg Infect Dis 16:1452

Karesh WB, Dobson A, Lloyd-Smith JO, Lubroth J, Dixon MA, Bennett M, Aldrich S, Harrington T, Formenty P, Loh EH, Machalaba CC, Thomas MJ, Heymann DL (2012) Ecology of zoonoses: natural and unnatural histories. Lancet 380:1936–1945. https://doi.org/10.1016/S0140-6736(12)61678-X

Kaysser P, Seibold E, Mätz-Rensing K, Pfeffer M, Essbauer S, Splettstoesser WD (2008) Re-emergence of tularemia in Germany: presence of *Francisella tularensis* in different rodent species in endemic areas. BMC Infect Dis 8:157

Kazlauskas D, Varsani A, Koonin Ev, Krupovic M (2019) Multiple origins of prokaryotic and eukaryotic single-stranded DNA viruses from bacterial and archaeal plasmids. Nat Commun 10:3425. https://doi.org/10.1038/s41467-019-11433-0

Kirillov AA, Kirillova NY, Ruchin AB (2022) Parasites, bacteria and viruses of the edible dormouse *Glis glis* (Rodentia: Gliridae) in the western palaearctic. Diversity 14:562. https://doi.org/10.3390/d14070562

Klempa B, Fichet-Calvet E, Lecompte E, Auste B, Aniskin V, Meisel H, Denys C, Koivogui L, ter Meulen J, Krüger DH (2006) Hantavirus in African wood mouse, Guinea. Emerg Infect Dis 12:838–840. https://doi.org/10.3201/eid1205.051487

Kondruweit M, Weyand M, Mahmoud FO, Geissdörfer W, Schoerner C, Ropers D, Achenbach S, Strecker T (2007) Fulminant endocarditis caused by *Streptobacillus moniliformis* in a young man. J Thorac Cardiovasc Surg 134:1579–1580. https://doi.org/10.1016/j.jtcvs.2007.08.010

Kvičerová J, Mikeš V, Hypša V (2011) Third lineage of rodent eimerians: morphology, phylogeny and re-description of *Eimeria myoxi* (Apicomplexa: Eimeriidae) from *Eliomys Quercinus* (Rodentia: Gliridae). Parasitology 138:1217–1223. https://doi.org/10.1017/S0031182011001107

Lane RS, Loye JE (1991) Lyme disease in California: interrelationship of Ixodid ticks (*Acari*), rodents, and *Borrelia burgdorferi*. J Med Entomol 28:719–725. https://doi.org/10.1093/jmedent/28.5.719

Lang J, Büchner S, Meinig H, Bertolino S (2022) Do we look for the right ones? An overview of research priorities and conservation status of dormice (Gliridae) in central Europe. Sustainability 14:9327. https://doi.org/10.3390/su14159327

Ledesma J, Fedele CG, Carro F, Lledó L, Sánchez-Seco MP, Tenorio A, Soriguer RC, Saz JV, Dominguez G, Rosas MF, Barandika JF (2009) Independent lineage of lymphocytic choriomeningitis virus in wood mice (*Apodemus sylvaticus*), Spain. Emerg Infect Dis 15:1677

Liu Y, Elworth RAL, Jochum MD, Aagaard KM, Treangen TJ (2022) De novo identification of microbial contaminants in low microbial biomass microbiomes with squeegee. Nat Commun 13:1–14. https://doi.org/10.1038/S41467-022-34409-Z

Liu Q, Jin X, Cheng J, Zhou H, Zhang Y, Dai Y (2023) Advances in the application of molecular diagnostic techniques for the detection of infectious disease pathogens (Review). Mol Med Rep. https://doi.org/10.3892/mmr.2023.12991

Lurz P, Gethöffer F, Bosch S, Ulrich R (2025) Die rolle der mit neozoen eingeführten krankheitserreger im interspezifischen konkurrenzkampf: das beispiel eichhörnchen und grauhörnchen. BMTW 138

Makarikov A (2017) A toxonomic review of hymenolepidids (Eucestoda, Hymenolepididae) from dormice (Rodentia, Gliridae), with descriptions of two new species. Acta Parasitol 62:1–21. https://doi.org/10.1515/ap-2017-0001

Makarikov AA, Georgiev BB (2020) Review of records of hymenolepidids (Eucestoda: Hymenolepididae) from dormice (Rodentia: Gliridae) in Europe, with a redescription of *Armadolepis spasskyi* Tenora & Baruš, 1958 and the description of A. genovi n. sp. Syst Parasitol 97:83–98. https://doi.org/10.1007/s11230-019-09891-7

Mas-Coma S (1977a) *Gongylonema pithyusensis* n. sp. (Nematoda: Spiruridae), a parasite of the oesophagus of the dormouse *Eliomys Quercinus ophiusae* Thomas, 1925 (Rodentia: Gliridae) in formentera (Balearic Islands). Ann Parasitol Hum Comp 52:13–18. https://doi.org/10.1051/parasite/1977521013

Mas-Coma S, Esteban JG (1982) *Kahmannia Eliomydis* n. gen., n. sp. (Nematoda: Heteroxynematidae), an intestinal parasite of *Eliomys Quercinus* (Linnaeus 1766) (Rodentia: Gliridae) in Minorca (Balearic Islands). Ann Parasitol Hum Comp 57:487–495. https://doi.org/10.1051/parasite/1982575487

Mas-Coma S, Gallego J (1977b) Pseudophysaloptera Kahmanni n. sp. (Nematoda: Physalopteridae), a parasite of the stomach of the dormouse *Eliomys Quercinus ophiusae* Thomas, 1925 (Rodentia: Gliridae) in formentera (Balearic Islands). Ann Parasitol Hum Comp 52:19–24. https://doi.org/10.1051/parasite/1977521019

Matuschka F-R, Spielman A (1986) The emergence of Lyme disease in a changing environment in North America and central Europe. Exp Appl Acarol 2:337–353

Matuschka F-R, Allgöwer R, Spielman A, Richter D (1999) Characteristics of garden dormice that contribute to their capacity as reservoirs for Lyme disease spirochetes. Appl Environ Microbiol 65:707–711. https://doi.org/10.1128/AEM.65.2.707-711.1999

Meerburg BG, Singleton GR, Kijlstra A (2009) Rodent-borne diseases and their risks for public health. Crit Rev Microbiol 35:221–270. https://doi.org/10.1080/10408410902989837

Mehl C, Adeyemi OA, Wylezich C, Höper D, Beer M, Triebenbacher C, Heckel G, Ulrich RG (2024) Lymphocytic choriomeningitis virus lineage V in wood mice, Germany. Emerg Infect Dis 30:399–401. https://doi.org/10.3201/eid3002.230868

Meseko C, Adedeji A, Shittu I, Obishakin E, Nanven M, Suleiman L, Okomah D, Tyakaray V, Kolade D, Yinka-Ogunleye A, Muhammad S, Morgan CN, Matheny A, Nakazawa Y, McCollum A, Doty JB (2023) Orthopoxvirus infections in rodents, Nigeria, 2018–2019. Emerg Infect Dis 29:433–434. https://doi.org/10.3201/eid2902.221411

Miquel J, Segovia JM, Feliu C, Torres J (1996) On *Physaloptera sibirica* petrow et Gorbunow, 1931 (Nematoda: Physalopteridae) parasitizing Iberian mammals. Wiad Parazytol 42:435–442

Mrochen DM, Schulz D, Fischer S, Jeske K, El Gohary H, Reil D, Imholt C, Trübe P, Suchomel J, Tricaud E, Jacob J, Heroldová M, Bröker BM, Strommenger B, Walther B, Ulrich RG, Holtfreter S (2018) Wild rodents and shrews are natural hosts of *Staphylococcus aureus*. Int J Med Microbiol 308:590–597. https://doi.org/10.1016/j.ijmm.2017.09.014

Nakamura I, Hang'ombe BM, Sawa H, Kobayashi S, Orba Y, Ishii A, Thomas Y, Isozumi R, Yoshimatsu K, Mweene AS, Takada A, Sugimoto C, Arikawa J (2013) Cross-reactivity of secondary antibodies against African rodents and application for sero-surveillance. J Vet Med Sci 75:819–825. https://doi.org/10.1292/jvms.12-0471

Nippert S, Rubbenstroth D, Geers J, Ebinger A, Hoffmann D, Breithaupt A, Wylezich C, Wang X, Haring V, Starcky P, Fruci P, Langner C, Trapp C, Schulz H, Stubbe W, Imholt C, Heckel G, Beer M, Pfaff F, Ulrich RG (2023) Continous presence of genetically diverse Rustrela virus lineages in yellow-necked field mouse reservoir populations in Northeastern Germany. Virus Evol 9:1–13

Ntumvi NF, Mbala Kingebeni P, Tamoufe U, Kumakamba C, Ndze V, Ngay Lukusa I, LeBreton M, Atibu Losoma J, Le Doux Diffo J, N'Kawa F, Takuo J-M, Mulembakani P, Nwobegahay J, Makuwa M, Muyembe Tamfum JJ, Gillis A, Harris S, Rimoin AW, Hoff NA, Fair JM, Monagin C, Ayukekbong J, Rubin EM, Wolfe ND, Lange CE (2018) High herpesvirus diversity in wild rodent and shrew species in central Africa. Intervirol 61:155–165. https://doi.org/10.1159/000493796

Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, Shamseer L, Tetzlaff JM, Akl ES, Brennan SE (2021) The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. BMJ 372

Parola P, Roux V, Camicas JL, Baradji I, Brouqui P, Raoult D (2000) Detection of ehrlichiae in African ticks by polymerase chain reaction. Trans R Soc Trop Med Hyg 94:707–708. https://doi.org/10.1016/s0035-9203(00)90243-8

Perez Gallardo F, Clavero G, Hernandez S (1951) Nota previa sobre La infección Del lirón español (*Eliomys Quercinus*) Por La *Rickettsia prowazeki* (Preliminary note on infection of *Eliomys Quercinus* with *Rickettsia prowazeki*). Rev Sanid Hig Publica 25:713–715

Perez Gallardo F, Clavero G, Hernandez S (1952) Investigaciones sobre La epidemiologia de La fiebre Q En españa; Los Conejos de Monte y Los Lirones Como reservorios de La *Coxiella Burneti* (Investigations on the epidemiology of Q fever in Spain; mountain rabbits and dormouses as a reservoir of *Coxiella Burneti*). Rev Sanid Hig Publica 26:81–87

Plyusnin A, Sironen T (2014) Evolution of hantaviruses: co-specification with reservoir hosts for more than 100 MYR. Virus Res 187:22–66. https://doi.org/10.1016/j.virusres.2014.01.008

Raafat D, Mrochen DM, Al'Sholui F, Heuser E, Ryll R, Pritchett-Corning KR, Jacob J, Walther B, Matuschka F-R, Richter D, Westerhüs U, Pikula J, van den Brandt J, Nicklas W, Monecke S, Strommenger B, van Alen S, Becker K, Ulrich RG, Holtfreter S (2020) Molecular epidemiology of methicillin-susceptible and methicillin-resistant *Staphylococcus aureus* in wild, captive and laboratory rats: effect of habitat on the nasal *S. aureus* population. Toxins 12:80. https://doi.org/10.3390/toxins12020080

Regnery RL, Spruill CL, Plikaytis BD (1991) Genotypic identification of rickettsiae and estimation of intraspecies sequence divergence for portions of two rickettsial genes. J Bacteriol 173:1576–1589. https://doi.org/10.1128/jb.173.5.1576-1589.1991

Richt JA, Rott R (2001) Borna disease virus: a mystery as an emerging zoonotic pathogen. Vet J 161:24–40. https://doi.org/10.1053/tvjl.2000.0533

Richter D, Matuschka F-R (2006) Perpetuation of the Lyme disease spirochete *Borrelia lusitaniae* by lizards. Appl Environ Microbiol 72:4627–4632. https://doi.org/10.1128/AEM.00285-06

Richter D, Schlee DB, Allgöwer R, Matuschka F-R (2004) Relationships of a novel Lyme disease spirochete, *Borrelia spielmani* sp. nov., with its hosts in central Europe. Appl Environ Microbiol 70:6414–6419. https://doi.org/10.1128/AEM.70.11.6414-6419.2004

Richter D, Postic D, Sertour N, Livey I, Matuschka F-R, Baranton G (2006) Delineation of *Borrelia burgdorferi* sensu lato species by multilocus sequence analysis and confirmation of the delineation of *Borrelia spielmanii* sp. nov. Int J Syst Evol Microbiol 56:873–881

Richter D, Schlee DB, Matuschka F-R (2011) Reservoir competence of various rodents for the Lyme disease spirochete *Borrelia spielmanii*. Appl Environ Microbiol 77:3565–3570. https://doi.org/10.1128/AEM.00022-11

Rubbenstroth D, Schlottau K, Schwemmle M, Rissland J, Beer M (2019) Human bornavirus research: back on track! PLoS Pathog 15:e1007873. https://doi.org/10.1371/journal.ppat.1007873

Runge M, von Keyserlingk M, Braune S, Voigt U, Grauer A, Pohlmeyer K, Wedekind M, Splettstoesser WD, Seibold E, Otto P, Müller W (2011) Prevalence of *Francisella tularensis* in brown hare (*Lepus europaeus*) population in lower Saxony, Germany. Eur J Wildlife Res 57:1085–1089

Rushton SP, Lurz PWW, Gurnell J, Nettleton P, Bruemmer C, Shirley MDF, Sainsburry AW (2006) Disease threats posed by alien species: the role of a poxvirus in the decline of the native red squirrel in Britain. Epidemiol Infect 134:521–533. https://doi.org/10.1017/s0950268805005303

Ryll R, Bernstein S, Heuser E, Schlegel M, Dremsek P, Zumpe M, Wolf S, Pépin M, Bajomi R, Müller G, Heiberg A, Spahr C, Lang J, Groschup M, Ansorge H, Freise J, Guenther S, Baert K, Ruiz-Fons F, Pikula J, Knap N, Tsakmakidis I, Dovas C, Zanet S, Imholt C, Heckel G, Johne R, Ulrich R (2017) Detection of rat hepatitis E virus in wild Norway rats (*Rattus norvegicus*) and black rats (*Rattus rattus*) from 11 European countries. Vet Microbiol 208:58–68

Scaramozzino N, Ferrier-Rembert A, Favier A-L, Rothlisberger C, Richard S, Crance J-M, Meyer H, Garin D (2007) Real-time PCR to identify variola virus or other human pathogenic orthopox viruses. Clin Chem 53:606–613. https://doi.org/10.1373/clinchem.2006.068635

Schlegel M, Jacob J, Krüger DH, Rang A, Ulrich RG (2014) Hantavirus emergence in rodents, insectivores and bats: what comes next? In: Johnson N (ed) The role of animals in emerging viral diseases. Academic, Boston, pp 235–292

Schlottau K, Hoffmann B, Homeier-Bachmann T, Fast C, Ulrich RG, Beer M, Hoffmann D (2017) Multiple detection of zoonotic variegated squirrel Bornavirus 1 RNA in different squirrel species suggests a possible unknown origin for the virus. Arch Virol 162:2747–2754

Schmidt S, Saxenhofer M, Drewes S, Schlegel M, Wanka KM, Frank R, Klimpel S, von Blanckenhagen F, Maaz D, Herden C, Freise J, Wolf R, Stubbe M, Borkenhagen P, Ansorge H, Eccard JA, Lang J, Jourdain E, Jacob J, Marianneau P, Heckel G, Ulrich RG (2016) High genetic structuring of Tula hantavirus. Arch Virol 161(5):1135–1149. https://doi.org/10.1007/s00705-016-2762-6

Schulze V, Große R, Fürstenau J, Forth LF, Ebinger A, Richter MT, Tappe D, Mertsch T, Klose K, Schlottau K, Hoffmann B, Höper D, Mundhenk L, Ulrich RG, Beer M, Müller K-E, Rubbenstroth D (2020) Borna disease outbreak with high mortality in an alpaca herd in a previously unreported endemic area in Germany. Transb Emerg Dis 67:2093–2107. https://doi.org/10.1111/tbed.13556

Seriki AT, Obi C, Olashile AA, Essiet UU, Akingboye DW, Ajayi A, Egwuatu TOG, Smith S (2025) Genomic analysis of multidrug resistant *Enterobacter hormaechei* strain AH1-NIMR isolated from a neonate with sepsis in Lagos, Nigeria. Infect Chemother 57:316. https://doi.org/10.3947/IC.2025.0040

Silva N, Igrejas G, Gonçalves A, Poeta P (2012) Commensal gut bacteria: distribution of *Enterococcus* species and prevalence of *Escherichia coli* phylogenetic groups in animals and humans in Portugal. Ann Microbiol 62:449–459. https://doi.org/10.1007/s13213-011-0308-4

Simanavicius M, Juskaite K, Verbickaite A, Jasiulionis M, Tamosiunas PL, Petraityte-Burneikiene R, Zvirbliene A, Ulrich RG, Kucinskaite-Kodze I (2018) Detection of rat hepatitis E virus, but not human pathogenic hepatitis E virus genotype 1–4 infections in wild rats from Lithuania. Vet Microbiol 221:129–133. https://doi.org/10.1016/j.vetmic.2018.06.014

Simpson VR, Davison NJ, Kearns AM, Pichon B, Hudson LO, Koylass M, Blackett T, Butler H, Rasigade JP, Whatmore AM (2013) Association of a *luk*M-positive clone of *Staphylococcus aureus* with fatal exudative dermatitis in red squirrels (*Sciurus vulgaris*). Vet Microbiol 162:987–991. https://doi.org/10.1016/j.vetmic.2012.10.025

Smallman TR, Perlaza-Jiménez L, Wang X, Korman TM, Kotsanas D, Gibson JS, Turni C, Harper M, Boyce JD (2024) Pathogenomic analysis and characterization of *Pasteurella multocida* strains recovered from human infections. Microbiol Spectr 12:e03805. https://doi.org/10.1128/SPECTRUM.03805-23

Stanojevic M, Nikolic V, Stajkovic N, Stamenkovic G, Bozovic B, Cekanac R, Marusic P, Gligic A (2015) Genetic detection of Dobrava-Belgrade hantavirus in the edible dormouse (*Glis glis*) in central Serbia. Epidemiol Infect 143:400–404. https://doi.org/10.1017/S0950268814001010

Stoddard RA, Gee JE, Wilkins PP, McCaustland K, Hoffmaster AR (2009) Detection of pathogenic *Leptospira* spp. through TaqMan polymerase chain reaction targeting the LipL32 gene. Diagn Microbiol Infect Dis 64:247–255. https://doi.org/10.1016/j.diagmicrobio.2009.03.014

Storch G (1978) Eliomys quercinus (Linnaeus, 1766) - gartenschläfer. niethammer. In: Krapp F (ed) Handbuch der Säugetiere Europas. Bd. 1 rotentia 1 (Sciuriddae, castoridae, gliridae, Muridae). Akademische Verlagsgesellschaft, Wiesbaden, pp 208–225

Tian H, Stenseth NC (2019) The ecological dynamics of hantavirus diseases: from environmental variability to disease prevention largely based on data from China. PLoS Negl Trop Dis 13:e0006901. https://doi.org/10.1371/journal.pntd.0006901

Tisza MJ, Belford AK, Dominguez-Huerta G, Bolduc B, Buck CB (2021) Cenote-taker 2 democratizes virus discovery and sequence annotation. Virus Evol. https://doi.org/10.1093/VE/VEAA100

Ulrich RG, Heckel G, Pelz H-J, Wieler LH, Nordhoff M, Dobler G, Freise J, Matuschka F-R, Jacob J, Schmidt-Chanasit J, Gerstengarbe FW, Jäkel T, Süss J, Ehlers B, Nitsche A, Kallies R, Johne R, Günther S, Henning K, Grunow R, Wenk M, Maul LC, Hunfeld K-P, Wölfel R, Schares G, Scholz HC, Brockmann SO, Pfeffer M, Essbauer SS (2009) Nagetiere und Nagetierassoziierte krankheitserreger: Das Netzwerk Nagetier-übertragene pathogene stellt Sich Vor (Rodents and rodent associated disease vectors: the network of rodent carrying pathogens introduces itself). Bundesgesundheitsblatt Gesundheitsforschung Gesundheitsschutz 52:352–369. https://doi.org/10.1007/s00103-009-0798-4

Ulrich RG, Drewes S, Jacob J, Böhmer M, Heckel G, Pfeffer M, Essbauer S (2025) Das netzwerk, nagetier-übertragene pathogene – eine nachhaltige infrastruktur der one health forschung (The network Rodent-borne pathogens – a sustainable infrastructure for one health research. BMTW Special Edition in

Vasiliūnaitė E, Repšytė M, Kramer EM, Lang J, Jelinek C, Ulrich RG, Buck CB, Gedvilaitė A (2024) Novel polyomavirus in the endangered garden dormouse *Eliomys quercinus*. Virol J 21:309. https://doi.org/10.1186/s12985-024-02581-x

Victoria B, Ahmed A, Zuerner RL, Ahmed N, Bulach DM, Quinteiro J, Hartskeerl RA (2008) Conservation of the *S10-spc-alpha* locus within otherwise highly plastic genomes provides phylogenetic insight into the genus *Leptospira*. PLoS ONE 7:e2752. https://doi.org/10.1371/journal.pone.0002752

Vieth S, Drosten C, Lenz O, Vincent M, Omilabu S, Hass M, Becker-Ziaja B, Meulen Jter, Nichol ST, Schmitz H, Günther S (2007) RT-PCR assay for detection of Lassa virus and related old world arenaviruses targeting the L gene. Trans R Soc Trop Med Hyg 101(12):1253–1264. https://doi.org/10.1016/j.trstmh.2005.03.018

Wang J, Wang B, Xiao J, Chen Y, Wang C (2024) *Chlamydia psittaci*: a zoonotic pathogen causing avian chlamydiosis and psittacosis. Virulence. https://doi.org/10.1080/21505594.2024.2428411

Wolcott KA, Margos G, Fingerle V, Becker NS (2021) Host association of *Borrelia burgdorferi* sensu lato: a review. Ticks and Tick-borne Diseases 12:101766

Wu Z, Lu L, Du J, Yang L, Ren X, Liu B, Jiang J, Yang J, Dong J, Sun L, Zhu Y, Li Y, Zheng D, Zhang C, Su H, Zheng Y, Zhou H, Zhu G, Li H, Chmura A, Yang F, Daszak P, Wang J, Liu Q, Jin Q (2018) Comparative analysis of rodent and small mammal viromes to better understand the wildlife origin of emerging infectious diseases. Microbiome 6:178. https://doi.org/10.1186/s40168-018-0554-9

Yarto-Jaramillo E (2015) Rodentia. In: Miller RE, Fowler ME (eds) Fowler's zoo and wild animal medicine, 8th edn. Elsevier, St. Louis, pp 384–422

Yebra G, Mrochen D, Fischer S, Pfaff F, Ulrich RG, Pritchett-Corning K, Holtfreter S, Fitzgerald JR (2024) Bacteriophage-driven emergence and expansion of *Staphylococcus aureus* in rodent populations. PLoS Pathog 20:e1012378. https://doi.org/10.1371/journal.ppat.1012378

Steere AC (1989) Lyme disease. N Engl J Med 321:586–589. https://doi.org/10.1056/NEJM198908313210906

Authors and Affiliations

Sarah P. Stubbe[1] · Eva Marie Kramer[1] · Sven Büchner[1,2] · Christine Jelinek[1,3] · Calvin Mehl[3,4] · René Ryll[3] · Elisa Heuser[3] · Dania Richter[5] · Donata Hoffmann[3] · Emilija Vasiliūnaitė[6] · Christopher B. Buck[7] · Indrė Kučinskaitė-Kodzė[6] · Alma Gedvilaitė[6] · Patricia König[3] · Viola C. Haring[3] · Vanessa Schulze[3] · Silva Holtfreter[8] · Christian Kohler[9] · Tobias Eisenberg[10] · Marie Christin Apfel[11] · Stephan Drewes[3] · Kathrin Jeske[3] · Cristian Raileanu[3,12] · Holger Meinig[1] · Anna Obiegala[13] · Martin Pfeffer[13] · Dina Raafat[8,14] · Dietrich Pöhle[15] · Claudia Ulber[15] · Cornelia Silaghi[3] · Rainer G. Ulrich[3,4] · Michael Lierz[1] · Johannes Lang[1]

✉ Sarah P. Stubbe
sarah.stubbe@vetmed.uni-giessen.de

[1] Clinic for Birds, Reptiles, Amphibians and Fish, Working Group for Wildlife Research, Justus-Liebig-University Giessen, Giessen 35392, Germany

[2] Senckenberg Museum for Natural History Görlitz, Görlitz 02826, Germany

[3] Federal Research Institute for Animal Health, Friedrich-Loeffler-Institut, Insel Riems, Greifswald 17493, Germany

[4] German Center for Infection Research, Partner site Hamburg-Lübeck-Borstel-Riems, Insel Riems, Greifswald 17493, Germany

[5] Institute of Geoecology, Landscape Ecology and Environmental Systems Analysis, Technische Universität Braunschweig, Braunschweig 38106, Germany

[6] Institute of Biotechnology, Life Sciences Center, Vilnius University, Vilnius 01513, Lithuania

[7] Laboratory of Cellular Oncology, Center for Cancer Research, National Cancer Institute, Bethesda, MD 20892-4263, USA

[8] Institute of Immunology, University Medicine Greifswald, Greifswald 17475, Germany

[9] Friedrich-Loeffler-Institut of Medical Microbiology, University Medicine Greifswald, Greifswald 17475, Germany

[10] Hessian State Laboratory, Giessen 35392, Germany

[11] Clinic for Birds, Reptiles, Amphibians and Fish, Justus-Liebig-University Giessen, Giessen 35392, Germany

[12] TRON gGmbH, Freiligrathstraße 12, Mainz 55131, Germany

[13] Institute for Animal Hygiene and Veterinary Public Health, Faculty of Veterinary Medicine, University of Leipzig, Leipzig 04103, Germany

[14] Department of Microbiology and Immunology, Faculty of Pharmacy, Alexandria University, Alexandria 21521, Egypt

[15] State Examination Office for Health and Veterinary Affairs of Saxony, Dresden 01074, Germany