The role of invasive alien species in the emergence and spread of zoonoses

This note has been drafted by IUCN within the framework of the contract No 07.0202/2019/812535/SER/ENV.D.2 "Technical and Scientific support in relation to the Implementation of Regulation 1143/2014 on Invasive Alien Species". The information and views set out in this note do not necessarily reflect the official opinion of the Commission, or IUCN. The Commission does not guarantee the accuracy of the data included in this note. Neither the Commission nor IUCN or any person acting on the Commission's behalf, including any authors or contributors of the notes themselves, may be held responsible for the use which may be made of the information contained therein. Reproduction is authorised provided the source is acknowledged. This document shall be cited as:

Purse, B. V., Tricarico, E., Hassall, R., and Roy, H. E. 2020. The role of invasive alien species in the emergence and spread of zoonoses. Technical note prepared by IUCN for the European Commission.

Date of completion: 06/10/2020

Comments which could support improvement of this document are welcome. Please send your comments by e-mail to ENV-IAS@ec.europa.eu.

Authors: Beth V. Purse[1], Elena Tricarico[2], Richard Hassall [1], Helen E. Roy[1]

[1]UK Centre for Ecology & Hydrology, UK

[2]University of Florence, Italy

Contents

Summary

This is a report on the role of invasive alien species (IAS) in the emergence and spread of zoonoses. It is based on review of the relevant literature. The role of IAS acting as reservoir host, vector, or by having indirect impacts on pathogen spread, is investigated. Particular attention is paid to IAS of Union concern under Regulation (EU) 1143/2014. Other alien species playing a role in pathogen spread are considered as well, even if they do not affect biodiversity and, therefore, are not considered as invasive alien species in the context of the definitions under Regulation (EU) 1143/2014.

Parasites and pathogens are two types of organisms that can adversely affect host organisms. Parasites live on or in another organism and feed on them and include for example protozoans and helminths. Pathogens are disease-causing agents. Pathogens include viruses, bacteria, fungi and prions. Some parasites are also disease-causing agents. Here we will use the term pathogen to include the subset of parasites that cause disease that is adverse symptoms or sickness to their host. Zoonotic diseases are those occurring following the natural and reciprocal transmission of a pathogen or parasite between animals and humans.

Pathogens can alter the outcomes of biological invasions in many different ways. The role of IAS in the transmission dynamics of emerging zoonotic diseases is often overlooked but the impacts of introduced pathogens can be devastating. Here we review the roles of IAS in zoonotic disease dynamics, recognising the rapid escalation in arrival and establishment of IAS into new regions coupled with the mounting evidence of links between zoonotic diseases and biodiversity.

We conducted a structured review of the published literature within Web of Knowledge. Using six sets of search terms we identified 603 unique references. The titles and abstracts of all the papers were reviewed and information from a subset that met specific inclusion criteria, agreed by the project team, was extracted by assessing the full text. Data on IAS-zoonotic disease interactions was extracted from the papers that met the inclusion criteria. The geographic scope was global.

Overall, 272 interactions between IAS (and other alien species) and zoonotic diseases, beyond the natural range of the alien host, were identified from the literature review. Of these, 213 corresponded to interactions between mammalian IAS (35 species of mammal) and the remaining 59 included pathogen interactions with birds (26 interactions involving 14 species of bird), fish (four interactions involving three species of fish), non-avian reptiles (three interactions involving two species of reptile), crustacean (one), molluscs as intermediate reservoirs (11 interactions involving six species of mollusc), insects (10 interactions involving five species of insect) and ticks (four interactions involving four species of tick) as biological vectors. Four species (non-avian reptile, two plants and a plant pathogen) were identified as having an indirect impact on zoonotic disease transmission, by altering host-vector pathogen dynamics.

Though a wide range of interactions between IAS (and other alien species) and zoonotic diseases were identified, there was evidence of an actual rather than a potential impact of the IAS on the zoonotic disease system and human health for only a few of the interactions. Species for which evidence of actual impacts on transmission to humans was found included the Norwegian rat, *Rattus norvegicus*, and the black rat, *Rattus rattus*, on the spread and maintenance of *Leptospira*, *Bartonella* and the *Yersinia* bacteria species and *Aedes* mosquito vectors (noting that *Aedes* are alien species that are not considered to have biodiversity or ecosystem impacts), including *Ae. albopictus*, providing the conditions for autochthonous outbreaks of arboviruses such as Dengue and Chikungunya.

There were 204 unique zoonotic pathogen – alien species interactions identified through the review and these represented the following diverse types of zoonotic pathogens: 52 bacteria, 23 viruses, 33

endoparasites. The mode of transmission was also highly variable; of the 204 zoonotic pathogens-alien species interactions, 22 were aerosol-transmitted, 33 were contact-transmitted, 119 orally-transmitted, 22 were water-borne, 55 were food-borne and 55 were vector-borne.

Policies and interventions can affect the outcomes of interactions between IAS and zoonotic disease systems; in some cases they can increase the role of the IAS in spill-over to humans. As an example, supplementary feeding to increase the density of wild boar for hunting can increase transmission risk to hunters. Additionally, trade of livestock, including the relatively uncontrolled transboundary trade in alien animals, increases the risk of disease transmission. Studies on the diversity and prevalence of pathogens in captive/farmed IAS are also important because they can reveal the potential zoonotic diseases these species can transmit to humans. However, we limited the scope of the review to IAS and other alien species in the wild but provide a case study on captive animals.

IAS are involved in endemic and epidemic disease contexts and there is a wide range of ecological and social mechanisms governing their role in disease transmission dynamics. There is an urgent need to build interdisciplinary capacity, expertise and coordination to increase understanding of the risks posed by IAS in the transmission of pathogens. Specifically there is a critical need to raise awareness among policy and decision-makers, wildlife managers, scientists and citizens of the risks to human health of IAS to disease transmission. Most forecasts of the risk of emerging diseases neglect the potential role of IAS and this consequently represents a gap in strategies underpinning responses for zoonoses. Additionally, risk assessments should be conducted for both IAS and associated pathogens alongside risk management which would need to be contextualised and co-developed with cross-sectoral managers. Furthermore, effective cross-disciplinary approaches to horizon scanning and biosecurity are required to prevent the introduction and spread of IAS and associated zoonoses including enhanced monitoring and surveillance (adopting citizen science approaches where appropriate) linking to integrated early warning systems. Collaborations through adoption of One Health initiatives (incorporating EcoHealth and Planetary Health) would improve representation of zoonoses and their interactions with IAS within legislation, policy and management frameworks.

Definitions

For the purpose of this report, the following definitions[1] are used:

Alien (=non-native) species: Animals, plants or other organisms transported beyond their natural range by humans.

Biological vector: Living organisms that can transmit infectious pathogens that can multiply within their bodies, between humans, or from animals to humans.

Definitive host: Living organism (host) in which the infectious agent reaches its mature form and at this stage is typically capable of reproduction.

Direct transmission: Transfer of an infectious agent from a reservoir to a susceptible host by direct contact or droplet spread.

Emerging and re-emerging infectious disease (EID): Disease whose incidence in humans has increased during the last two decades or which threatens to increase in the near future. The term includes newly appearing infectious diseases or those spreading to new geographical areas. It also refers to those that were easily controlled by chemotherapy and antibiotics but have developed resistance to such treatments.

Endemic: Constant presence and/or usual prevalence of a disease or infectious agent in a population within a geographic area. More explicitly, a disease is endemic when its annual prevalence is predictable (by previous data) and oscillating in between an upper and below limits.

Epidemic: An increase, often sudden, in the number of cases of a disease above what is normally expected in that population in that area i.e., in relation to incidence, the number or proportion of new cases which surpass previous records (if any).

Indirect transmission: Transfer of an infectious agent from a reservoir to a susceptible host by suspended air particles, food or water, inanimate objects (vehicles), or animate intermediaries (vectors).

Intermediate host: Living organism (host) in which the infectious agent primarily grows but not to the point of reaching (sexual) maturity.

Invasive alien (=non-native) species (IAS): Plants, animals, pathogens and other organisms that are introduced directly or indirectly by people into places out of their natural range of distribution, and which may establish, spread and threaten or adversely impact upon biodiversity and related ecosystem services. It is important to note that in this context some of the alien species documented within this report are not considered invasive alien species, for example mosquitoes can have adverse impacts on human health but not biodiversity and ecosystems; as such in this report mosquitoes would be termed alien species.

---

[1] Some definitions have been taken from the World Health Organisation (WHO), the Centre for Disease Control (CDC), the European Food Standards Agency (EFSA) or other references where specified.

Invasive alien species of Union concern: IAS regulated in the framework of Regulation (EU) 1143/2014 across the territory of the European Union (excluding the outermost regions).

Mechanical vector: Living organisms that can transmit infectious pathogens on the outside of their bodies and transmit them through physical contact.

Neglected Tropical Diseases (NTD): Group of mainly communicable diseases that primarily affect communities in resource poor settings in tropical and subtropical conditions (1).

Pandemic: Epidemic that has spread over most or all continents, usually affecting a large number of people.

Parasites: Organisms that live on or in another organism and feed on them and include protozoans and helminths.

Pathogens: Organisms that can cause disease and include viruses, bacteria, fungi and prions. Both parasites and pathogens can adversely affect host organisms. Some parasites are as well disease-causing agents. Here we will use the term pathogen to include the subset of parasites that cause disease.

Re-emerging disease: Diseases that reappear after they have been on a significant decline.

Reservoir: Following Haydon et al. (2) "one or more epidemiologically connected populations or environments in which the pathogen can be permanently maintained and from which infection is transmitted to the defined target population".

Reservoir host: Populations or species in which a pathogen can be maintained and that serve as a source of infection for the recipient host.

Spillback: Spread of a pathogen in an introduced host and movement back to the original host, resulting in higher prevalence than expected in the absence of the new host.

Spillover: Pathogen is transmitted from reservoir population to novel host population and then may or may not be transmitted within the host population.

Sporadic: Occurrence of cases or outbreaks that are unpredictable.

Vector: Living organisms that can transmit infectious pathogens between humans, or from animals to humans. In the context of human diseases, vectors are almost exclusively arthropods, with the exception of the vampire bat (*Desmondus rotundus*), which inoculate (by biting or sting) the pathogen through an ecological relationship usually through feeding on the host organism.

Zoonosis (plural zoonoses, or zoonotic diseases): A zoonosis is a human disease occurring following the natural and reciprocal transmission of a pathogen or parasite between animals and humans.

Introduction

The adverse effects of invasive alien species (IAS) on biodiversity, ecosystems, economies and human health are widely documented (3). In particular, the human health impacts of a few alien species have received considerable attention (4), notably common ragweed, *Ambrosia artemisiifolia*, which has highly allergenic pollen, giant hogweed, *Heracleum mantegazzianum*, which causes contact dermatitis and Asian tiger mosquito, *Aedes albopictus*, which is a vector of several pathogens. However, the number of alien species arriving in new regions is escalating (5). Additionally there appears to be no sign of saturation in the accumulation of alien species globally (6). The role of alien species in the transmission dynamics of emerging zoonotic diseases is often overlooked (7–9). However, the interaction of alien species with environmental degradation has been postulated to be of similar magnitude to the threat of climate change in shifting the distribution of hosts, vectors and reservoirs of pathogens (7).

Pathogens (including pathogenic bacteria, fungi and viruses[2]) and parasites are frequently implicated in biological invasions. Pathogens can be introduced into an invaded range alongside an alien species; additionally, both introduced and endemic pathogens can alter the outcome of a biological invasion by changing the strength of interactions between species (8). Emerging Infectious Diseases (EID), which spread into new host populations or species, are rarely treated as biological invasions but it is recognised that the introduction of novel organisms (those without evolutionary analogues in the recipient environment) have potential to cause disruption (10,11). Zoonotic diseases[3] make up 60% of emerging infectious disease events worldwide (12) and disproportionately affect tropical communities (13,14) accounting for around 26% of Disability Life Adjusted Years lost to infectious diseases in Lower Middle Income Countries (15).

The impacts of these complex, multi-host pathogens are evolving in response to social-ecological and environmental changes including environmental degradation, forest loss, human settlement, climate change (16–18) and linked large-scale changes in the distribution, abundance and habitat use of animal species (19). Social-ecological and environmental change can alter the behaviour, social structure or dispersal of any or all the interacting species within a disease transmission network in many different ways (18). Anthropogenic changes to landscapes can dramatically alter the distribution of species; for example, habitat fragmentation or the creation of nature reserves can result in increased densities of animals within restricted areas. Host and vector ecology are key factor in determining pathogen transmission rates and therefore such changes can create novel sources of zoonotic infection. Furthermore, habitat loss (including drainage), degradation and fragmentation can increase overlap and encounter rates between humans and animals, which in turn can increase

---

[2] There is a longstanding debate on whether or not viruses are classified as living organisms but viral outbreaks have characteristics that are typical of biological invasions: sudden emergence, rapid proliferation and spread, adaptation to new environments (or hosts), large-scale geographic dispersal via human transportation networks, and significant impacts (10)

[3] According to WHO, "a zoonosis is any disease or infection that is naturally transmissible from vertebrate animals to humans. Zoonoses may be bacterial, viral, or parasitic, or may involve unconventional agents".

multidirectional transmission of pathogens amongst the interacting species. Alterations to the composition and diversity of local communities can increase or decrease pathogen transmission. One potential mechanism for this is the so-called, "dilution effect". This refers to the way in which increased community diversity can lead to decreased transmission risk for any particular host species because as diversity increases the occurrence of low quality hosts or non-host species disrupts transmission.

In some cases new alien species within a community may be suitable hosts for existing pathogens and so can increase pathogen transmission through "spillback" to original hosts. The connectedness between natural and anthropogenic systems highlights the importance of whole systems approaches to understanding the changing dynamics of pathogens in response to global environmental change (20). A recent topical study highlighted the complex nature of the interactions among IAS and zoonotic disease. Following an outbreak of SARS-CoV-2 on a farm mink, *Neovison vison*, there was strong evidence to suggest the mink had seemingly contracted the infection from spill-over from the human pandemic, at least two farm workers have subsequently caught the virus from the mink (21). The clinical and pathological characteristic of the SARS-CoV-2 outbreaks in mink farms was an acute interstitial pneumonia coupled with acute alveolar damage (22). Infectivity pattern analysis has illustrated that mink and bat coronaviruses have similar infectivity patterns with 2019-nCoV and confirm that bats and mink maybe two candidate reservoirs of SARS-CoV-2 (23).

The roles that IAS or alien species could play in zoonotic disease transmission are wide-ranging (7), from direct effects of acting as a vector, reservoir host or pathogen, to indirect effects that change the balance of vector-host-pathogen interactions to favour spill-over to humans (Fig. 1). Although robust evidence implicating IAS in increased transmission rates of a zoonotic pathogen is often lacking, IAS and alien species may have a disproportionate impact on zoonotic disease transmission for a number of reasons – summarised from (7):

- Alien species maybe more effective hosts or vectors in the transmission of existing diseases than other species
- Alien species may facilitate the establishment of new emerging diseases which they have co-evolved with in their native range
- Alien species often thrive in anthropogenic environments so have high encounter rates with people and often exhibit high dispersal rates. Indeed, IAS often spread rapidly through human-mediated dispersal and, as an example, virus transmission risk has been highest from animal species that have increased in abundance and expanded in range by adapting to human-dominated landscapes (19)
- The integration of a new host into an established zoonotic network can dramatically increase disease transmission

Distribution and intensity of infection in reservoir hosts

- Reservoir host distribution
- Reservoir host density
- Prevalence and intensity of host infection

Distribution and intensity of infection in vectors

- Vector distribution
- Vector host density
- Prevalence and intensity of vector infection

	Excretion	Slaughter of food or prey	Vector-borne
Parasite release from reservoir host	Shedding rates	Harvesting rates	Vector-reservoir biting-rate
Parasite survival, development and dissemination	Pathogen survival and management	Parasite survival and transport in food	Vector survival and movement

Parasite pressure

Human exposure to parasite

Human behaviour, resource and ecosystem use that leads to contact with pathogens

Food contact and consumption
Livestock and wildlife management

Vector-human biting-rate

Dose and route of exposure

Human host susceptibility

Structural barriers   Immune response
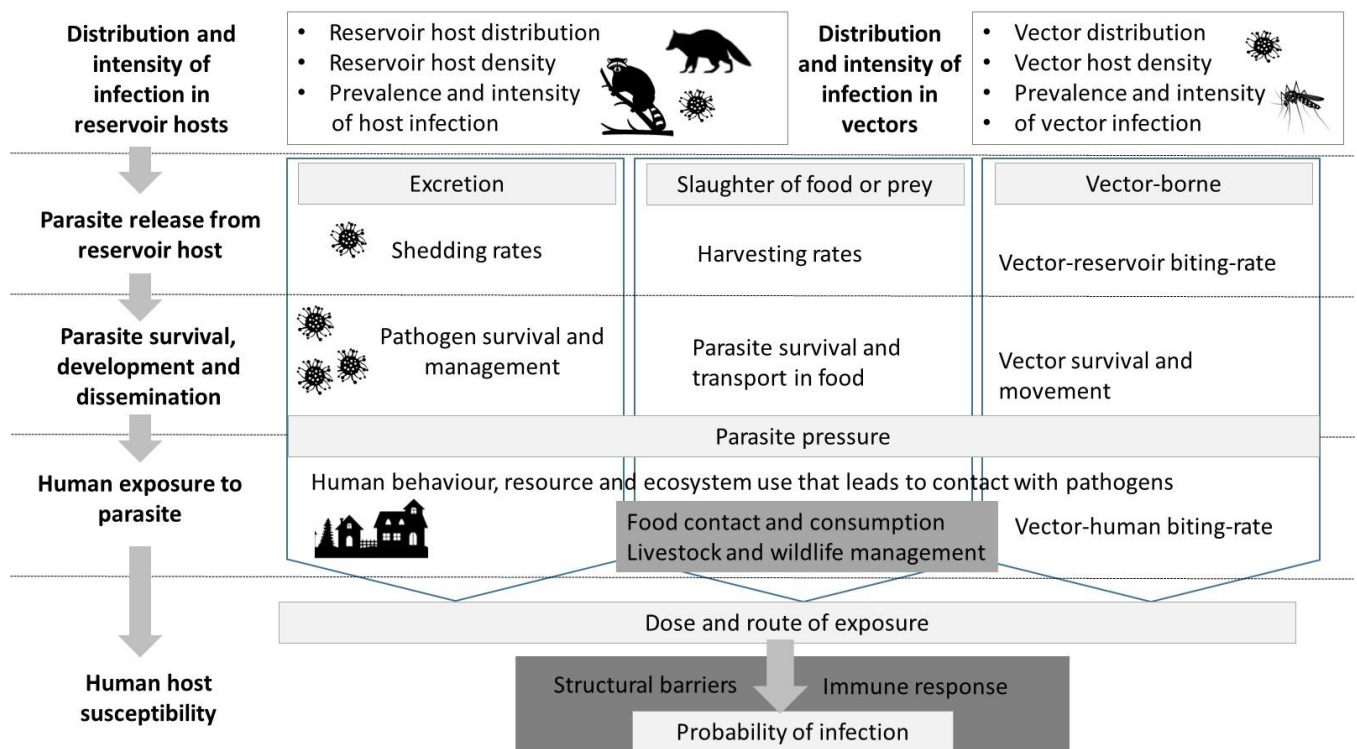
Probability of infection

Figure 1. Pathways of zoonotic disease spill-over, modified from (24). This figure highlights the linkages between the ecological dynamics of infection in reservoir hosts, the determinants of pathogen survival and dissemination outside of reservoir hosts, sometimes in arthropod vectors, the anthropogenic and ecological determinants of exposure such as human and vector behaviour and ecosystem use and the within-human biological factors that determine susceptibility. IAS may play several roles in these spill-over pathways from direct roles as vectors, reservoir hosts or pathogens, or by indirect effects (e.g. on vector or host habitats or demography) that change the balance of vector-host-pathogen interactions to favour spill-over to humans.

Given this complexity, there is a critical need for a synthesis of available information on the prevalence and abundance of pathogens and vectors of human diseases associated with IAS and other alien species coupled with an understanding of the epidemiological risks associated with transmission. It is also important to consider the global context of zoonotic diseases and the roles of a wide diversity of native hosts, pathogens in spill-over when weighing up the evidence for the involvement of alien species in transmission. It should also be noted that emphasis is often given to widespread IAS presumed to pose a risk to human health such as raccoons in Europe (7). Therefore, we present a review of the literature on the role of alien species broadly in the emergence and spread of zoonoses recognising the rapid escalation in arrival and establishment of alien species into new regions coupled with the mounting evidence of links between zoonotic diseases and biodiversity (10,19).

We examined the available literature to assess the extent to which the impacts of IAS, and indeed other alien species, on zoonotic disease transmission have already been realised, the context in which these impacts have occurred, the direct or indirect role the IAS have played in promoting transmission, and the ecological and evolutionary processes involved. Ultimately, as outlined in the task scoping brief, we aim to:

- provide an overview of IAS and associated pathogens that are or could become a Public Health concern in Europe;

- understand the magnitude of impacts that IAS are already having in the context of zoonoses, as opposed to the potential impacts that have been postulated, and the mechanisms involved in spill-over to humans;
- delineate which types of zoonotic diseases, with which type of transmission and in which epidemiological contexts, are most sensitive to involvement of IAS;
- determine which types of IAS are most likely to impact on zoonotic disease transmission and at which stage of invasion or establishment these can occur;
- examine biases and highlight knowledge gaps affecting our understanding of IAS in zoonotic disease transmission.

We also consider the policy landscape and highlight potential options for monitoring the role that IAS (and other alien species) play in zoonotic disease transmission but also approaches for prevention and intervention, including, for example, ways to integrate understanding of alien species into health system responses or health priorities into environmental IAS policy. We highlight key opportunities for improving our scientific understanding of the role IAS play in zoonotic disease transmission to inform interventions and policy.

Methods

We conducted a systematic review of published literature following PRISMA guidelines using the Web of Knowledge which includes references from 1960 onwards. All databases within Web of Knowledge were searched which included Web of Science Core Collection, BIOSIS Citation Index, BIOSIS Previews, KCI Korean Journal Database, MEDLINE, Russian Science Citation Index, SciELO Citation Index (search date: 12th July 2020). We utilised six sets of search terms to retrieve literature (Table 1), which yielded 603 unique references once duplicates were removed. No special operators were used which effectively performs an AND operation between the words in the set.

Table 1. Sets of search terms used to retrieve literature linking zoonotic diseases and invasive alien species and the number of references returned for each set.

Sets of search terms	Number of references returned
alien species zoonoses	48
alien species zoonotic diseases	50
invasive species zoonoses	262
invasive species zoonotic diseases	272
non-native species zoonoses	312
non-native species zoonotic diseases	290

For extraction of data into summary tables, we agreed on inclusion and exclusion which aligned with the scope of the task (Table 2). Full papers were identified following screening of all titles and abstracts and further reviewed as necessary for eligibility and inclusion by three of the study authors (BVP, ET, HER). Overall, 369 papers out of the 603 were excluded from the study.

Table 2. Inclusion and exclusion criteria used to select studies for the review.

Inclusion Criteria
Contains primary data on populations of alien species established in the wild outside their native range and causing (or having potential to cause) zoonotic disease.
Contains primary data on the role of alien species (or potential role) as a vector or reservoir species for a zoonotic disease in the wild outside their native range
Reviews the role of alien species in zoonotic disease transmission and spread in the wild outside their native range (either considering only the alien species or the alien species in comparison to native species)
Contains primary laboratory data on competence of alien species which are vectors or reservoirs for a zoonotic pathogen where the laboratory test populations arefrom outside the native range
Exclusion Criteria
Contains only ecological, taxonomic, genetic or physiological data on the alien species with no data on a zoonotic disease
Contains data on alien species involved as a vector or reservoir species for a zoonotic disease in the native range of the IAS only and with no information from outside the native range
Contains data on invasiveness of a pathogen inside host tissue as opposed to data on an alien species
Contains data on a non-invasive scientific method as opposed to data on alien species
Contains data on zoonotic disease in humans without linkage to alien species
Contains data on zoonotic disease links to alien species hosts but the hosts are not identified to species
Contains data on alien species links to zoonotic disease where alien species populations are captive or kept as pets [4]only with no free living alien species populations
Contains data on bites by an alien species as health problem rather than infectious zoonotic disease
Reviews that do not explicitly link alien species and zoonotic diseases (e.g. of invasion and biosecurity policy, zoonotic diseases and ecosystems, zoonotic diseases and biogeography, wildlife trade)
Paper not in the English language or lacking an abstract, It should be noted that literature in other languages would undoubtedly add to the information available.

Data synthesis and summary measures

Data on IAS-zoonotic disease interactions from relevant papers was extracted into summary tables (Tables 4-13). The first columns identified the Order, Family, Species of the IAS, and the species or genus name of the pathogen. The role of the IAS in zoonotic disease transmission was classified within broad categories of direct and indirect roles. Direct roles in transmission included being an IAS pathogen of humans, being a reservoir host for a zoonotic pathogen, being an arthropod vector for the zoonotic pathogen (biological or mechanical). Indirect roles included being a host for arthropod vectors of zoonotic pathogens, being a transport vector for a zoonotic pathogen, or altering vector-host-pathogen dynamics in ways that increase human spill-over.

The type of study was also categorised for each paper. Some of the studies were laboratory-based such as those considering the competence of vectors or reservoirs within the context of zoonoses and others on molecular phylogenetics. Many of the studies were field-based including relatively simple

---

[4] Although we excluded information from captive (zoos, aviaries, aquaria, farms) within the main results we have included a short case study recognising the potential of such animals as future IAS.

screening approaches to assess pathogen prevalence within an IAS host through to complex ecological studies investigating the mechanisms behind zoonotic transmission. There were also a number of biogeographic studies and review papers identified. For each study and where available the following contextual factors were collected: the region and country in which the study took place, the timing of introduction of the alien species and current extent of establishment and spread in the country, information on the status of the zoonotic disease in the study region.

To clarify and quantify the extent of impact that IAS and other alien species are having on zoonotic disease spill-over in each interaction, we extracted further information on the precise role of the IAS in the pathways to zoonotic disease spill-over (24) (Plowright et al. 2017, Fig. 1) from all the papers identified as relevant (conforming to the inclusion criteria outlined in Table 2). This information was compiled in a free text field and included information on:

- prevalence and diversity of pathogens in IAS established in the wild. Including, where information was available comparisons to native species and those strain/species shared with humans in the invaded range ;
- evidence of pathogen development within the IAS (for vectors and reservoirs), shedding (release into the environment) from the IAS and contact rates with vectors (for reservoirs only) that mediates the IAS role in transmission;
- ecological characteristics of the IAS that might favour or disfavour spill-over to humans such as high densities and (human-mediated) dispersal rates and adaptation to or association with anthropogenic environments;
- ecological mechanisms by which the IAS was reported to impact on zoonotic disease transmission, including how species may be modifying ecological networks.

Once this information had been extracted for all the alien species and zoonosis interactions from the relevant papers, the evidence for each individual IAS and zoonotic disease interaction was revisited to evaluate the extent of impact that IAS are having on transmission from a potential impact to an actual (=realised) impact along a continuum (identified by the authors) of available supporting evidence (Table 3). This provided an opportunity to give context to the interaction and specifically some measure of confidence in the extent and magnitude of the impact on humans. Pathogen type and transmission pathways were retrospectively retrieved for pathogens involved in the interactions using a wide range of literature sources (see Appendix 1).

The EU Regulation (EU) No 1143/2014 (hereafter IAS Regulation) on the prevention and management of the introduction and spread of IAS came into force on 1st January 2015. The IAS Regulation outlines measures to be taken across the EU for species included within the list of IAS of Union Concern (https://ec.europa.eu/environment/nature/invasivealien/docs/R_2016_1141_Union-list-2019-consolidation.pdf). Therefore, a summary is provided of the zoonoses (potential and actual) that are relevant to the IAS included within this list. It is important to note that the EU Regulation focuses on IAS that adversely affect biodiversity and ecosystems. Therefore, although some of the IAS listed will also have social and economic impacts, those only exerting human health impacts would not be included in the list of IAS of Union concern.

Table 3. Continuum of potential and actual impacts of alien species and IAS on zoonotic disease spill-over with types of supporting evidence.

Type of impact	Certainty of impact	Type of supporting evidence
Potential	Very low	detection of sporadic pathogen presence or low prevalence (< 5%) in populations of IAS in outside their native range
Potential	Low	detection of medium pathogen prevalence in populations of IAS (5-20%) in outside their native range, especially where less than native species
Potential	Medium	high pathogen prevalence in populations of IAS outside their native range, especially where the same or higher than native species
Potential	High	high pathogen prevalence in populations of IAS outside their native range, especially where higher than native species, widespread and abundant in anthropogenic habitats, laboratory/dissection studies supporting role in transmission
Actual	Low	IAS shown to play a role in transmission to people but low case number or prevalence outside their native range
Actual	Medium	IAS shown to overlap spatially or temporally with the distribution of human outbreaks outside the native range of the IAS
Actual	High	IAS shown to have changed the distribution or spread of autochthonous transmission or human outbreaks outside the native range of the IAS
Actual	High	IAS shown to alter strain diversity and population structure of pathogens and strains shared with humans outside the native range of the IAS

Additionally, information is provided on type of transmission and broad host associations and human health impact in Europe (Supplementary Information 1). Transmission was coded as: A = aerosol transmission, C= contact (skin and mucosal) transmission, O = oral transmission through food (F) or water (W) or vector-borne transmission (V) by either flea (F), tick (T), mite (MI), lice (LI), biting flies (BF), Triatminae (Tri) or mosquitoes (MOS). The annual cases and case fatality rates are also reported within the tables and all information is taken from European Centre for Disease Prevention and Control (2012-2018) where data are available.

Results

Overall 272 interactions between alien species or IAS and zoonotic diseases in the IAS invaded range, conforming to our inclusion criteria, were identified from the literature review (as well as other recent review papers (7,25)). The vast majority of direct interactions identified involved invasive alien vertebrate as potential or actual reservoir species for zoonotic diseases, with 213 (78.3%) IAS species-pathogen genus interactions identified for mammals, 26 (9.6%) for birds, 3 (1.1%) for reptiles and 4 (1.5%) for fish. For invertebrates, 14 (5.1%) IAS-pathogen interactions involved invasive ticks (4) or insects (10) as biological vectors, whilst one (0.4%) involved a Crustacean IAS and 11 (4.0%) involved Mollusc IAS as intermediate reservoir hosts for zoonotic diseases. Four species (a reptile, two plants, and a plant pathogen) were identified as having an indirect impact on zoonotic disease transmission, by altering host-vector pathogen dynamics. Six nematodes and five platyhelminthes were identified as zoonotic endo-parasites that had been recently introduced to Europe, with some degree of impact on human health.

Though a wide range of interactions between IAS and zoonotic diseases were identified, for only a small fraction was there evidence of an actual rather than a potential impact of the IAS on the zoonotic disease system and human health. The clearest evidence of actual impacts on transmission were for the well-studied impacts of the Norwegian rats, *Rattus norvegicus*, and the black rat, *Rattus* rattus, on the spread and maintenance of serious human pathogens such as the bacteria *Leptospira*, *Bartonella* and the *Yersinia* species. The evidence for the actual impacts on transmission was based on global biogeographical studies of these pathogens facilitated by advances in molecular methods (26,27)(28) alongside meticulous empirical studies on host-vector-pathogen interactions (29). Other significant actual impacts come from more recent invaders to Europe, such as the invasive *Aedes* mosquito vectors including *Ae. albopictus* providing the conditions for autochthonous outbreaks of arboviruses such as Dengue and Chikungunya in Europe. Additionally there was evidence that the raccoon dog, *Nyctereutes procyonoides*, an invasive alien species of Union concern, was modulating rabies transmission in Eastern Europe. Among the pathogens for which spill-over was found to be affected by IAS or other alien species, these included epidemics such as Chikungunya and Dengue outbreaks facilitated by the spread of *Ae. albopictus* or the East Coast Fever outbreaks facilitated by the brown ear tick *Rhipicephalus appendiculatus*.

The following groups of pathogens were implicated (actual or potential) with alien or IAS vectors or hosts in transmission, 52 bacteria, 23 viruses, 33 endoparasites and these combined with the IAS to give 204 zoonotic pathogen – alien or IAS interactions. Of these 22 were aerosol-transmitted, 33 were contact-transmitted, 119 orally-transmitted, 22 were water-borne, 55 were food-borne and 55 were vector-borne (details in Supplementary Information 1). In all cases the transmission of pathogens should be considered within the context of a complex system including interconnections amongst biological, economic, social and cultural variables. The high number of orally-transmitted, food-borne and vector-borne pathogens implicated with alien or IAS vectors or hosts perhaps highlights an increased sensitivity of these to involvement in spill-over. This is perhaps a consequence of the strength of the interconnections of these ecologically-complex pathogens with people and nature.

In the results section, for each major taxon in turn, with particular direct or indirect roles in transmission, we summarise the interactions identified and their public health importance, particularly for Europe. We then evaluate the evidence that IAS are having an equivalent or disproportionate impact on zoonotic disease transmission relative to native species, and outline some of the ecological, evolutionary and social mechanisms involved in IAS impacts on spill-over.

Ticks

Three interactions were identified where alien tick species were implicated as potentially affecting transmission of zoonotic Rickettsial bacteria species, due to the sporadic presence of these pathogens in ticks in the invaded ranges or links to human cases (Table 4a). The clearest example of where an invasive alien tick species has already altered the distribution of human disease outbreaks, the introduction of *Rhipicephalus appendiculatus* to the Comoros Islands (Indian Ocean) through cattle imports that lead to epidemics of East Coast Fever (*Theileria parva*) in 2004 (30). There was some concern also over the potential impact of *Haemaphysalis longicornis* in its invaded range in the United States on Lyme Borrelia transmission but behavioural evidence suggests these ticks might avoid key rodent reservoirs as biting hosts (31).

Mosquitoes

Previous studies have highlighted successive waves of invasion of vector mosquitoes since the 15th century largely due to worldwide ship transport, most notably *Aedes aegpyti* and the *Culex pipiens* complex, as well as *Ae. albopictus* (32). An increase in the spread of alien mosquitoes in Europe has been seen since the 1990s, linked to increased global trade and travel (33), with six invasive *Aedes* mosquito species now established in continental Europe - *Ae.albopictus, Ae. aegypti, Aedes japonicus, Aedes koreicus, Aedes atropalpus*, and *Aedes triseriatus*. This intensification of trade and travel has not only promoted the expansion of alien mosquito species, but has also increased the rate of imported cases of dengue, chikungunya or Zika viruses in continental Europe, resulting in local outbreaks in several European countries (34).

Mosquito species that occupy transportable container habitats, such as water-holding automobile tires, have been especially successful as recent invaders. Propagule pressure, previous success, and adaptations to human habits appear to favor successful invasions by vectors (32,35). The most significant Public Health threats from alien mosquitoes arise from their ability to transmit zoonotic arboviruses, particularly flaviviruses, alphaviruses, bunyaviruses and orthabunyaviruses (33) but they also transmit other important pathogens like filarial worms and protozoan parasites (33). Since the invasion status of mosquito species is often not an explicit consideration in vector incrimination studies, particularly for long-standing invaders, our search terms captured only a fraction of relevant literature on interactions between invasive mosquitoes and pathogens (Table 4). Therefore, we also included existing review studies (32–35) that have integrated field evidence and laboratory competence and infection studies and largely limit our focus here to mosquito species alien to Europe (35).

Ae. albopictus has played the greatest role in facilitating the autochthonous transmission of arboviruses in Europe. This species spread dramatically across Europe, largely through the trade in used tyres, since it arrived in Albania in 1979. *Ae. albopictus* breeds in urban water containers and is aggressively anthropophilic, preferring and seeking humans as hosts, but also has the widest range of competence for arboviral pathogens amongst native and alien mosquito species in Europe (34). Considering vector roles in the recent Chikungunya virus outbreaks in 2007 (Italy, France), only *Ae. albopictus* (in France) and *Ae. japonicus* (Germany) have been shown to be competent for transmission and their adult activity seasons (coincide with the seasonal peak of imported cases, promoting autochthonous transmission. *Ae. aegypti* and *Ae. albopictus* are the main vectors of Chikungunya virus but *Ae. Koreicus* has also been shown to be a competent vector under optimal rearing conditions (36). Temperature fluctuations reduce the risk of transmission by *Ae. Koreicus* and so transmission by this vector species is likely to be limited in Europe. Furthermore, there is evidence that adaptive envelope glycoprotein substitutions in the Central African Chinkungunya virus strained enhanced transmission by *Ae. Albopictus* (37). Sporadic local outbreaks of Dengue in France and Croatia in 2010, 2013 and 2015 (causing >1500 cases from 2012-2016) have also been attributed to

the establishment of *Ae.albopictus* (33). *Ae. albopictus* and *Ae. aegypti* are the main vectors of Dengue in urban cycles globally (32,33) and thus known to be competent, but *Ae. japonicus* populations in Germany have also shown competence to transmit tropical Dengue strains and the adult activity periods of all three of these species overlap with the part of the year when imported cases occur.

In terms of future potential risk of Zika virus transmission in Europe, *Ae. albopictus* is also expected to take the most prominent vector role. Only *Ae. albopictus* (France, Germany) and *Ae. japonicus* (Germany) are competent mosquitoes, the latter only poorly competent, whilst native Culex species have not been found competent for Zika virus (34). Thus, Martinet and others (34) conclude that the three species alien to Europe *Ae. albopictus, Ae. koreicus* and *Ae. japonicus* are the species most likely to play a role in circulation of Chikungunya, Dengue and Zika virus in Europe. To date, *Ae. japonicus* is well established in Belgium, France, Luxembourg, Germany, The Netherlands, and Switzerland, and *Ae. koreicusis* has invaded Germany, Switzerland, and Belgium. By contrast, native *Culex* species would likely play a stronger role in transmission of Usutu and West Nile viruses, because of high competence and their ability to act as bridge vectors between avian and mammalian hosts (34).

These six *Aedes* species have been linked to a wide range of other arboviruses in their native ranges as well as elsewhere in their invaded ranges, through field infection rates and laboratory competence studies (33), though their precise roles in transmission under natural conditions is often still unclear. For a full list of these interactions see Schaffner et al. (38). Furthermore, several mosquito species including *Ae. aegypti*, *C. pipiens*, *Ae. japonicus*, and *Ae. albopictus*, have been linked to transmission of zoonotic filaroid helminths, *Dirofilaria repens* and *D. imiitis*, outside the native range of the mosquito species, either through laboratory competence studies or findings of infective stages of the pathogens in wild-caught adults. These filarioid helminths use domestic and wild canids as main hosts and mosquitoes as vectors, and only occasionally infect humans, though autochthonous cases of human dirofilariosis are now increasing in Italy, anecdotally linked with *Ae. albopictus* (Table 11).

Overall, it is clear that introduced arthropod species can alter the transmission of zoonotic diseases quite rapidly (<10 years) following their introduction to new regions. Increasing travel and pathogen introduction, expansion of vector distribution, and both environmental and climatic changes are likely to raise the risk of pathogen transmission in Europe, and indeed globally, by these alien *Aedes* mosquitoes (33,34,39–41). Several research priorities have been highlighted that would improve our ability to predict health outcomes from *Aedes*-parasite interactions (35,42). These include understanding how and why alien vector species are becoming locally abundant in urban habitats, understanding their basic behaviour, the developmental and life-history parameters that contribute to vectorial capacity alongside vector competence, and how these are modulated by environmental variability (42).

Alien arthropods (Crustacea) as hosts for enteric bacterial diseases and food-borne trematodes

In one study from the UK, an introduced barnacle, *Austrominius (Elminius) modestus*, was found to act as a significant reservoir of coliform enteric bacteria on shell-fish beds, harbouring higher concentrations of the bacteria than other barnacle species or the native mussel, *Mytilus edulis* (Table 5) (43). Surface-dwelling barnacles, such as *A. modestus*, are commonly associated with shellfish and are recognised as a potential source of contaminants for commercially harvested mussels and so pose a risk to humans when shell-fish are ingested. In terms of introduced Crustacea listed as invasive alien species of Union concern, the mitten crab, *Eriocheir sinensis*, and the red swamp crayfish, *Procambarus clarkii*, are intermediate hosts for the lung fluke, *Paragonimus westermani*, in Asia which, if eaten, can cause tuberculosis-like and influenza-like symptoms in humans (7,25). This lung fluke is widely distributed in south-east Asia and Japan but only rarely found in Europe.

Alien molluscs as intermediate hosts for zoonotic diseases

Invasive alien molluscs, especially freshwater species, can act as intermediate hosts for nematode, trematode and Platyhelminthes and can infect humans that eat raw or undercooked molluscs. Our literature search identified 11 interactions between IAS of mollusc and such parasitic worms (Table 6), in North and South America, though it was rare for the introduced species to have been explicitly linked to human cases of disease. *Melanoides tuberculata*, the Red-rimmed melania, was found to be an intermediate host for a particularly wide range of such parasitic worm pathogens, being linked to human haplorchiasis cases in Venezuela. This species is native to eastern Africa and the Middle East but has spread throughout the tropics, with sporadic records in Spain, Netherlands and Germany. The Giant African Land Snail, *Achatina fulica*, is implicated as an intermediate host of the rat lung worm, but again human cases have rarely been linked to this species (25), and the species is localized (Spain) or under eradication in Europe (Italy). Some species of Planorbid snail that have been recently introduced into Eastern Europe (Romania), *Biomphalaria glabrata* and *Biomphaliaria tenagophila* (44), can act as intermediate hosts for *Schistosoma mansoni*. This species of trematode causes Schistosomiasis, and the associated intermediate host snails are increasingly imported into Europe by immigrants from endemic areas (7). However, explicit links between these species and Schistosomiasis transmission have yet to be made for Europe. The establishment of another tropical *Schistosoma* species, *Schistosoma haematobium*, in southern Europe has been linked to transmission by native snail species in Corsica (45).

Table 4. Alien arthropods as biological vectors for vector-borne zoonotic diseases (*=invasive alien species of Union concern). V = vector borne transmission by either flea (F), tick (T) or mosquito (MOS). Case fatality is mean of case fatalities reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

(a) Arthropoda: Arachnida								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Trans mission	Case fatality rate (%)				
Ixodida: Ixodidae	*Rhipicephalus microplus*	*Candidatus Rickettsia senegalensis*	V(F)	-	Pathogens found in 1-2 ticks of this IAS recovered from Philippine deer in invaded range	Guam	Potential (very low)	(46)
Ixodida: Ixodidae	*Hyalomma marginatum*	*Rickettsia aeschlimannii*	V(T)	-	Adult *Hyalomma marginatum* tick positive for *Rickettsia aeschlimannii*	Austria	Potential (very low)	(47)
Ixodida: Ixodidae	*Rhipicephalus appendiculatus*	*Theileria parva* (East Coast Fever)	V(T)	-	Alien tick is a highly competent vector for East Coast fever, previously absent from island. Alien species introduction through cattle imports probably led to subsequent outbreaks	Comoros Islands, Indian Ocean	Actual (high)	(30)
Ixodida: Ixodidae	*Rhipicephalus sanguineus*	*Rickettsia conorii*	V(T)	-	Implicated as only potential local vector of five cases of Mediterranean boutonneuse fever. Alien status in Switzerland is unclear	Switzerland	Actual (low)	(48)
(b) Arthropoda: Insecta								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Trans mission	Case fatality rate (%)				
Diptera: Culicidae	*Aedes aegypti*	*Dirofilaria immitis* *Dirofilaria repens*	V(MOS)	-	Pathogens only rarely transmitted from dogs to humans. Non-infective larval stage of these pathogens found in adult *Ae. aegypti* in Argentina. Laboratory colonies (Switzerland) found to be refractory to the pathogen	Argentina Switzerland	Potential (low)	(49, 50)(51)
Diptera: Culicidae	*Culex pipiens*	*Dirofilaria immitis* *Dirofilaria repens*	V(MOS)	-	Non-infective larval stage of these pathogens found in adult *Cx. pipiens* in Argentina	Argentina	Potential (low)	(49, 50)

Order:Family	Species	Pathogen	Role	Value	Description	Location	Status	Ref
Diptera: Culicidae	*Aedes japonicus*	*Dirofilaria immitis* *Dirofilaria repens*	V(MOS)	-	Efficient a vector in the field for *both D. immitis* and *D. repens* as the native *Ae. geniculatus* (lab. competence of colony and field populations)	Switzerland	Potential (medium)	(51)
Diptera: Culicidae	*Aedes albopictus*	*Dirofilaria immitis* *Dirofilaria repens*	V(MOS)	-	The infective stage of this pathogen has been found in adult populations of *Ae. albopictus* in Italy and been anecdotally linked within an increase in human dirofilariosis	Italy	Actual (low)	(52) (33)
Diptera: Culicidae	*Aedes aegypti*	Eastern equine encephalitis virus	V(MOS)	-	Adults were found to acquire transmissible viral infections from infected starling hosts in the laboratory	United States	Potential (low)	(53)
Diptera: Culicidae	*Aedes japonicus japonicus*	Cache Valley virus	V(MOS)	-	In the lab, vector competence of *Ae. j. japonicus* mosquitoes was equivalent to other species that are part of the CVV transmission cycle	United States	Potential (high)	(54)
Diptera: Culicidae	*Aedes japonicus japonicus*	West Nile Virus	V(MOS)	9.13	Introduced populations are highly susceptible to WNV, even more so than native vector *Culex pipiens*. Also feeds opportunistically on avian and mammalian hosts and highly abundant in late summer and autumn when human WNF cases occur, making it the ideal bridge vector	Switzerland	Potential (high)	(55, 56)
Diptera: Culicidae	*Aedes japonicus japonicus*	Dengue virus	V(MOS)	-				(38)
Diptera: Culicidae	*Aedes japonicus japonicus*	Chikungunya virus	V(MOS)	-				(38)
Diptera: Culicidae	*Aedes japonicus japonicus*	Zika virus	V(MOS)	-				(38)
Diptera: Culicidae	*Aedes albopictus*	West Nile Virus	V(MOS)	9.13	*Ae. albopictus* has been found to be competent for West Nile Virus in laboratory and field populations in the US and Europe	Europe United States		(34)
Diptera: Culicidae	*Aedes albopictus*	Chikungunya virus	V(MOS)	-	Where *Ae. albopictus* is established, viraemic travel-related cases may generate local urban transmission of the virus as demonstrated by the sporadic events of chikungunya virus transmission since 2007. Field populations of the species have also been shown to be competent in the laboratory for this virus in Europe and the United States.	Europe United States	Actual (very high)	(57–60) (33) (61)

| Diptera: Culicidae | *Aedes albopictus* | Dengue Virus | V(MOS) | - | Where *Ae. albopictus* is established, viraemic travel-related cases may generate local urban transmission of the virus as demonstrated by the sporadic dengue outbreaks since 2010 in Europe | France, Croatia | Actual (very high) | (33) |
| Diptera: Culicidae | *Culex quinquefasciatus* | West Nile Virus | V(MOS) | 9.13 | The species has established as a primary vector for WNV in the US, human cases shown to correlate with infection rates in this species | United States | Actual (medium) | (62) |

Table 5. Alien arthropods (Crustacea) as hosts for zoonotic diseases (*=invasive alien species of Union concern). C = transmission through contact. The criteria for actual or potential impact are outlined in Table 3.

(a) Maxillopoda								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Trans mission	Case fatality rate (%)				
Sessilia: Austrobala nidae	*Austrominius (Elminius) modestus*	Colliforms	C	-	Coliform concentrations were significantly higher in the species than in the native *Mytilus edulis*, per unit area, across all surveyed sites	United Kingdom	Potential (low)	(43, 63)

Table 6. Alien molluscs as hosts for zoonotic diseases (*=invasive alien species of Union concern). O =oral transmission through food (F) or water (W). Case fatality is mean of case fatalities reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

(a) Gastropoda								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Trans missi on	Case fatality rate (%)				
Planorbidae	*Biomphalaria glabrata*	*Schistosoma mansoni*	O(W)	-	Intermediate hosts for *Schistosoma mansoni* which itself is increasingly imported into Europe by immigrants from endemic areas	Romania	Potential (low)	(44)
Planorbidae	*Biomphaliaria tenagophila*	*Schistosoma mansoni*	O(W)	-	Intermediate hosts for *Schistosoma mansoni* which itself is increasingly imported into Europe by immigrants from endemic areas	Romania	Potential (low)	(44)
Achatinidae	*Achatina fulica*	*Angiostrongylus cantonensis* *A. costaricensis*	O(F)	-	Intermediate host for this pathogen (the rat lungworm), facilitating establishment in Florida	United States	Potential (low)	(64)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Philophthalmus gralli* *P.lucipetus* *P. gralli*	O(W)	-	IAS established as an intermediate host for these eye trematodes. When definitive hosts were experimentally removed, pathogen prevalence decreased in the IAS intermediate host	Costa Rica Peru Brazil	Potential (low)	(65) (66) (67)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Centrocestus formosanus*	O(F, W)	-	IAS infested with this pathogen so probably intermediate host	Brazil	Potential (low)	(67)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Clonorchis sinensis*	O(F, W)	-	IAS established as an intermediate host though not yet linked to infections causing human cases in Brazil	Brazil	Potential (low)	(67)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Haplorchis pumilio*	O(F)	-	IAS established as an intermediate host and linked to haplorchiasis in humans in Venezuela	Venezuela	Realised (low)	(67)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Paragonimus westermani*	O(F)	-	IAS established as an intermediate host though not yet linked to infections causing human cases in Brazil	Brazil	Potential (low)	(67)
Caenogastropoda : Thiaridae	*Melanoides tuberculata*	*Philophthalmus gralli*	O(W)	-	IAS infested with this pathogen so probably intermediate host	Brazil	Potential (low)	(67)
Neritopsina: Helicinidae	*Alcadia striata*	*Angiostrongylus cantonensis*	O(F)	-	intermediate host for this pathogen (the rat lungworm), facilitating establishment in Florida	United States	Potential (low)	(64)

Stylommatophora :Bradybaenidae	*Bradybaena similaris*	*Angiostrongylus cantonensis*	O(F)	-	intermediate host for this pathogen (the rat lungworm), facilitating establishment in Florida	United States	Potential (low)	(64)
Stylommatophora :Bradybaenidae	*Zachrysia provisoria*	*Angiostrongylus cantonensis*	O(F)	-	intermediate host for this pathogen (the rat lungworm), facilitating establishment in Florida	United States	Potential (low)	(64)

Alien fish species as hosts for food-borne zoonotic diseases

Alien fish species can act as an important source of zoonotic pathogens, especially such as trematode, cestode and nematode parasitic worms that are acquired by consuming raw or undercooked fish products (25) and can cause wide-ranging symptoms, depending on the pathogen species. For example, the WHO estimates that over 2 million disability-adjusted life years worldwide are lost to food-borne trematode parasites each year, concentrated in Africa, Asia and Latin America. We identified 5 interactions between introduced fish species and fish-borne pathogens (Table 7) while Zhu et al. (25) identify a further 60 interactions for IAS in China, though few studies document actual as opposed to potential impact on human disease cases or outbreaks. Of greatest significance to Europe is the finding that introduced salmon species, *Oncorhynchus keta* and *Oncorhynchus nerka*, used for food, harbour the nematode *Anisakis simplex*, and were the source of several human cases of Anisakidosis, an emerging disease in Europe.

Alien bird species as hosts for zoonotic diseases

The role of alien birds species as hosts for zoonotic diseases was under-researched with few studies, mostly from prior to 2000 and few studies documenting actual (as opposed to potential) impacts on zoonotic disease spill-over, which is perhaps the most significant role that invasive alien birds could play in zoonotic disease dynamics. Table 8 identifies 26 interactions between invasive alien bird species and zoonotic disease systems, mostly from studies in the United States or New Zealand (only three studies were found for Europe). Most suggestions of invasive alien bird species as hosts in zoonotic disease transmission relied on relatively weak evidence of presence or low prevalence levels of the pathogen in sampled populations.

Perhaps the most significant role that alien/introduced birds could play in human spill-over of zoonotic diseases is as maintenance hosts for mosquito-borne arboviruses (MBAs). This is particularly relevant in the United States, where several alphaviruses (Eastern equine encephalitis virus, Western equine encephalomyelitis virus, Togaviridae: Alphavirus) and flaviviruses (West Nile virus, Saint Louise encephalitis virus Flaviviridae: Flavivirus) are relatively widespread and cause febrile illnesses and encephalitis in people (occasionally resulting in neurological problems and death). These viruses tend to be maintained by cycles between infected birds and mosquitoes, with transmission to humans requiring "bridge vector" mosquitoes that bite mammals as well as birds. Many of the introduced bird species sampled in peridomestic settings in the United State in 2000 were found to have a very low prevalences (<5%) of Saint Louise encephailitis, Japanese encephalitis and Western equine encephalomyelitis viruses (68), indicating that they probably are not maintenance hosts for these viruses (Table 5). By exception, the introduced sparrow, *Passer domesticus*, and the European Starling, *Sturnus vulgaris*, had levels of viremia to Eastern equine encephalomyelitis that were as or more intense and lasted longer than those of other native bird and mammal species (53,69), making them likely maintenance hosts.

Of significance for Public Health is the finding that some birds that have been introduced to Europe can harbour Influenza A viruses that have been implicated in human outbreaks, including the Mandarin duck, *Aix galericulata*, in its native range (H5N1 strains) (70) and the ring-necked parakeet, *Psittacula krameri*, in its invaded range (H9N2 strains) (71). Avian influenza viruses represent a major concern for animal and human health worldwide (72). Indeed the emergence of Avian influenza virus H5 (highly pathogenic) and H7N9 (low pathogenic) have led to socioeconomic losses in the poultry industry and fatal human infections. Timely data sharing is seen as critical to address the threat of Avian influenza viruses (and indeed other zoonoses). Real-time epidemiological and sequence data are essential for feeding into models to demonstrate transmission patterns and virus evolution. Ecological studies are also crucial for describing host range and bird migration patterns.

Several introduced birds, including Canada geese, *Branta canadensis*, and the ring-necked parakeet, *Psittacula krameri*, were implicated as hosts of *Crytosporidium* and *Giardia* in farmland settings in New Zealand (73) and the UK (74,75), with human cases of Giardia being relatively common in New Zealand. Psittacosis is an acute respiratory disease (ranging from mild illness to pneumonia) caused by infection with the bacterium, *Chlamydia psittaci*, following inhalation of airborne particles secreted by bird hosts. Some IAS have been found to be key hosts of this pathogen in urban park or farmed settings in Europe and New Zealand, (75–77) but the risk is soley restricted to the small number of people who come into direct contact with birds.

Alien amphibians as hosts for zoonotic diseases

The search terms we used did not identify some of the potential interactions amongst IAS and pathogens. No references were revealed through the structured search relating to amphibians and zoonotic disease. However, there are a few examples in the literature such as the isolation of *Aeromonas hydrophila* from bullfrog, *Lithobates catesbeianus (78)*.

Table 7. Alien fish species as hosts for food-borne zoonotic diseases (*=invasive alien species of Union concern). O = oral transmission through food (F) or water (W). Case fatality is mean of case fatalities reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

Actinopterygii								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Transmission	Case fatality rate (%)				
Cichliformes: Cichlidae	*Oreochromis niloticus*	Echinostomatidae	O(F)	-	A very low prevalence (1.5%) of trematode infections found in farmed Nile tilapia (n=388)	China	Potential (low)	(79)
Cichliformes: Cichlidae	*Oreochromis niloticus*	Heterophyidae	O(F)	-	A very low prevalence (1.5%) of trematode infections found in farmed Nile tilapia (n=388)	China	Potential (low)	(79)
Cypriniformes: Cyprinidae	*Cyprinus carpio*	*Contracaecum bancrofti*	O(F, W)	-	Intermediate host for *Contracaecum bancrofti*, linked to human infections	Australia	Actual (low)	(80)
Salmonidae	*Oncorhynchus keta*	*Anasakis simplex*	O(F)	-	Host for nematodes, which is prevalent in Baltic and Barent seas, causes anisakidosis	Europe	Actual (low)	(81)
Salmonidae	*Oncorhynchus nerka*	*Anasakis simplex*	O(F)	-	Host for nematodes, which is prevalent in Baltic and Barent seas, causes anisakidosis	Europe	Actual (low)	(81)

Table 8. Alien bird species as hosts for zoonotic diseases. A = aerosol transmission. C= contact transmission. O = oral transmission through food (F) or water (W). V = vector-borne transmission by either tick (T) or mosquito (MOS). Case fatality is mean of case fatalities reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

Aves								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Transmission	Case fatality rate (%)				
Passeriformes: Sturnidae	*Sturnus vulgaris*	*Salmonella enterica*	O(F)	0.2	The species is reservoir host. 2.5% prevalence in sampled individuals. Contamination of both cattle troughs significantly related to numbers of starlings	United States	Potential (medium)	(82)
Passeriformes: Sturnidae	*Sturnus vulgaris*	*Anaplasma phagocytophilum*	V(T)	-	Pathogen detected in 1/13 individuals	United States	Potential (very low)	(82)
Passeriformes: Sturnidae	*Sturnus vulgaris*	Cryptosporidium	O(F, W)	0.01	Pathogen detected in 1/2 individuals	New Zealand	Potential (very low)	(82)
Passeriformes: Sturnidae	*Sturnus vulgaris*	Eastern equine encephalitis virus	V(MOS)	-	The bird is likely maintenance host. Longer, more intense viremia than in other birds	United States	Potential (medium)	(53)
Anseriformes: Anatidae	*Branta canadensis*	*Chlamydia psittaci*	A	-	Role of IAS as host indicated by high prevalence (>90%) of *C. psittaci* antibodies	Belgium	Potential (low)	(75)
Anseriformes: Anatidae	*Branta canadensis*	*Cryptosporidium sp.*	O(F, W)	0.01	Presence of Cryptosporidium found in free-living United Kingdom populations	United Kingdom	Potential (very low)	(74)
Galliformes: Phasianidae	*Alectoris chukar*	*Chlamydia psittaci*	A	-	Role of species as host indicated by high prevalence (>50%) of *C. psittaci* antibodies in farm setting	United States	Potential (low)	(83)
Psittaciformes: Psittacidae	*Myiopsitta monachus*	*Cryptosporidium sp.*	O(F, W)	0.01	It is a host, around 20% of sampled populations of this IAS harboured Cryptosporidium in Chile	Chile	Potential (low)	(84)
Psittaculidae	*Psittacula krameri*	*Chlamydia psittaci*	A	-	IAS as host, low levels of shedding found in 30% of IAS individuals in urban park	France	Potential (low)	(77) (85)
Psittaculidae	*Psittacula krameri*	Influenza A virus (H9N2)	A;C	-	Parakeets imported (Pakistan to Japan) harbor H9N2 influenza A viruses, closely related to human strains from Hong Kong	Japan	Potential (low)	(71)

Order: Family	Species	Pathogen	Transmission	Value	Notes	Country	Risk	Ref
Columbiformes: Columbidae	*Columba livia*	St. Louis encephalitis virus (SLEV)	V(MOS)	-	Alien bird is a host for the virus in peridomestic settings, 3.4% prevalence is greater than for native species	United States	Potential (low)	(68)
Columbiformes: Columbidae	*Columba livia*	western equine encephalomyelitis virus (WEEV)	V(MOS)	-	Alien bird is a host for the virus in peridomestic settings, though <1% prevalence, equivalent to native species	United States	Potential (low)	(68)
Columbiformes: Columbidae	*Streptopelia chinensis*	Japanese encephalitis virus (JEV)/ Saint Louise Encephalitis virus (SLEV)	V(MOS)	-	Potential host for virus, <1% of sampled populations had neutralising antibodies to JEV/SLEV in Hawaii	United States	Potential (very low)	(86)
Estrildidae	*Padda oryzivora*	Japanese encephalitis virus (JEV)/ Saint Louise Encephalitis virus (SLEV)	V(MOS)	-	Potential host for virus, <1% of sampled populations had neutralising antibodies to JEV/SLEV in Hawaii	United States	Potential (very low)	(86)
Passeriformes: Fringillidae	*Fringilla coelebs*	*Giardia* sp.	O	0.05	Alien bird is host, 60% of sampled birds (10) carried *Giardia* in farmland settings	New Zealand	Potential (low)	(73)
Passeriformes: Turdidae	*Turdus philomelos*	Whataroa virus	V(MOS)	-	Whataroa virus is mosquito-borne and causes influenza like symptoms in humans. Antibodies found in 15% of sampled birds (>4000), suggesting IAS hosts plays maintenance role	United States	Potential (medium)	(87)
Passeriformes: Turdidae	*Turdus merula*	*Giardia* sp.	O	0.05	Alien bird is host, 35% of sampled birds (20) carried *Giardia* in farmland settings	New Zealand	Potential (low)	(73)
Passeriformes: Turdidae	*Turdus philomelos*	*Cryptosporidium*	O(F, W)	0.01	Alien bird is host, 21.4% of sampled birds (14) carried *Cryptosporidium* in farmland settings	New Zealand	Potential (low)	(73)
Passeriformes: Turdidae	*Turdus philomelos*	*Giardia* sp.	O	0.05	Alien bird is host, 50% of sampled birds (14) carried *Giardia* sp. in farmland settings	New Zealand	Potential (low)	(73)
Passeriformes: Prunellidae	*Prunella modularis*	*Giardia* sp.	O	0.05	Alien bird is host, 14.3% of sampled birds (14) carried *Giardia* in farmland settings	New Zealand	Potential (low)	(73)
Passeriformes: Passeridae	*Passer domesticus*	*Toxoplasma gondii*	O(F)	2.11	Alien bird is host, <2% of sampled birds were infected, much less than native hosts	United States	Potential (very low)	(88)
Passeriformes: Passeridae	*Passer domesticus*	*Cryptosporidium* spp.	O(F, W)	0.01	Alien bird is host, 8.2% of sampled birds (61) carried *Cryptosporidium* in farmland settings	New Zealand	Potential (very low)	(73)
Passeriformes: Passeridae	*Passer domesticus*	*Giardia* sp.	O	0.05	Alien bird is host, 15.4% of sampled birds (104) carried *Giardia* in farmland settings	New Zealand	Potential (low)	(73)

Passeriformes: Passeridae	Passer domesticus	Eastern equine encephalitis virus	V(MOS)	-	Sparrows found to be reservoir host for this mosquito-borne alphavirus equally susceptible to *Rattus* species, with viraemia lasting 4-5 days	United States	Potential (medium)	(69)
Passeriformes: Passeridae	Passer domesticus	Western equine encephalomyelitis virus (WEEV)	V(MOS)	-	Alien bird is a host for the virus in peridomestic settings, though <1% prevalence	United States	Potential (low)	(68)
Passeriformes: Passeridae	Passer domesticus	St. Louis encephalitis virus (SLEV)	V(MOS)	-	Alien bird is a host for the virus in peridomestic settings, though <1% prevalence	United States	Potential (low)	(68)

Alien reptile species (=non-avian Reptilia) as hosts for zoonotic diseases

Many studies examining interactions between turtles and tortoises and zoonotic pathogens have been conducted in captive populations, particularly for bacterial pathogens such as Chlamydia and Salmonella. For free-living IAS populations, three such interactions were identified (Table 9), the most important for Europe being the ability of the red-eared slider, *Trachemys scripta elegans*, to harbour both Chlamydia and Salmonella. A high proportion of captive *Testudo hermanni* and *Testudo marginata* populations tested positive for Chlamydiaceae in Poland, but have not yet been detected in free-living populations. It should be noted that some sources of information were not captured by the structured review and as examples the Life Project *Informes Trachemys* includes further information on disease in *T. scripta elegans* and there has been an observation of anti-leptospiral agglutinins from *T. scripta elegans* in three urban ponds in Italy (89).

Alien mammal species as hosts for zoonotic diseases

The diversity and global distribution of mammalian hosts of zoonotic pathogens is vast and it is perhaps not surprising that the majority of emerging human diseases originate from mammals (1). A number of mammalian IAS have been very well-studied and dominate in terms of numbers and diversity of potential interactions with zoonoses (Table 10). Such IAS are often widely distributed beyond the native range and have close association with humans because they thrive in anthropogenic habitats (rats, *Rattus* spp*.,* mice, *Mus* spp*.,* raccoon dog, *Nyctereutes procyonoides,* raccoon, *Procyon lotor*) or are managed by humans in one way or another (wild board, *Sus scrofa,* feral American mink, *N. vison*). Although such human association may result in reporting bias, it is also intuitive that increased contact between humans and animals carrying zoonotic pathogens will increase the probability of transmission of such zoonoses. A number of the pathogens are associated with a diverse range of hosts. *Giardia* sp. was reported in wild boar, *Sus scrofa*, ferrets, *Mustela putorius furo*, hedgehogs, *Erinaceus europaeus*, rabbits, *Oryctologus cuniculus*, muskrat, *Ondatra zibethicus*, house mice, *Mus musculus* and black rats, *R. rattus*, with incidences ranging from 4.3 – 42.1% of individuals infected (2,3,4,5).

Rodents are known to be the most species rich of zoonotic mammalian hosts; 17 species were identified through this literature review (Table 10). Rodent reservoir hosts are characterised by high reproductive potential (reproducing early in life and with high frequency) which favours pathogen transmission and maintenance within reservoir populations. Furthermore, many of the rodents favour urban habitats and as such live in close proximity with humans increasing the probability of human exposure to the zoonotic pathogens they carry. Many studies highlight the risk of increased zoonotic disease with increasing urbanisation and habitat degradation globally (6–8). Many studies reported rodents as reservoir hosts of *Leptospira spp*.; Leptospirosis, caused by these spirochetes, is the most common bacterial zoonosis worldwide (9). Humans can acquire infection through direct contact with animals or through an environment contaminated by animal urine including ingestion of contaminated food or water. Urbanisation alongside climate change, including increased frequency of extreme weather events such as flooding, are predicted to increase the incidence and magnitude of leptospiroris outbreaks (9).

Norway rats (*R. norvegicus*) and black rats (*R. rattus*) are considered to be amongst the most damaging IAS globally (90) and inhabit every continent except for Antarctica. There role in transmitting a number of zoonotic pathogens has been well documented (91). Leptospira and hantaviruses, particularly Seoul virus) are the most important in terms of human morbidity and mortality (91). It is intriguing to note the vast variability in prevalence of pathogens bourne by rats, even with limited geographical distances (91) which has implications for surveillance and monitoring. Furthermore, molecular studies have shown that rats are carrying an expanding range of pathogens for which the human health implications are unknown. Further demonstrating the dynamic nature of the role of IAS in zoonoses transmission and epidemiology.

Hosts from the order Carnivora are considered to carry almost as many unique zoonoses as rodents (1), perhaps a consequence of accumulation of infectious agents such as endo-parasitic worms from their prey. Ten species of Carnivora were identified in our study with the raccoon dog, *N. procyonoides*, and the raccoon, *P. lotor*, being the most frequently cited as zoonotic reservoir hosts. A number of well-studied pathogens are associated with these species including rabies. While it is recognised that the red fox, *Vulpes vulpes*, is the main wildlife rabies vector in Europe, the raccoon dog has become an increasingly important host particularly in the Baltic regions (10). In some regions the density of each of the reservoir hosts might be too low to sustain a rabies epidemic but the community of foxes and raccoon dogs increases the risk.

Human behaviour can alter dramatically influence the risk of transmission of a pathogen from an animal to a human host. Wild boar, *Sus scrofa*, are reservoirs for many pathogens and pathogens transmissible to humans including foodborne zoonoses including bacterial diseases (brucellosis, salmonellosis, tuberculosis and yersiniosis), parasitic diseases (toxoplasmosis and trichinellosis) and the viral 19 hepatitis E. Supplemental feeding to increase the density of wild boar for hunting can increase transmission risk and hunters are at highest risk. Pathogen prevalence can vary with habitat; incidence of *Brucella suis* and *Escherichia coli* were highest in boar from forested and agricultural regions respectively (11). Furthermore, hunting with dogs compared to other management practices can increase the risk of pathogen transmission from wild boar to humans (12).

Table 9. Alien reptiles as hosts for zoonotic diseases. A = aerosol transmission. C= contact transmission. O = oral transmission through food (F). Case fatality is mean of case fatality rate reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

Key: Species in bold with * = IAS of Union concern

Reptilia								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Transmission	Case fatality rate (%)				
Squamata: Gekkonidae	*Hemidactylus frenatus*	*Salmonella enterica* *Salmonella enterica* (sero. Weltevreden)	O(F)	0.2	The species is host for *Salmonella*, pathogen found at low prevalence of 4.3%-7%, ubiquitous in houses	Costa Rica	Potential (low)	(92) (93)
Testudines: Emydidae	**Trachemys scripta***	*Chlamydiaceae*	A;C	-	Alien turtle is host for *Chlamydia* spp., pathogen found in 20% of free-living individuals tested (63), detected strain related to *Chlamydia* (C.) *pneumoniae* strains and *Candidatus C. sanzinia*. Group	Poland	Potential (low)	(94)
Testudines: Emydidae	**Trachemys scripta elegans***	*Salmonella*	O(F)	0.2	Alien turtle is host for *Salmonella*, pathogen found in 39% of sampled individuals in China (41) and 15% of individuals (117) in ponds in Spain	China Spain	Potential (low)	(95) (96)

Table 10. Invasive alien mammals as hosts for zoonotic diseases: A = aerosol transmission. C= contact transmission. O = oral transmission through food (F) or (W). V = vector-borne transmission by either flea (F), tick (T), mite (MI), lice (LI), biting flies (BF), Triatminae (Tri) or mosquitoes (MOS). Case fatality is mean of case fatality rate reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

*Key: Species in bold with * = IAS of Union concern, species underlined with # = IAS species listed in the Horizon scanning (97).*

Mammalia								
Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Transmission	Case fatality rate (%)				
Artiodactyla: Suidae	*Sus scrofa*	*Brucella sp. (B. suis, B. canis*	O(F)	0.73	4.3- 15% of samples tested positive *Brucella* is a bacterium that causes brucellosis or undulant fever in humans. Hunters and those working in the livestock industries are particularly at risk. It should be noted that in Europe only an avirulent strain of *B. suis* is prevalent on wild-boars which cause abortions in pigs but a very limited number of humans cases (despite a huge exposure of hunters) in immunocompromised humans	United States Georgia Australia	Realised (medium)	(98) (99) (100) (101) (102–106)
Artiodactyla: Suidae	*Sus scrofa*	*Campylobacter sp. (Campylobacter coli, Campylobacter fetus, Campylobacter hyointestinalsis, Campylobacter jejuni, Campylobacter lanienae and Campylobacter sputorum)*	O(F)	0.13	Zero - 40% of samples tested positive. Food -borne Campylobacter infections are usually mild but considered the most common bacterial cause of human gastroenteritis in the world	United States Georgia	Potential (medium)	(107) (104)
Artiodactyla: Suidae	*Sus scrofa*	*Coxiella burnetii*	A;O(F)	0.69	22- 50% of samples tested positive. Air- and food-borne infections of the bacterium. *Coxiella burnetii* causes Q-fever. Some people are asymptomatic but others have flu-like symptoms. Livestock workers are particularly vulnerable	Australia United States	Potential (medium)	(108) (99)

Artiodactyla: Suidae	*Sus scrofa*	*Cryptosporidium sp. (C. scrofarum and C. suis)*	O(F, W)	0.01	1.6-5.4% of feral pigs were shedding oocysts. Water- and food-borne infections of the bacterium *Cryptosporidium* sp. cause gastroenteritis. Contamination of water sources is seen as increasingly problematic	United States	Potential (very low)	(109) (110)
Artiodactyla: Suidae	*Sus scrofa*	*Ehrlichia chaffeensis*	V(T)	-	Possibility of antibodies in feral pigs. Tick-borne bacterium that can cause Ehrlichiosis in humans which results in mild to moderate flu-like symptoms	United States	Potential (very low)	(111)
Artiodactyla: Suidae	*Sus scrofa*	*Escherichia coli*	O(F)	0.3	Presence in 28% of samples Detection of the bacterium in *S. scrofa* at higher levels in agricultural regions compared to forested regions	Georgia	Potential (low)	(104)
Artiodactyla: Suidae	*Sus scrofa*	*Giardia sp.*	O	0.05	4.3 – 7.6% of feral pigs were shedding *Giardia*. Water- and food-borne infections can occur from a variety of livestock. Feral *S. scrofa* maybe a reservoir of *Giardia* transmitting to humans and livestock	United States	Potential (very low)	(109) (110)
Artiodactyla: Suidae	*Sus scrofa*	Hepatitis E	O(F)	-	4.4% seroprevalence Low prevalence of this virus in feral *S. scrofa*	United States	Potential (very low)	(101)
Artiodactyla: Suidae	*Sus scrofa*	Influenza (H1N1, H3N2, Influenza A)	A;C	-	H1N1 virus has been detected in feral *S.scrofa*. 10.8% seroprevalence for influenza A	United States	Potential (low)	(112) (113) (101)
Artiodactyla: Suidae	*Sus scrofa*	*Leptospira spp. (L. pomona, L. hardjo, L. interrogans, Leptospira interrogans serovar Pomona, Leptospira borgpetersenii serovar tarassovi*	A;C;O (W)	3.08	10 - 87% seroprevalence. Leptospirosis is a severe flu-like illness caused by bacteria in the genus *Leptospira*. Increased seroprevalence of *Leptospira* spp. occurred in years preceded by flooding and high rodent abundance in Australia, suggesting the potential for zoonotic infection is much greater than previously realised	Australia United States	Potential (medium)	(103) (99) (103) (114) (115)
Artiodactyla: Suidae	*Sus scrofa*	*Mycobacterium avium*	A	-	85% seroprevalence Tuberculosis in humans due to *M. avium* most often occur in immunocompromised individuals	United States	Potential (medium)	(99)
Artiodactyla: Suidae	*Sus scrofa*	Pseudorabies virus (PRV)	A;O	-	2.52 - 3% seroprevalence	United States	Potential (very low)	(99) (106)

					PRV primarily infects swine and has several secondary hosts, including cattle, dogs, and cats. It may infect humans. Higher prevalence of pseudorabies in feral *S. scrofa* hunted with dogs compared to other harvesting methods			(105)
Artiodactyla: Suidae	*Sus scrofa*	*Salmonella* sp.	O(F)	0.2	50% of animals possessed antibodies for *Salmonella* sp.	United States	Potential (low)	(116)
Artiodactyla: Suidae	*Sus scrofa*	*Streptococcus suis*	O(F)	-	94.4% of animals tested positive for *Streptococcus suis*. It should be noted that human infection can be severe, with a short incubation leading to death. Few cases have been recorded in meat production industry. Very few cases in hunters	United States	Potential (low)	(116)
Artiodactyla: Suidae	*Sus scrofa*	*Toxoplasma gondii*	O(F)	2.11	Infection levels ranged from 11% to 27.7% Protozoan that can infect humans causing toxoplasmosis, most humans are asymptomatic but some have flu-like symptoms. More serious complications occur in immunocompromised individuals. lack of sanitary management of feral animals increases the incidence of infections, and the consumption of raw or inadequately cooked meat may become a potential source of infection for humans	Brazil United States	Potential (low)	(117) (118) (99) (119) (120) (121)
Artiodactyla: Suidae	*Sus scrofa*	*Trichnella sp. (T. spiralis)*	O(F)	0.42	Prevalence was low ranging from 1.8 to 13.3% Food-borne transmission of this nematode can cause Trichinellosis which is widely distributed worldwide	Chile United States	Potential (low)	(118) (101) (122) (123) (121) (120)
Artiodactyla: Suidae	*Sus scrofa*	*Trypanosoma cruzi*	V(TRI)	-	6% of *S. scrofa*, reservoir for the protozoan, tested positive. Eleven species of kissing bugs (Hemiptera: Reduviidae) are found in the United States with ranges possibly expanding northward. At least eight of the species, perhaps all, vector *Trypanosoma cruzi*, the cause of Chagas disease.	United States	Potential (low)	(124)

					Infection can also occur through food- or water-borne transmission			
Artiodactyla: Suidae	*Sus scrofa*	*Yersinia pestis*	A;V(FL)	-	15% of *S. scrofa* tested positive for *Y. pestis*. Plague causing bacterium transmitted by fleas. It should be noted that comparison between continents is difficult because of differences in the epidemiological contexts	United States	Potential (very low)	(99)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Alaria alata*	O(F)	-	30 – 94.3% infection of the trematode.	Poland Estonia Denmark Lithuania Austria	Potential (low)	(125) (126) (127) (128) (129)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Anaplasma phagocytophilum*	V(T)	-	Bacterium spread by ticks to humans causing anaplasmosis. 23% infection of raccoon dogs compared to 8.2% of red foxes	Germany	Potential (low)	(130)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Apophallus sp*	O(F)	-	15.1% intestinal helminth infection of raccoon dogs compared to 7.6% of red foxes	Poland	Potential (low)	(125)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Echinococcus multilocularis*	O	0.64	Low prevalence with 1.6% in Estonia as an example	Poland Germany Netherlands Estonia	Potential (very low)	(125) (131) (132) (133)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Francisella tularensis*	V(T,BF,MOS)	3.05	Lower prevalence of bacterium in raccoon dog (12.8%) than red fox (18.4%)	Germany	Potential (low)	(134,135)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Ancylostoma sp.*	C	-	Higher prevalence of hookworm in raccoon dog (83%) than red fox (68.2%)	Poland	Potential (medium)	(125)
Carnivora: Canidae	**Nyctereutes procyonoides***	*Mesocestoides spp.*	O	-	Lower prevalence of helminth in raccoon dog (24.5%) compared to red fox (57.6%). Only approximately 3% of raccoon dogs infected in Germany	Poland Germany	Potential (very low)	(125) (136)
Carnivora: Canidae	**Nyctereutes procyonoides***	Rabies	C	100	Prevalence of rabies increased from 11.8% in 1994 to 28.9% in 2004 in raccoon dogs in Lithuania. Variable prevalence across studies from 0-100% infection in samples. However, raccoon dog is now a new maintenance host of rabies in North East of	Estonia Lithuania Latvia Poland	Potential (medium)	(137) (138) (139) (140) (141) (142)

Carnivora: Canidae	Taxon	Pathogen	Type	Value	Description	Location	Status	Ref
					Europe but the number of human cases in Europe remains less than one per year			(143)
Carnivora: Canidae	*Nyctereutes procyonoides**	*Taenia sp.*	O(F)	-	Lower prevalence of helminth in raccoon dog (1.9%) compared to red fox (40.9%)	Poland	Potential (very low)	(125)
Carnivora: Canidae	*Nyctereutes procyonoides**	*Toxocara/Toxascaris* nematodes	O	-	Lower prevalence of helminth in raccoon dog (15.1%) compared to red fox (33.3%)	Poland	Potential (very low)	(125)
Carnivora: Canidae	*Nyctereutes procyonoides**	Trematodes, cestodes, nematodes	-	-	4 trematodes, 4 cestodes and 9 nematodes. Number and range of raccoon dogs in Europe and the relatively high number of zoonotic pathogen taxa that it harbours suggests that this species should be considered an important source of environmental contamination	Estonia	Potential (low)	(126)
Carnivora: Canidae	*Nyctereutes procyonoides**	*Trichinella spiralis* (also *T. britovi, T. nativa, T. pseudospiralis*)	O(F)	0.42	Higher prevalence of *Trichinella* sp. in foxes (28.9–40.6%) than raccoon dogs (32.5–42%) across Lithuania, Latvia and Estonia. In Poland only 0.8% infection rate; 5% in Germany; 1 out of 9 raccoon dogs in the Netherlands	Lithuania Latvia Estonia Poland Germany Netherlands	Potential (medium)	(144) (145) (123) (132) (146) (147) (148)
Carnivora: Canidae	*Nyctereutes procyonoides**	*Uncinaria stenocephala*	O	-	97.6% infection in hunted raccoon dogs	Estonia	Potential (medium)	(126)
Carnivora: Canidae	*Canis lupus*	*Echinococcus granulosus*	O	0.64	2.2% faecal samples tested positive for *E. granulosus*	Estonia	Potential (very low)	(149)
Carnivora: Canidae	*Canis lupus familiaris*	*Leptospira sp. (L. mayottensis, L. borgpetersenii, L. kirschneri)*	A;C;O (W)	3.08	Reservoir of *L. mayottensis*; main reservoirs of L. borgpetersenii and *L. kirschneri*, both bacteria being prevalent in local clinical cases	Madagascar	Realised (medium)	(150)
Carnivora: Canidae	*Canis lupus dingo*	*Coxiella burnetii*	A;O(F)	0.69	Lower prevalence (17.3%) of the bacterium in dingoes compared to native species *Isoodon macrourus* (23.9%) but higher than possum (10.7%)	Australia	Potential (low)	(108)
Carnivora: Canidae	*Vulpes vulpes*	*Bartonella henselae, Bartonella clarridgeiae*	V(F)	-	*B. henselae* and *B. clarridgeiae* were detected in fleas (*Ctenocephalides felis*) from red foxes (*Vulpes vulpes*)	Australia	Potential (very low)	(151)
Carnivora: Canidae	*Vulpes vulpes*	*Coxiella burnetii*	A;O(F)	0.69	Higher prevalence (43.8%) of the bacterium in foxes compared to native species *Isoodon macrourus* (23.9%) and possum (10.7%)	Australia	Potential (medium)	(108)

Carnivora: Canidae	*Vulpes vulpes*	*Echinococcus granulosus*	O	0.64	Presence only cited	Australia	Potential (very low)	(152)
Carnivora: Felidae	*Felis catus*	*Helminths (Angiostrongylus cantonensis, Toxocara cati, Ancylostoma braziliense, Taenia taeniaeformis, Moniliformis moniliformis, Hymenolepis nana)*	-	-	Sixty-one (92%) of cats harboured one or more helminth species	Australia	Potential (medium)	(153)
Carnivora: Felidae	*Felis catus*	*Coxiella burnetii*	A;O(F)	0.69	Higher prevalence (38.7%) of the bacterium in cats compared to native species *Isoodon macrourus* (23.9%) and possum (10.7%)	Australia	Potential (medium)	(108)
Carnivora: Felidae	*Felis catus*	*Leptospira* spp.	A;C;O(W)	3.08	*Leptospira* was detected in the 42.4% of sampled cats in Christmas Island, but no in cats sampled in Dirk Hartog Island or southwest Western Australia	Australia	Potential (low)	(153)
Carnivora: Felidae	*Felis catus*	*Toxoplasma* sp. *(Toxoplasma gondii)*	O(F)	2.11	Antibody test to *Toxoplasma,* yielded a prevalence rate of about 16%. In a further study DNA of *Toxoplasma gondii* was detected in 5% of faecal samples	United States	Potential (low)	(154) (155)
Carnivora: Mustelidae	*Neovison vison*	Influenza A	A;C	-	2.2% seropositive	Spain	Potential (very low)	(156)
Carnivora: Mustelidae	*Neovison vison*	*Ascaridinae*	O(F, W)	-	Presence only cited	Chile	Potential (very low)	(157)
Carnivora: Mustelidae	*Neovison vison*	*Cryptosporidium* sp.	O(F, W)	0.01	Presence only cited	Chile	Potential (very low)	(157)
Carnivora: Mustelidae	*Neovison vison*	*Echinococcus* sp.	O	0.64	Presence only cited	Poland	Potential (very low)	(158)
Carnivora: Mustelidae	*Neovison vison*	*Leptospira* spp. *(L. interrogans, L. borgpetersenii)*	A;C;O(W)	3.08	54.4% of samples. Lakes and rivers also contaminated	Chile Patagonia	Potential (medium)	(157) (159)
Carnivora: Mustelidae	*Neovison vison*	*Pterygodermatites (Paucipectines)* spp.	O	-	Presence only cited	Chile	Potential (very low)	(157)
Carnivora: Mustelidae	*Neovison vison*	*Toxocara* sp.	O	-	Evidence of increase in seropositivity over time for *Toxocara*	Poland	Potential (low)	(158)

Carnivora: Mustelidae	*Neovison vison*	*Toxoplasma gondii*	O(F)	2.11	78.8% were seropositive	Spain	Potential (medium)	(160)
Carnivora: Procyonidae	***Procyon lotor***	Influenza H5N1	A;C	-	Presence only cited	Japan	Potential (very low)	(161)
Carnivora: Procyonidae	***Procyon lotor***	*Baylis ascaris procyonis*	O	-	1.9 – 100 % prevalence of the helminth	Denmark Germany Poland Norway China Japan	Potential (medium)	(162) (163) (164) (165) (166) (167) (168) (169) (170)
Carnivora: Procyonidae	***Procyon lotor***	*Campylobacter* sp.	O(F)	0.13	1.3% prevalence	Japan	Potential (very low)	(171)
Carnivora: Procyonidae	***Procyon lotor***	*Borrelia afzelii; Borrelia garinii*	V(T, LI)	-	0.9% prevalence	Japan	Potential (very low)	(172)
Carnivora: Procyonidae	***Procyon lotor***	*Capillaria* sp.	O	-	3.2% prevalence	Poland	Potential (very low)	(166)
Carnivora: Procyonidae	***Procyon lotor***	*Cryptosporidium* sp.	O(F, W)	0.01	34.7% prevalence	Germany; Poland	Potential (medium)	(173)
Carnivora: Procyonidae	***Procyon lotor***	*Enterocytozoon bieneusi*	O(W)	-	4.1% prevalence	Germany; Poland	Potential (very low)	(173)
Carnivora: Procyonidae	***Procyon lotor***	*Francisella tularensis*	V(T,B F,MO S)	3.05	0.5% prevalence	Japan	Potential (very low)	(172)
Carnivora: Procyonidae	***Procyon lotor***	*Listeria* sp.	O(F)	15.91	2 - 5%	Poland	Potential (very low)	(174)
Carnivora: Procyonidae	***Procyon lotor***	*Molineus* sp.	O	-	Presence only cited	Austria	Potential (very low)	(129)
Carnivora: Procyonidae	***Procyon lotor***	*Orientia tsutsugamushi*	V(MI)	-	1.4% prevalence	Japan	Potential (very low)	(172)
Carnivora: Procyonidae	***Procyon lotor***	*Rickettsia japonica*	V(T)	-	7.3% prevalence	Japan	Potential (low)	(172)
Carnivora: Procyonidae	***Procyon lotor***	*Salmonella* sp. *(S. enterica)*	O(F)	0.2	2 – 5.7% prevalence	Japan Poland	Potential (very low)	(171) (174)

Carnivora: Procyonidae	*Procyon lotor**	*Sarcocystis kirkpatricki*	O(F)	-	8.3% prevalence	Germany	Potential (low)	(175)
Carnivora: Procyonidae	*Procyon lotor**	*Staphylococcus* sp.	A;C	-	35% prevalence	Poland	Potential (medium)	(174)
Carnivora: Procyonidae	*Procyon lotor**	*Strongyloides procyonis*	C	-	28.3% prevalence and infection of one person	Japan	Realised (medium)	(176)
Carnivora: Procyonidae	*Procyon lotor**	*Toxascaris* sp.	O	-	2 farmed raccoons	Norway	Potential (very low)	(167)
Carnivora: Procyonidae	*Procyon lotor**	*Toxocara* sp.	O	-	2 farmed raccoons	Norway	Potential (very low)	(167)
Carnivora: Procyonidae	*Procyon lotor**	*Yersinia* sp.	A;O(W)(F);V(F)	0.07	7 - 38.6% prevalence	Japan Poland	Realised (medium)	(171) (174)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Anoplocephalidae*	O	-	1.5% prevalence	Germany	Potential (very low)	(177)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Cryptosporidium parvum*	O(F, W)	0.01	Heavily infested individuals	Poland	Potential (very low)	(178)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Echinococcus multilocularis*	O	0.64	0.7 – 4.1% prevalence	Germany France	Potential (very low)	(177) (179) (180)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Giardia* sp.	O	0.05	75.2% prevalence	Germany	Potential (medium)	(181)
Rodentia: Cricetidae	*Ondatra zibethicus**	Hantavirus	A;C	-	8% of tested animals (n=266) were found positive to infection; 14% had antibodies	Germany	Potential (low)	(182)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Leptospira* spp.	A;C;O(W)	3.08	Presence only cited	France	Potential (very low)	(183)
Rodentia: Cricetidae	*Ondatra zibethicus**	*Taenia* spp. (*T. taeniaeformis, T. crassiceps, T. polyacantha, T. martis*)	O(F)	-	0.4 – 42.3% metacestodes with *T. taeniaeformis* at highest prevalence	France Germany	Potential (medium)	(180) (177)
Rodentia: Echimyidae	*Myocastor coypus**	*Aeromonas* spp. (*A. hydrophila, A. caviae, and A. dhakensis*)	O(W)	-	Presence only cited	Korea	Potential (very low)	(184)
Rodentia: Echimyidae	*Myocastor coypus**	*Echinococcus multilocularis*	O	0.64	>1% (2 of 531 individuals)	France	Potential (very low)	(180)

Rodentia: Echimyidae	*Myocastor coypus**	*Strongyloides myopotami*	C	-	99% prevalence	Japan	Potential (medium)	(185)
Rodentia: Echimyidae	*Myocastor coypus**	*Taenia* sp. *(T. taeniaeformis)*	O(F)	-	3.8% prevalence	France	Potential (very low)	(180)
Rodentia: Echimyidae	*Myocastor coypus**	*Toxoplasma gondii*	O(F)	2.11	59.4% prevalence with higher incidence in male (68.2%) compared to female (31.8%) individuals	Italy	Potential (medium)	(186)
Rodentia: Muridae	*Mus musculus*	*Bartonella* sp.	V(F)	-	Presence only cited	Senegal	Potential (very low)	(187)
Rodentia: Muridae	*Mus musculus*	*Brucella* sp.	C; O(F)	0.73	Brucella was not identified, and it was concluded that prevalence was below 12%	Australia	Potential (low)	(188)
Rodentia: Muridae	*Mus musculus*	*Cryptosporidium*	O(F, W)	0.01	11.8% prevalence	New Zealand	Potential (low)	(73)
Rodentia: Muridae	*Mus musculus*	*Giardia* sp.	O	0.05	30.5% prevalence	New Zealand	Potential (medium)	(73)
Rodentia: Muridae	*Mus musculus*	*Hantavirus*	A;C	-	Presence only cited	Senegal	Potential (very low)	(189)
Rodentia: Muridae	*Mus musculus*	*Hepatozoon canis*	V(T)	-	Presence only cited but notes lower levels of pathogen prevalence compared to native species sampled in same study	Senegal	Potential (very low)	(190)
Rodentia: Muridae	*Mus musculus*	*Helminths*	-	-	8% were infected with *Syphacia obvelata*, 8% with *Hetereakis spumosa*, 12% with *Taenia taeniaeformis*, 36% with *Nippostrongylus brasiliensis*	Argentina	Potential (low)	(191)
Rodentia: Muridae	*Mus musculus*	*Leptospira* spp.	A;C;O (W)	3.08	23 – 59% prevalence	Madagascar Puerto Rico Chile	Potential (medium)	(29) (192) (193)
Rodentia: Muridae	*Mus musculus*	*Toxoplasma gondii*	O(F)	2.11	11% prevalence	Senegal United States	Potential (low)	(194) (88)
Rodentia: Muridae	*Mus musculus*	*Trypanosoma lewis*	V(F)	-	8.6% prevalence	Nigeria	Potential (low)	(195)
Afrosoricida: Tenrecidae	*Tenrec ecaudatus*	*Leptospira mayottensis*	A;C;O (W)	3.08	27% prevalence; acute human infections reported	Mayotte (Indian Ocean Islands)	Realised (medium)	(150)

Order: Family	Species	Pathogen	Route	Ro	Prevalence	Location	Risk	Ref
Carnivora: Herpestidae	**Herpestes javanicus***	Hepatitis E virus (HEV)	O(F)	-	21% prevalence	Japan	Potential (medium)	(196)
Carnivora: Mustelidae	*Mustela putorius furo*	*Giardia* sp.	O	0.05	33.3% prevalence	New Zealand	Potential (medium)	(73)
Carnivora: Procyonidae	**Nasua nasua***	*Coccidia*	O	-	50% prevalence	Norway	Potential (medium)	(167)
Carnivora: Therapsid	*Felis catus*	*Alaria alata*	O(F)	-	3% prevalence	Denmark	Potential (very low)	(197)
Carnivora: Viverridae	*Paguma larvata*	*Campylobacter* spp.	O(F)	0.13	7.2% prevalence	Japan	Potential (low)	(171)
Carnivora: Viverridae	*Paguma larvata*	*Salmonella enterica*	O(F)	0.2	2% prevalence	Japan	Potential (very low)	(171)
Carnivora: Viverridae	*Paguma larvata*	*Yersinia* sp.	A;O(W)(F);V(F)	0.07	10.5% prevalence	Japan	Potential (low)	(171)
Didelphimorphia: Didelphidae	*Didelphis marsupialis*	*Rickettsia typhi*	V(F)	-	10.6% prevalence	United States (California)	Potential (low)	(198)
Diprotodontia: Phalangeridae	*Trichosurus vulpecula*#	*Cryptosporidium*	O(F, W)	0.01	12.8% prevalence	New Zealand	Potential (low)	(73)
Diprotodontia: Phalangeridae	*Trichosurus vulpecula*#	*Giardia* sp.	O	0.05	23.6% prevalence	New Zealand	Potential (medium)	(73)
Eulipotyphla: Erinaceidae	*Erinaceus europaeus*	*Giardia* sp.	O	0.05	33.3% prevalence	New Zealand	Potential (medium)	(73)
Lagomorpha: Leporidae	*Lepus europaeus*	*Fasciola hepatica*	O(F, W)	-	14.2% prevalence	Patagonia	Potential (low)	(199)
Lagomorpha: Leporidae	*Oryctolagus cuniculus*	*Giardia* sp.	O	0.05	20% prevalence	New Zealand	Potential (low)	(73)
Primates: Cercopithecidae	*Chlorocebus aethiops sabaeus*	*Klebsiella pneumoniae*	A	-	20% prevalence	St Kitts (Caribbean islands)	Potential (low)	(200)
Primates: Cercopithecidae	*Macaca mulatta*	B-virus	C	-	Around 70% prevalence	Puerto Rico	Potential (high)	(201)

Primates: Cercopithecidae	*Macaca mulatta*	macacine herpesvirus 1 (McHV-1)	C	-	25% prevalence	United States (Florida)	Potential (medium)	(202)
Rodentia: Chinchillidae	*Chinchilla lanigera*	*Taenia crassiceps*	O(F)	-	One individual infected	Switzerland	Potential (very low)	(203)
Rodentia: Muridae	*Gerbillus nigeriae*	*Borrelia crocidurae*	V(T, LI)	-	5% prevalence	Senegal	Potential (low)	(190)
Rodentia: Muridae	*Herpestes auropunctatus*#	*Leptospira spp.*	A;C;O (W)	3.08	13% prevalence	Puerto Rico	Potential (low)	(192)
Rodentia: Muridae	*Herpestes auropunctatus*#	*Leptospira spp.*	A;C;O (W)	3.08	8.1% prevalence	St Kitts (Caribbean islands)	Potential (low)	(204)
Rodentia: Soricidae	*Suncus murinus*	*Leptospira*	A;C;O (W)	3.08	25% prevalence	Madagascar	Potential (medium)	(29)
Rodentia: Sciuridae	*Callosciurus finlaysonii*#	variegated squirrel bornavirus 1 (VSBV-1)	A	-	16.7% prevalence	Germany	Potential (low)	(205)
Rodentia: Sciuridae	*Callosciurus prevostii*	variegated squirrel bornavirus 1 (VSBV-1)	A	-	17.3% prevalence	Germany; Croatia	Potential (low)	(205)
Rodentia: Sciuridae	***Sciurus carolinensis***	*Borrelia burgdorferi Sensu Lato*	V(T)	-	11.9% prevalence	Scotland	Potential (low)	(206)
Rodentia: Sciuridae	***Sciurus carolinensis***	Tick-borne encephalitis virus (TBEV)	V(T)	-	1.9-2.5% prevalence	Italy	Potential (very low)	(207)
Rodentia: Sciuridae	***Sciurus carolinensis***	Usutu virus (USUV)	V(MOS)	-	3.2-3.8% prevalence	Italy	Potential (very low)	(207)
Rodentia: Sciuridae	***Sciurus carolinensis***	West Nile virus (WNV)	V(MOS)	-	0.6% prevalence	Italy	Potential (very low)	(207)
Rodentia: Sciuridae	***Sciurus carolinensis***	variegated squirrel bornavirus 1 (VSBV-1)	A	-	50% prevalence. Borna virus found in a captive colony. The virus is indigenous and carried by a shrew	Germany	Potential (high)	(205)
Rodentia: Sciuridae	*Sciurus variagata*	variegated squirrel bornavirus 1 (VSBV-1)	A	-	Detection of pathogen in people that is same as pathogen in exotic squirrels. Borna virus found in a	Germany	Potential (low)	(208)

					captive colony. The virus is indigenous and carried by a shrew			
Rodentia: Sciuridae	*Tamias sibiricus barberi**	*Borrelia burgdorferi* species complex	V(T)	-	Greater flea infestation in alien species (no reported values)	France	Potential (medium)	(209)
Rodentia: Sciuridae	*Tamiops swinhoei*	variegated squirrel bornavirus 1 (VSBV-1)	A	-	1.3% prevalence	Germany	Potential (very low)	(205)
Rodentia: Muridae	*Rattus norvegicus*	*Anaplasma phagocytophilum*	V(T)	-	Presence only cited	United States	Potential (very low)	(210)
Rodentia: Muridae	*Rattus norvegicus*	*Ehrlichia muris*	V(T)	-	Presence only cited	United States	Potential (very low)	(211)
Rodentia: Muridae	*Rattus norvegicus*	*Angiostrongylus cantonensis*	O(F)	-	Presence only cited	Grenada	Potential (very low)	(212)
Rodentia: Muridae	*Rattus norvegicus*	*Aspiculuris tetraptera*	O(F)	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Eucoleus sp.*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Heterakis spumosa*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Mastophorus muris*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Protospirura sp.*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Strongyloides ratti*	C	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Syphacia obvelata, Syphacia muris*	C;O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Trichuris sp.*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Trichosomoides crassicaud*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Inermicapsifer madagascariensis*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus norvegicus*	*Hydatigera taeniaeformis*	O	-	Presence only cited	South Africa	Potential (very low)	(213)

Rodentia: Muridae	*Rattus norvegicus*	*Bartonella sp. (Bartonella elizabethae)*	V(F)	-	12.5% prevalence of *Bartonella elizabethae*	United States	Potential (very low)	(214) (215)
Rodentia: Muridae	*Rattus norvegicus*	*Brucella spp.*	C;O(F)	0.73	Not identified presumed below 12%	Australia	Potential (very low)	(188)
Rodentia: Muridae	*Rattus norvegicus*	*Calodium hepatica*	O	-	Presence only cited	United States	Potential (very low)	(214)
Rodentia: Muridae	*Rattus norvegicus*	*Capillaria hepatica*	O	-	25.9 – 36% *Capillaria hepatica*	Canada Argentina British Columbia	Potential (low)	(216) (191) (217)
Rodentia: Muridae	*Rattus norvegicus*	*Enterococcus* sp.	O	-	Presence only cited	Canada	Potential (very low)	(216)
Rodentia: Muridae	*Rattus norvegicus*	*Escherichia coli*	O(F)	0.3	Presence only cited	Canada	Potential (very low)	(216)
Rodentia: Muridae	*Rattus norvegicus*	*Eucoleus* sp.	0	-	Eucoleus sp. in the upper gastrointestinal tract (164 of 399; 41%)	Canada	Potential (medium)	(216)
		Hantavirus	A;C	-	Highest prevalence of the virus in rats (20%) than in other native rodents	United States	Potential (medium)	(218) (219)
Rodentia: Muridae	*Rattus norvegicus*	Hepatitis E	O(F)	-	77% of rats from Maryland, 90% from Hawaii, and 44% from Louisiana were seropositive for anti-HEV. Not considered a zoonotic strain	United States	Potential (low)	(215) (220) (214)
Rodentia: Muridae	*Rattus norvegicus*	*Hymenolepis* sp. (*Hymenolepis diminuta, Hymenolepis nana*	O(F)	-	7.4% with *Hymenolepis diminuta*; 33.3% with Hymenolepis nana	South Africa Argentina United States British Columbia	Potential (low)	(213) (191) (214) (217)
Rodentia: Muridae	*Rattus norvegicus*	*Leptospira spp.(Leptospira icterohaemorrhagiae [L. interrogans]; L. copenhageni)*	A;C;O (W)	3.08	23-48% prevalence. 20% of Norway rats	Madagascar United States Puerto Rico Chile British Columbia	Potential (medium)	(29) (214) (192) (193) (217)

Rodentia: Muridae	*Rattus norvegicus*	*Monoliformis moniliformis*	O	-	25.9% infected with *Monoliformis moniliformis*	Argentina	Potential (medium)	(191)
Rodentia: Muridae	*Rattus norvegicus*	*Nippostrongylus brasiliensis,*	C	-	81.5% infected with *Nippostrongylus brasiliensis*	Argentina Australia South Africa	Potential (medium)	(213) (188) (191)
Rodentia: Muridae	*Rattus norvegicus*	*Hetereakis spumosa*	O	-	88.9% infected with *Hetereakis spumosa*	Argentina	Potential (medium)	(191)
Rodentia: Muridae	*Rattus norvegicus*	*Gongylonema neoplasticum*	O	-	3.7% infected with *Gongylonema neoplasticum*	Argentina	Potential (very low)	(191)
Rodentia: Muridae	*Rattus norvegicus*	*Nematospiroides dubius*	O	-	Presence only cited	British Columbia	Potential (very low)	(217)
Rodentia: Muridae	*Rattus norvegicus*	*Trichostrongylus* spp.	O(F)	-	Presence only cited	British Columbia	Potential (very low)	(217)
Rodentia: Muridae	*Rattus norvegicus*	*Coccidia*	O	-	Presence only cited	British Columbia	Potential (very low)	(217)
Rodentia: Muridae	*Rattus norvegicus*	*Entamoeba*	C;O(W)	-	Presence only cited	British Columbia	Potential (very low)	(217)
Rodentia: Muridae	*Rattus norvegicus*	*Salmonella panama*	O(F)	0.2	Presence only cited	British Columbia	Potential (very low)	(217)
Rodentia: Muridae	*Rattus norvegicus*	*Rickettsia typhi*	V(F)	-	Presence only cited	United States	Potential (very low)	(211) (214) (215)
Rodentia: Muridae	*Rattus norvegicus*	Seoul virus (Hantavirus)	A;C	-	Presence only cited	United States	Potential (very low)	(214) (215)
Rodentia: Muridae	*Rattus norvegicus*	*Staphylococcus aureus*	A;C	-	Presence only cited	Canada	Potential (very low)	(216)
Rodentia: Muridae	*Rattus norvegicus*	*Taenia taeniaeformis*	O	-	22.2% with *Taenia taeniaeformis*	Argentina	Potential (medium)	(191)
Rodentia: Muridae	*Rattus norvegicus*	*Toxoplasma gondii*	O(F)	2.11	3% of rats	United States	Potential (very low)	(88)
Rodentia: Muridae	*Rattus norvegicus*	*Trichosomoides crassicauda*	O	-	*Trichosomoides crassicauda* in the urinary bladder (59 of 194; 30%)	Canada	Potential (medium)	(216)
Rodentia: Muridae	*Rattus norvegicus*	*Trypanosoma lewis*	V(F)	-	68.8% of the sampled individuals	Nigeria	Potential (medium)	(195)
Rodentia: Muridae	*Rattus rattus*	*Angiostrongylus species*	O(F)	-	84% of rats harboured helminths	Australia	Potential (medium)	(221) (222)

						United States		(223)
Rodentia: Muridae	*Rattus rattus*	*Toxocara cati*	O	-	84% of rats harboured helminths	Australia	Potential (medium)	(221)
Rodentia: Muridae	*Rattus rattus*	*Ancylostoma braziliense*	C	-	84% of rats harboured helminths	Australia	Potential (medium)	(221)
Rodentia: Muridae	*Rattus rattus*	*Toxocara cati*	O	-	84% of rats harboured helminths	Australia	Potential (medium)	(221)
Rodentia: Muridae	*Rattus rattus*	*Hetereakis spumosa*	O	-	14.3% with *Hetereakis spumosa*	Argentina Australia South Africa	Potential (low)	(191) (213) (221)
Rodentia: Muridae	*Rattus rattus*	*Hymenolepis spp.*	O(F)	-	14.3% with *Hymenolepis diminuta* 3.6% *Hymenolepis nana* from South Africa	Argentina Australia South Africa	Potential (low)	(191) (213) (221)
Rodentia: Muridae	*Rattus rattus*	*Moniliformis moniliformis*	O	-	7.1% with *Moniliformis moniliformis*	Argentina South Africa	Potential (low)	(191) (213)
Rodentia: Muridae	*Rattus rattus*	*Aspiculuris tetraptera*	O(F)	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Eucoleus* sp.	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Heterakis spumosa*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Mastophorus muris*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Strongyloides ratti*	C	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Trichuris* sp.	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Protospirura* sp.	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Trichosomoides crassicauda*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Inermicapsifer madagascariensis*	O	-	Presence only cited	South Africa	Potential (very low)	(213)

Rodentia: Muridae	*Rattus rattus*	*Hydatigera taeniaeformis*	O	-	Presence only cited	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus rattus*	*Babesia* sp.	V(T)	-	Presence only cited	Italy	Potential (very low)	(224)
Rodentia: Muridae	*Rattus rattus*	*Bartonella* sp.	V(F)	-	1.3% (three of 228)	Chile Uganda Madagascar Senegal	Potential (very low)	(225) (226) (227) (187)
Rodentia: Muridae	*Rattus rattus*	*Borrelia burgorferi*	V(T)	-	Highest prevalence of the bacterium compared to native species (two out of six rats: 33.3%)	United States	Potential (medium)	(228)
Rodentia: Muridae	*Rattus rattus*	*Brucella* spp.	C; O(F)	0.73	Not identified presumed below 12%	Australia	Potential (very low)	(188)
Rodentia: Muridae	*Rattus rattus*	*Coxiella burnetii*	A; O(F)	-	Not identified presumed below 12%	Australia	Potential (very low)	(188)
Rodentia: Muridae	*Rattus rattus*	*Salmonella* spp.	O(F)	0.2	*Salmonella choleraesuis* ssp. *arizonae* (14.29%)	Australia	Potential (low)	(188)
Rodentia: Muridae	*Rattus rattus*	*Syphacia obvelata; Syphacia muris*	C;O	-	*Syphacia obvelata* (2.86%)	Australia South Africa	Potential (very low)	(188) (191)
Rodentia: Muridae	*Rattus rattus*	*Nippostrongylus brasiliensis*	C	-	*Nippostrongylus brasiliensis* (14.3 - 85.71%)	Australia Argentina South Africa	Potential (medium)	(188) (191) (213)
Rodentia: Muridae	*Rattus rattus*	Various parasites	-	-	*Laelaps* spp. (41.17%), *Polyplax* spp. (23.53%), *Hoplopleura* spp. (17.65%), *Ixodes holocyclus* (17.64%) and *Stephanocircus harrisoni* (5.88%)	Australia	Potential (medium)	(188)
Rodentia: Muridae	*Rattus rattus*	*Capillaria hepatica*	O	-	Histology revealed 15 (75%) of the rats sampled had a current or previous infection with *C. hepatica*	Diego Garcia - British Overseas Territories	Potential (medium)	(229)
Rodentia: Muridae	*Rattus rattus*	*Cryptosporidium*	O(F, W)	0.01	37.5% carried *Cryptosporidium*	New Zealand	Potential (medium)	(73)
Rodentia: Muridae	*Rattus rattus*	*Giardia* sp.	O	0.05	42.1% carried *Giardia*	New Zealand	Potential (medium)	(73)
Rodentia: Muridae	*Rattus rattus*	Hantavirus	A;C	-	Presence only cited	Senegal	Potential (very low)	(230)
Rodentia: Muridae	*Rattus rattus*	*Hymenolepis* sp.	O(F)	-	3.6% with *Hymenolepis nana*, 14.3% with *Hymenolepis diminuta*	South Africa Argentina	Potential (low)	(213) (191)

Rodentia: Muridae	*Rattus rattus*	*Leishmania* spp.	V(BF)	-	17.5% infected	Italy Senegal	Potential (low)	(224) (230)
Rodentia: Muridae	*Rattus rattus*	*Leptospira* spp.	A;C;O (W)	3.08	2.9 - 42.5% prevalence	Madagascar La Réunion Mauritius Seychelles South Africa Swaziland Mozambique Madagascar Puerto Rico Australia Malayasia Borneo Australia	Potential (medium)	(188) (29) (231) (192) (150) (153) (232)
Rodentia: Muridae	*Rattus rattus*	Mammarenavirus	A	-	Presence only cited	Senegal	Potential (very low)	(189)
Rodentia: Muridae	*Rattus rattus*	*Aspicularis tetraptera*	O(F)	-	25% prevalence	Argentina	Potential (medium)	(191)
Rodentia: Muridae	*Rattus rattus*	Sin Nombre Virus (Hantavirus)	A;C	-	1.7% of infected individuals, less than native rodents	United States	Potential (very low)	(233)
Rodentia: Muridae	*Rattus rattus*	*Taenia taeniaeformis*	O	-	Presence only cited	Argentina Australia	Potential (very low)	(191) (221)
Rodentia: Muridae	*Rattus rattus*	*Toxoplasma gondii*	O(F)	2.11	38.2% prevalence	Italy Brazil	Potential (medium)	(224) (234)
Rodentia: Muridae	*Rattus rattus*	*Trypanosoma* sp.	O;V(TRI)	-	25.2% - 71% prevalence	Nigeria Benin Senegal	Potential (medium)	(195) (235) (236) (230)
Rodentia: Muridae	*Rattus rattus*	West Nile Virus	V(MOS)	9.13	30% prevalence	United States	Potential (medium)	(237)
Rodentia: Muridae	*Rattus tanezumi*	Oxyurids	-	-	90%	South Africa	Potential (medium)	(213)
Rodentia: Muridae	*Rattus tanezumi*	*Mastophorus muris*	O	-	0.45%	South Africa	Potential (very low)	(213)

Rodentia: Muridae	*Rattus tanezumi*	*Nippostrongylus brasiliensis*	C	-	2.86%	South Africa	Potential (very low)	(213)
Rodentia: Muridae	*Rattus tanezumi*	*Hydatigera taeniaeformis*	O	-	6.7%	South Africa	Potential (low)	(213)

Alien parasites as causal agents for zoonotic diseases in Europe

There is evidence that several exotic endoparasite species have been introduced to Europe (Table 11) (7). Of most immediate significance is the introduction of the threadworm, Strongyloides stercoralis into Europe, and consequent increased in strongyloidiasis (respiratory, skin and/or digestive symptoms, with complications in immune-compromised individuals) case and infection rates in people. Domesticated small ruminants act as reservoir hosts and are thought to be enhancing establishment of this parasite in Europe (238). Also significant is the Raccoon roundworm, *Baylisascaris procyonis* that causes a severe or fatal neural condition called baylisascariasis in infected people. Though only one human case has been reported in Europe to date, transmission of this parasite is now widespread in the invaded range of the raccoon dog in Europe (see Table 12), the Public Health consequences of which should be monitored carefully, given the severe clinical symptoms in infected people. A number of Platyhelminthes have also been introduced, linked to the trade and consumption of fish, particularly where fish are not frozen during transport, but these have caused low numbers of human cases in Europe to date (Table 8).

Alien species with indirect impacts on zoonotic disease transmission

Only four studies addressed indirect impacts of IAS on disease transmission (Table 13). IAS can alter the habitat use by native species and indirectly increase the human risk of exposure to a disease as reported by Allan et al. (239). In Missouri (U.S.) the white-tailed deer, *Odocoileus virginianus*, the dominant host for the tick *Amblyomma americanum* carrying the bacteria *Ehrlichia* spp. (agents of human ehrlichiosis), used areas invaded by the Amur honeysuckle, *Lonicera maackii,* more frequently. This led to considerably greater numbers of ticks infected with pathogens in honeysuckle-invaded areas than the adjacent honeysuckle-uninvaded areas. When honeysuckle was experimentally removed, a decrease in deer activity and infected tick numbers was observed. On the contrary, IAS can reduce the quality of habitat for vector-host contact, thus decreasing the risk: an experiment carried out in USA showed that Japanese stiltgrass, *Microstegium vimineum*, changes soil surface microclimate conditions, reducing habitat quality for ticks (240). Similarly, in Illinois (USA), the management of invasive plants *Typha* spp. and *Phragmites australis* in storm-water dry detention basins during the growing season can increase West Nile Virus transmission risk, while in unmanaged patches the presence of communal bird roosts can decrease this risk(241). IAS can also alter vector-host-pathogen dynamics, increasing human spill-over. In Florida, the invasive Burmese python, *Python bivittatus*, heavily predated the large mammals of the area (i.e. deer, raccoons and opossums), inducing the native mosquito, *Culex cedecei*, to feed more on hispid cotton rat *Sigmodon hispidus* (the primary reservoir host) and even on humans(242). The final example concerns a forest pathogen, the oomycete *Phytophthora ramorum*, that causes tree dieback and the tick-borne Lyme Borrelia pathogen in the United States. Forest structure changes arising from dieback altered host and vector abundance in coastal woodlands in a manner expected to increase the risk from Borrelia-infected nymphal ticks (243).

Table 11. Nematode parasites alien in Europe as causal agents for zoonotic diseases. C= contact transmission. O = oral transmission through food (F) or water (W). V = vector-borne transmission by mosquitoes (MOS). The criteria for actual or potential impact are outlined in Table 3.

Nematoda							
Order: Family	Parasite	Transmission type	Health impacts	Evidence for introduction into Europe and links to human disease in Europe	Countries of impact	Actual or potential impact (impact level)	Refs
Rhabditida: Onchocercidae	*Dirofilaria immities Dirofilaria repens*	V(MOS)	Filarioid helminths with domestic and wild canids as main hosts and mosquitoes as vectors. Cause primarily pulmonary *(D . immitis)*, ocular (D . repens), and subcutaneous (*D . repens*) dirofilariosis	Prior cases tended to be introduced but finding of D. repens in mosquito vectors now suggests the parasite has established in some parts of Europe. Burden: 33 cases reported since 2012	Austria	Actual (low)	(244)
Secernentea: Ascarididae	*Baylisascaris procyonis*	O	Larvae of the Raccoon roundworm causes a severe or fatal neural larva migrans called baylisascariasis, in humans. Eggs excreted in raccoon feces are infective after 2–4 weeks and can remain so for years	Raccoon roundworm has been found in raccoon populations in Germany, Norway, Denmark and Poland (refs in Table 7). Despite widespread transmission in its introduced host, only 1 human case has been notified in Europe	Germany Denmark Norway Poland	Actual (low)	(245)
Secernentea: Strongyloididae	*Strongyloides myopotami* *Strongyloides stercoralis* *Strongyloides procyonis*	C	Nutria/coypu roundworm where larvae burrow into skin causing nutria or swimmer's itch Threadworm causing strongyloidiasis with respiratory, skin and/or digestive symptoms, complications in immune-compromised individuals Raccoon threadworm demonstrated can cause short-lived intestinal infection in healthy humans	Infection rates of *S. stercoralis* are increasing in Europe, nearing those in endemic areas. Domesticated small ruminants act as reservoir hosts and are thought to be enhancing establishment	central, south and east Europe	Actual (medium)	(238)

Table 12. Platyhelminthes parasites alien in Europe as causal agents for zoonotic diseases C= contact transmission. O = oral transmission through food (F) or water (W). V = vector-borne transmission by mosquitoes (MOS). The criteria for actual or potential impact are outlined in Table 3.

Platyhelminthes							
Order: Family	Parasite	Transmission type	Health impacts	Evidence for introduction into Europe and links to human disease in Europe	Countries of impact	Actual or potential impact (certainty)	Refs
Plagiorchiida: Heterophyidae	*Centrocestus formosanus*	O(F,W)	In humans, *C. formosanus* infections result in epigastric pain, indigestion, and diarrhea	Species spreading in freshwater fish trade (ornamental and research), sporadically reported in European fish populations. Human cases have not been recorded in Europe	Italy	Potential (low)	(246)
Cestoda: Diphyllobothriidea	*Diphyllobothrium pacificum* *D. dendriticum* *D. nihonkaiens* *D. balanopterae*	O(F)	Tapeworm causing diphyllobothriasis due to human consumption of raw or undercooked freshwater fish	Only *D. latum* is autochthonous in north-east Europe. Most of the cases in Europe are imported or caused by consumption of fish imported from endemic areas, particularly where fish have not been frozen. Very few cases reported overall.	Spain Switzerland	Actual (low)	(247)

Table 13. Alien species with indirect impacts on zoonotic disease transmission. V = vector-borne transmission by tick (T) or mosquitoes (MOS). Case fatality is mean of case fatality rate reported by ECDC from 2012-2018 (where data are available). The criteria for actual or potential impact are outlined in Table 3.

Order: Family	Name of Alien Species	Pathogen genus impacted			Evidence for role in zoonotic disease transmission	Countries of impact	Actual or potential impact (certainty)	Refs
		Species within genus	Trans missi on	Case fatality rate (%)				
Poales:Poaceae	*Phragmites australis*	West Nile Virus	V(MOS)	9.13	Management of the species increases disease risk by altering habitat quality for vectors (immatures) and avian host (roosts)	United States	Actual (low)	(241)
Poales:Typhaceae	*Typha* spp.	West Nile Virus	V(MOS)	9.13	IAS management increases disease risk by altering habitat quality for vectors (immatures) and avian host (roosts)	United States	Actual (low)	(241)
Peronosporales: Peronosporaceae	*Phytophthora ramorum*	Borrelia burgdorferi	V(T)	-	Introduced forest oomycete pathogen found in models to reduce nymphal infection prevalence through its impacts on forest structure, affecting hosts and tick abundance in coastal woodlands	United States	Actual (low)	(243)
Squamata: Pythonidae	*Python bivittatus*	Everglades virus, Venezuelan equine encephalitis complex	V(MOS)	9.13	Invasive python heavily predated the large mammals (i.e. deer, raccoons and opossums), inducing native mosquito *Culex cedecei* to feed more on hispid cotton rat *Sigmodon hispidus* (the primary reservoir host) and even on humans	United States	Actual (low)	(242)

Role of IAS of Union concern in the emergence and spread of zoonoses

There are 30 animals on the list of invasive alien species of Union concern and a further 36 plants. A number of the plants could have an indirect role in the emergence and spread of zoonoses, primarily by altering the habitat use by animals, but the animals are most relevant in the context of zoonoses transmission. Of the 30 listed animals, there was evidence, from the literature reviewed, for 11 species of having a role in the emergence and spread of zoonoses somewhere in the world (Table 14). It was notable that there was a lack of studies on all groups other than mammals. The highest diversity of pathogens was apparent for raccoons, *P. lotor*, and raccoon dogs, *N. procyonoides*, with diseases such as rabies documented within the literature reviewed in this study. A number of studies compared IAS host- and native host-pathogen dynamics and raccoon dogs were widely mentioned in studies alongside red fox, *V. vulpes*. In most cases, the prevalence of the pathogen was lower or similar in the raccoon dogs but for four there was a higher pathogen prevalence in the IAS. As an example rabies was confirmed in all raccoon dogs tested in a study of animals surveyed in Poland (141).

Table 14. IAS on the list of EU Concern highlighted from the structured review as being associated with potential or actual (in bold) zoonotic pathogen or parasite transmission. Note: There is some evidence that American bullfrog, *Lithobates catesbeianus*, has potential for zoonotic transmission but the relevant literature was not revealed from our structured review.

Order: Family	Species name	Pathogen or Parasite
Carnivora: Canidae	*Nyctereutes procyonoides*	*Alaria alata*
		Anaplasma phagocytophilum
		Apophallus sp.
		Echinococcus multilocularis
		Francisella tularensis
		Ancylostoma sp.
		Mesocestoides spp.
		Rabies
		Taenia sp.
		Toxocara/Toxascaris spp.
		Trichinella spp.
		Uncinaria stenocephala
Carnivora: Herpestidae	*Herpestes javanicus*	Hepatitis E Virus
Carnivora: Procyonidae	*Nasua nasua*	Coccidia
Carnivora: Procyonidae	*Procyon lotor*	Influenza H5N1
		Baylis ascaris procyonis
		Campylobacter sp.
		Borrelia spp.
		Capillaria sp.
		Cryptosporidium sp.
		Enterocytozoon bieneusi
		Francisella tularensis
		Listeria sp.
		Molineus sp.
		Orientia tsutsugamushi
		Rickettsia japonica
		Salmonella sp.
		Sarcocystis kirkpatricki
		Staphylococcus sp.
		Strongyloides procyonis

		Toxascaris sp.
		Toxocara sp.
		Yersinia sp.
Rodentia: Cricetidae	*Ondatra zibethicus*	*Anoplocephalidae*
		Cryptosporidium parvum
		Echinococcus multilocularis
		Giardia sp.
		Hantavirus
		Leptospira sp.
		Taenia sp.
Rodentia: Echimyidae	*Myocastor coypus*	*Aeromonas* sp
		Echinococcus multilocularis
		Strongyloides myopotami
		Taenia sp.
		Toxoplasma gondii
Rodentia: Sciuridae	*Sciurus carolinensis*	*Borrelia burgdorferi*
		Tick-borne encephalitis virus
		Usutu virus
		West Nile virus
		variegated squirrel bornavirus 1
Rodentia: Sciuridae	*Tamias sibiricus barberi*	*Borrelia burgdorferi* species complex
Testudines: Emydidae	*Trachemys scripta*	*Chlamydia*
		Salmonella
Decapoda: Varunidae	*Eriocheir sinensis*	**Paragonimus westermani**
Decapoda: Cambaridae	*Procambarus clarkii*	**Paragonimus westermani**

Evidence for IAS playing an equivalent or disproportionate role in zoonotic disease spill-over

Many of the studies reviewed compared host-pathogen interactions between IAS and native host species, usually for a single pathogen at a time, but sometimes for multiple native hosts and multiple pathogen species. Of the 65 host-pathogen interactions identified from these comparative studies, 57 focused on mammalian hosts including 13 host species with the most numerous being raccoon dog, *N. procyonoides* (32%; n=21), black rat, *R. rattus* (26%; n=17), Norway rat, *R. norvegicus* (11%; n= 7), house mouse, *M. musculus* (5%; n=3). The remaining eight IAS were birds (8%; n=5) and insects (5%; n=3). Across all the comparative studies, the pathogen prevalence in the IAS host was lower than in the native host in 15 studies, equivalent to the native host in 14 studies, and higher than the native host in 33 studies.

In all the comparisons of insect IAS host-pathogen interactions, the pathogen prevalence was considered equivalent in the IAS and native vectors. Although interestingly the non-native reservoir host, *Sturnus vulgaris* - European starling was seen to infect more mosquitoes than the native reservoir hosts including American robin, *Turdus migratorius* (53). Further interesting transmission dynamics were revealed for several viruses whereby European house sparrows, *Passer domesticus*, may have provided a link for the St. Louis encephalitis (SLE) between endemic house finches, *Carpodacus mexicanus*, and invading pigeons, *Columba livia* (68). It is suggested that house sparrows are pre-adapted, competent reservoir hosts for SLE virus (a flavivirus) following association with Old World flavivirus. Furthermore, the phenology of the house sparrow appears to have further contributed to the SLE virus-mosquito cycle; house sparrows perturb the endemic enzootic cycle by making SLE virus available during the summer months when there are high abundance and activity of the vectors, *C. tarsalis* and *C. quinquefasciatus*. Prior to the introduction of house sparrows, the potential for human SLE cases in the Los Angeles Basin was low primarily because of the winter and spring emergence of SLE virus in house finches, which did not coincide, with the peak of mosquito activity (68).

Of the 57 mammalian host-pathogen interactions assessed there were only 14 documented examples of the IAS and native host being similar with respect to pathogen prevalence and 16 examples whereby the IAS host had a lower prevalence than the native host. In most cases the IAS host was considered to have higher prevalence of the pathogen than the native host (n=33). However, there was considerable variability even within a given host. As an example, of the six papers comparing 21 interactions between raccoon dogs, *N. procyonoides*, and native hosts (in all but one case red fox, *V. vulpes*), for 10 of the interactions the prevalence was lower in raccoon dogs than the native host, for four there was an increase and a further four the prevalence was the same. Although interestingly the prevalence of *Leptospira* species was consistently higher in all cases of IAS host-pathogen interaction compared to native host-pathogen interactions, noting the IAS hosts included house mouse, *M. musculus*, Norway rat, *Rattus norvegicus*, black rat, *R. rattus*, and Indian musk shrew, *Suncus murinus*.

Raccoon dogs, *N. procyonoides*, were assessed in a number of studies as a reservoir host for a range of intestinal pathogens, the bacterial pathogen *Francisella tularensis* and rabies. A number of the traits that have contributed to the invasion success of raccoon dogs are also considered important in the altering the spatial and temporal dynamics of the tapeworm *Echinococcus multilocularis*; Raccoon dogs can colonise wide areas over a short time and have a high reproductive rate. They are considered to be an important definitive host for the tapeworm. The disease, *Alveolar echinococcosis*, caused by the larval form of this tapeworm is a highly lethal helminthic disease in humans; the prevalence of the disease is increasing in Europe (248) particularly in western Europe and has been attributed to the abundance of foxes and meadow voles. Studies from Poland, Germany and Estonia all demonstrated

a lower prevalence of the tapeworm in raccoon dogs compared to the native red foxes sampled in the same period. It is thought that this might be a consequence of diet. Red foxes consumed more arvicolid rodents, the main intermediate hosts of the tapeworm, particularly during the coldest period of the year when raccoon dogs are in hibernation (133). However, raccoon dogs can reach very high densities and so are potentially an important additional definitive host for *E. multilocularis*.

Box 1. Zoonotic pathogens and captive-bred IAS populations

Studies on pathogens present in captive/farmed alien species are important because they can reveal the potential zoonotic diseases these species can transmit to humans. Considering the close contact between humans and alien species in captivity, animal breeders and keepers, if not following appropriate measures, can be infected by their animals. Eleven studies were retrieved from the literature research on captive/farmed animals, six of them dealing with mammals, and two of them reporting realised impacts to humans.

In China (165) and Norway (167), captive individuals of raccoon *P. lotor* were found to host the nematode *Baylisascaris procyonis* that causes fatal or severe neural larva migrans in animals and humans. In Norway, *Toxocara* and *Toxascaris sp.* eggs were detected in the faeces of two raccoons, while *Echinococcus* was not detected. In the same study conducted in Norway, two coatis *Nasua nasua* out of four had coccidia oocysts. In a zoological garden in German (249), banded mongooses, *Mungos mungo*, and jaguarundis, *Herpailurus yagouaroundi*, were infected by cowpox virus (CPXV) with a prevalence of 100% and a mortality of 30%. A subsequent serological investigation of other exotic animal species living in this zoo provides evidence for subclinical infection before the onset of clinical cases in the mongoose colony. Moreover, the authors reported a time-delayed CPXV infection with an identical virus strain occurring in different geographical areas, indicating a common source of infection. In Germany, following the discovered variegated squirrel bornavirus 1 (VSBV-1) causing the death of three squirrel breeders in Germany, Schlottau et al. (205) assessed the possible presence of this virus on 17 captive squirrel species, with infected animals found in four species (*Callosciurus prevostii, C. finlaysonii, Tamiops swinhoei, Sciurus granatensis*). In Canada, an individual of Rhesus macaque, *Macaca mulatta*, maintained in laboratory was found infected by *Arcobacter butzleri* causing diarrhoea (250), while one adult male Chinchella, *Chinchilla lanigera*, kept in an animal shelter in Switzerland by *Taenia crassiceps* (203).

Alien reptiles, particularly turtles, can also pose a risk to human health. In Poland, 11 species were tested for the presence of Chlamydiaceae. A higher prevalence of positive individuals was found both in free-living (13 of 63) and captive (22 out of 63) pond sliders, *T. scripta elegans*, compared to other alien and native turtles, but not to alien tortoises (*Testudo spp.*) having 23 out of 35 individuals positive to *Chlamydia spp*. (94). In the Netherlands, a breeder was infected by his turtle, the common musk turtle, *Sternotherus odoratus*; both serotyping and amplified fragment-length polymorphism analysis revealed that the *Salmonella* strains obtained from the patient, the pond water, and the freshwater turtle were identical(251).

In Brazil, captive ostriches *Struthio camelus* were infected with *Giardia duodenalis* (252), highlighting the potential to transmit it to breeders. On the contrary, a very low prevalence (1.5%) of trematode infections was found in the 388 examined tilapia, *Oreochromis niloticus*, farmed in China (79), showing how well managed aquaculture can reduce the transmission of zoonosis to humans.

Notably a recent study on farmed American mink, *N. vison*, demonstrated the spill-over of SARS-CoV-2, cause of coronavirus, from humans into the mink. At least two farm workers have subsequently caught the virus from the American mink (21).

Policy perspectives

Policies and interventions modulating the impacts of IAS on zoonotic disease spill-over

Policies and interventions have affected the outcomes of interactions between IAS and zoonotic disease systems, sometimes increasing the role of the IAS in spill-over to humans. Considering the introduction phase of the invasion process, transboundary trade of livestock, including the relatively uncontrolled transboundary trade in exotic and pet animals, has the potential to disseminate vector arthropods harbouring zoonotic pathogens (253). We can see several instances above where vector arthropods disseminated in this way have gone on to cause disease in humans (Table 4). Ticks and mites are particularly likely to be transported through trade, due to their long association (from several hours or days up to a month) with their blood meal hosts following a blood meal, compared to insect ecto-parasites. For example, the introduction of the brown ear tick, *Rhipicephalus appendiculatus* to the Comoros Islands through live cattle imports led to human outbreaks of East Coast Fever there in 2004, because this tick species is a highly competent vector for *Theileria parva*, the protozoan parasite causal agent (30). However, for Europe, although diversity of tick species reported on imported reptiles are high, truly invasive tick species are rarely reported and onward spread into natural environments has only reported twice, for *Hyalomma aegyptium*, whilst reports of tick-borne pathogens linked to imported reptile ticks are even rarer(254). However, this study included data from Italy, Poland, Spain, Netherlands, Belgium, Slovenia and UK, and the need for more data collection through tighter veterinary policy was highlighted.

In terms of population management, eradication and population reduction programs for invasive alien hosts have varied in their effectiveness, with outcomes modulated by underlying ecological and evolutionary processes and interactions between native and IAS. In Florida, United States, for example it has been shown use of hunting with dogs to control populations of invasive non-native wild pigs, *Sus scrofa*, led to a higher risk of emergence of zoonotic pathogens from these IAS hosts (105). The overall prevalence of pseudo-rabies virus (animal disease not zoonotic disease) and rate of co-infections with pseudo-rabies virus and *Brucella spp.* was higher in *Sus scrofa* in areas in which dog hunting was used compared to areas in which other culling methods were used. It is postulated that hunting with dogs may elevate stress and birth rates, leading to higher rates of pathogen excretion, but may also alter animal movements and social structure in ways that increase contact rates and pathogen transmission (105). As the range and population size of invasive non-native wild pigs (*S. scrofa*) has expanded, the opportunity for hunting has expanded but education programs are required for hunters to understand the risk of exposure to the wide range of food-borne zoonotic diseases linked with the species, during the cleaning process and meat consumption (117,118).

Vaccination campaigns targeted at native reservoir hosts host can have unintended consequences for the role of IAS in transmission. For rabies, a fatal zoonosis, that kills up to 70,000 people globally each year (in the EU less han one human case is reported per year),, considerable success in eradicating the disease was achieved in Western and some Central European countries using oral rabies vaccination (ORV) of the native red fox host, *V. vulpes*, developed in the late 1970s(137). In Estonia, the successful eradication of rabies produced large population increases in an invasive alien host species, raccoon dog, *N. procyonoides,* with potential impacts on the transmission of other zoonotic pathogens shared between this IAS and native species such as the tapeworm *Echinococcus multilocularis* (133). The rabies example also highlights the need to account for differential ecology of IAS and native reservoir hosts when planning interventions. Across Estonia, Latvia and Lithuania since 2005-6, raccoon dog has been shown to have significantly lower uptake of oral rabies vaccination compared with red foxes, possibly due to the long hibernation of the raccoon dog from November to March, which may reduce ORV effectiveness in areas with high densities of this IAS (137).

A number of the host-pathogen interactions varied with land use. In Mediterranean Chile *Leptospira* species in rodent communities inhabiting agricultural areas were almost three times more infected than in wild areas (193) and the invasive murid the Norwegian rat was the most infected species (38.1%). The association between the black rat and sewers resulting in high population densities of this IAS was seen to be a contributing factor to the increased prevalence of *Leptospira* in the western Indian Ocean islands and neighbouring Africa (231). Urbanisation has led to conditions that favour highly adaptable species such as mice and rats and in a study of the cities of southern Benin the infection rates of black rats, *R. rattus*, and Norwegian rats, *R. norvegicus*, with *Trypanosoma lewisi* was higher than in native rodents (236).

Policy options to address the threat posed by IAS in zoonotic disease transmission

There are many challenges in ensuring responses to IAS and wildlife management also consider Public Health priorities and vice versa (7–9). This mainly arises from the different regulatory and biosecurity strategies which are aimed at tackling plant, animal, or human health separately, with wildlife diseases often falling between the gaps amongst these strategies. Member countries of the World Organization for Animal Health (OIE), and the International Plant Protection Convention (IPPC) are mandated to report listed or emerging animal and plant diseases, respectively, and to manage the introduction and spread of these diseases. However, the policies of OIE and IPPC are focused mainly on animals and plants of economic importance, paying less attention to pathogens that affect wildlife (9). At the EU level, there is relevant legislation including Regulation 2016/2031 on protective measures against plant pests (Plant Health law), Council Directive 2006/88/EC dealing with the market of aquaculture animals and products (255), and Regulation 2016/429 (Animal Health Law) on transmissible animal diseases (that provides a legal basis to tackle diseases with significant negative impact on biodiversity through biosecurity, contingency planning, surveillance, and eradication). However, not all the relevant diseases are listed under the Regulations, leading to uncoordinated and late (or even absent) responses (9). EU Regulation 2016/429 also tackles wild animals and animals used in research, where there is a risk for transmitting disease to other animals or to humans, and is strongly linked to the international standards set by OIE and the EU's obligations under the Sanitary and Phytosanitary Measures Agreement in the context of WTO (255).

Alien mosquitoes, as vectors of pathogens that cause disease in humans, are managed in cooperation with WHO Europe, the European Centre for Disease Prevention and Control, the European Mosquito Control Association and Member States, under a regional framework for surveillance and control of invasive mosquitoes and re-emerging mosquito-borne diseases. Guidelines have also been developed (256). However, a similar framework has not yet been developed for other IAS that are vectors, hosts or ectoparasites.

Concerning international wildlife trade regulations, there is insufficient attention to some traded species that may hide new or existing zoonotic agents of public health concern (7). In Japan, for example, Goka and others (257) highlight how the national Invasive Species Act does not cover organisms such as mites, viruses and bacteria that are not easily visible. It is also noted that exotic ticks and mites are being introduced through the importation of wild reptiles that are unregulated because the associated risks of passing infectious diseases such as tick-borne Rickettsioses and Lyme *Borrelia* species to humans and animals is unknown. Under the WTO Agreement of the Application of Sanitary and Phytosanitary Measures and General Agreement on Tariffs and Trade, individual countries can restrict trade to protect animal or plant health or food safety, but they cannot cooperate to apply trade restrictions in order to limit pest or pathogen transmission except in cases of emerging human diseases (8). Other shortcomings are due to the fragmentation of policy and legislation on IAS

and wildlife pathogens, the lack of international cooperation, the unclear mandatory rules and the difficulty in identifying the responsible actors (8,9,255).

Adoption of the One Health approach

Adoption of the One Health approach is considered critical to tackle and understand threats posed by IAS-pathogen interactions. Indeed, One Health approaches consider that human, domestic animal and wildlife, and ecosystem health are linked and interdependent. Therefore, promoting the monitoring and managing of their interactions is optimal for public health. The One Health approach could be considered the umbrella term for two other closely related approaches ("EcoHealth" which advocates understanding and promoting health and well-being in the context of social and ecological interaction, and "Planetary Health" focussed on human health in relation to global sustainability; revised in (258)). The One Health and EcoHealth approaches require "a multidisciplinary collaboration for holistic interventions that attain not only human health goals but also animal and environment health targets, the latter two of which are central to improving the control of neglected and emerging infectious diseases, many of which are zoonoses" (258). Embracing such an approach, in 2008, to tackle the bird flu pandemic, WHO, OIE and FAO, together with UNICEF, the United Nations System Influenza Coordination, and the World Bank developed a strategic framework for reducing the risks of emerging zoonoses (258). In 2010, FAO, OIE and WHO started collaborative work to address risks at the human-animal-ecosystems interface as described in the FAO/OIE/WHO Tripartite Concept, updated in 2019 (revised in UNEP & ILFRI 2020(258)). This multi-sector approach led to some successes reported in the recent UNEP & ILRI report (258), such as controlling rabies in the Serengeti ecosystem in Tanzania, understanding the human and animal burden of brucellosis in Mongolia, and elucidating the transmission dynamics of Rift Valley fever and forecasting its outbreaks.

In Europe, there are already examples of the application of One Health approaches. Examples include HevNET, a network and database for sharing sequences and accompanying metadata collected from human, animal, food and environmental sources to explore the root cause of hepatitis E (259); the *Campylobacte*r mitigation system that includes human and poultry surveillance data-sharing within a multi-sectorial platform in Switzerland (260). A similar approach should be applied to tackle IAS-pathogen interactions, establishing partnerships between environmental, medical and veterinary sector that involves dedicated networks of different professionals such as invasion scientists, wildlife ecologists, conservation biologists, environmental biologists, disease ecologists, epidemiologists, veterinary and medical scientists, medical microbiologists (4,10,255,261). Indeed, according to the IPBES conceptual framework, zoonotic diseases and biological invasions play a shared role for human well-being as components of One Health approach (261). In South Africa, for example, the transdisciplinary approach "invasion science for society" considers a social–ecological system with wider implications included, such as health and socio-economic impacts, recalling the One Health approach (261).

Linking IAS and pathogen process to inform relevant management and action

It is important to note that IAS will likely have reached the establishment or spread stage of the invasion process, before they affect pathways by which zoonotic spill-over to humans occur. The approach used for invasion biology (the stage-based processes, the expansion phase, the hierarchical approach in management) should be applied also to the role of IAS in zoonotic diseases (10) (Fig. 2).
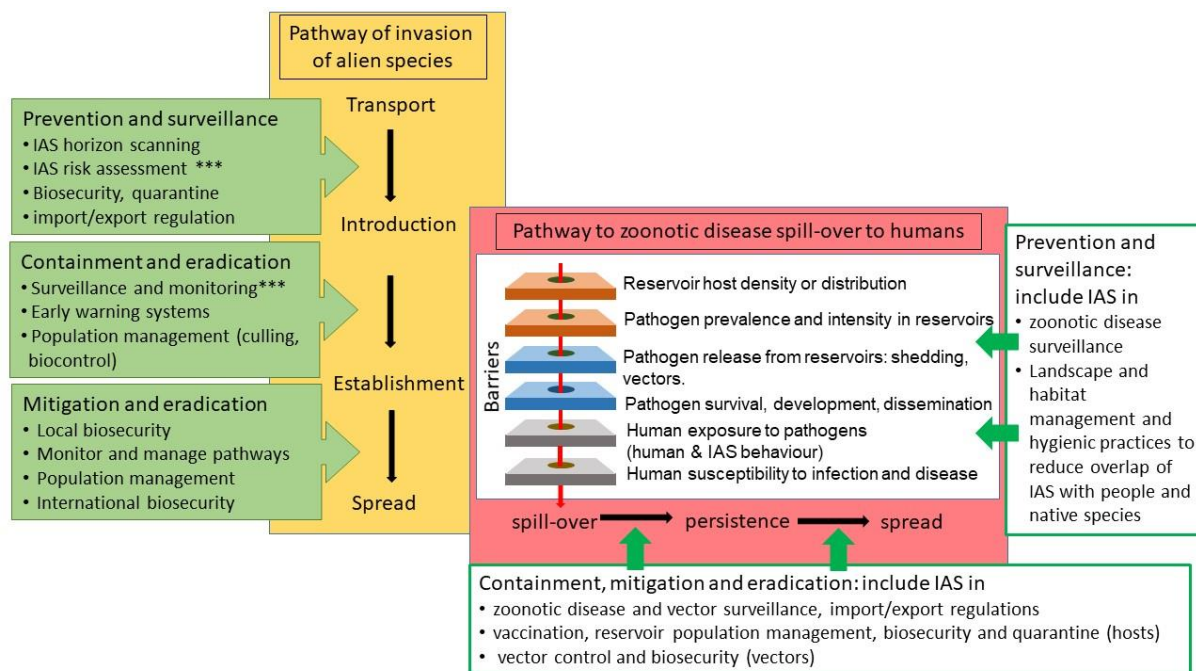
*Figure 2. Stage-specific cross-sectoral control strategies for reducing impacts of invasive alien species on zoonotic disease transmission. Invasive alien species will likely have reached the establishment or spread stage of the invasion process, before they affect pathways by which zoonotic spill-over to humans occur. Green boxes indicate stage-specific control strategies normally targeted at IAS. White boxes with green outlines indicate how zoonotic disease control strategies could be modified to account for IAS roles in spill-over. * indicate potential for cross-sectoral linkage of policy on IAS and zoonotic diseases.*

Specific policy recommendations

As a priority, and as stated in EU Regulation 2016/429, it is necessary to implement biosecurity measures to tackle IAS implicated in disease transmission. Such coordinated action and increasing controls and health surveillance of wildlife imports are needed to prevent introduction of IAS (9). However, this requires a better knowledge of zoonotic diseases, meaning that lists of pathogens and centralised cross-sectoral databases on IAS-pathogen interactions are necessary (7,9,262). To update the database, studies are needed to provide evidence implicating alien species in measurably increased transmission rates of a zoonotic pathogen (7,42,263), accounting for the roles of native species and other key contextual factors affecting transmission.

The three scenarios developed for mosquitoes (256) could be adopted for other IAS and associated pathogens, hosts or vectors:

1) surveillance at the entry points in case of pathogen/reservoir or vector host being absent in an area
2) surveillance to quantify establishment and detecting possible spread of the pathogen/reservoir or vector host locally established
3) surveillance to assess abundance and population structure of pathogen/reservoir or host vector, and impacts to humans to implement appropriate management strategies (and evaluate their efficacy).

Surveillance activities should involve different actors, for example

(256):

- Ministry of human health, of environment and of agriculture/animal production could coordinate and share risk assessment and management procedures with one another
- Public health services at national, regional, local levels could contribute to the surveillance and the assessment of health impact of control measures,
- Veterinary services at national, regional, local levels could contribute to the surveillance of zoonotic diseases
- Regions/provinces/municipalities could participate in management plan definition and implementation
- Environment agencies could contribute to surveillance, management plan definition and implementation
- Research institutes participating in surveillance, collecting data on ecological, social and environmental risk factors, and risk assessment procedures

Currently, there are already inspections for species relevant to animal health at entry points (Regulation (EU) 2017/625) and for IAS of Union concern under the EU Regulation 1143/2014. Therefore, screening for zoonotic diseases could be included in these inspections. A similar screening could be performed when managing IAS already established to assess the possible presence of pathogens and their spread, in order to combine and maximize field survey (261). Molecular tools coupled with bioinformatics could be used across all three surveillance scenarios and could be particularly powerful when integrated into Early Warning Systems and predictive frameworks (264), as has been demonstrated through the joint WHO-OIE-FAO Global Early Warning System (GLEWS)[5] for emerging risks in the context of the human–animal–ecosystems interface, active detection of EID events from the media and also from volunteers participating in public health surveillance, infectious disease, veterinary, microbiology and academic experts in systems such as Promed[6] and Health Map[7] (264).

Citizens can also contribute to surveillance activities and could assist in collecting distribution data on reservoir and vector hosts, allowing detection at the early stages of invasion (264). Examples are the NASA Citizen Science App Tackles Mosquito-Borne Disease[8] and the Global Mosquito Alert[9] consortium. Strong engagement with affected communities will also increase sharing of knowledge and raise awareness of the risks posed by IAS linked to zoonotic diseases. Targeted information campaigns are particularly important for highlighting the risks from food-borne pathogens linked to IAS and for stakeholders having a close contact with IAS hosts, such as farmers, hunters and animal keepers.

Prevention and early detection could be implemented using Horizon scanning and Risk Assessment protocols (7–9,255,261). Horizon scanning, a systematic approach for rapid evaluation of possible IAS currently absent in a certain area, combines expert opinion, consensus methods, and data/literature search, and could provide relevant information for policy, early warning and subsequent detailed screening alongside a risk assessment. This approach has already been shown to be of value for identifying potential new IAS. In Britain, within two years of publication of a Horizon Scanning list (265), seven of the species ranked in the top ten had been reported . In a similar way, this approach

---

[5] http://www.glews.net/
[6] https://www.promedmail.org/
[7] https://www.healthmap.org/en/
[8] https://www.nasa.gov/feature/nasa-citizen-science-app-tackles-mosquito-borne-disease
[9] https://www.wilsoncenter.org/global-mosquito-alert

could be applied to identify potential new zoonotic diseases arising from IAS-pathogen interactions to inform appropriate control measures and prioritise IAS for risk assessment.

Risk assessment protocols are already considered in plant health regulation, EU Regulation 1143/2014 on IAS, Animal Health Codes developed by the OIE and also in the guidelines for conservation translocations drafted by the IUCN in 2013. Indeed the risk assessment framework used to underpin the list of IAS of Union concern (EU Regulation 1143/2014 on IAS) includes consideration of human health impacts and so could be an important tool for assessing risk of zoonoses in this context. Ideally risk assessments would be conducted for the IAS and pathogen alongside risk management which would need to be contextualised and co-developed with cross-sectoral managers. There are many protocols developed for predicting the potential risks posed by alien species, but most do not adequately quantify potential impacts on human health (7). An exception is represented by Pandora, a risk screening protocol developed for emerging or re-emerging, pathogenic or parasitic micro-organisms (266). Following the steps identified by OIE, the stages in Pandora are Entry, Exposure and Consequence: entry and exposure determine the Emergence status of the screened pathogen, while consequence refers to concerns for the environmental, plant, animal, human and other domains. There is also an advanced version, Pandora⁺, screening the risk of a particular pathogen to be introduced by a particular host species (266). Pandora and Pandora⁺ results can feed directly into Harmonia⁺, a risk assessment protocol developed to identify the high risk IAS.

Modelling can also inform prevention and early warning of zoonotic diseases carried or hosted by alien species. There has been considerable research focus on predicting geographical spread of invasive mosquitoes and their impacts on transmission under current and future climates (39) and on predicting vector or reservoir host species roles in zoonotic disease transmission from ecological traits and phylogenetic relationships (267,268). In the light of "invasion science for society" and the interconnection among humans, animals and the environment as recognised by One Health, network approaches for representing and analysing these interdependencies offer promising solutions (269). Network theory that integrates ecological and socioeconomic systems may examine ecosystem services but can also assess how drivers and management actions can directly and indirectly alter ecosystem services, and thus human wellbeing (270). Recently, Wardeh et al. (271) transformed a dataset of mammal–pathogen interactions into networks with hosts linked via their shared pathogens. They used ensemble models coupled with network characteristics, phylogeny and life-history traits to predict key hosts and quantify the roles they undertake in pathogen transmission. Consequently, they were able to predict reservoirs of zoonoses of various pathogen taxa and quantify the extent of pathogen sharing between humans and mammals.

Key policy priorities

- Raise awareness among policy and decision-makers, wildlife managers, scientists and citizens of the risks to human health of alien species to disease transmission. Most forecasts of the risk of emerging diseases neglect the potential role of alien species (10) and this consequently represents a gap in strategies underpinning responses for zoonoses (7).
- Implement effective cross-disciplinary approaches to biosecurity to prevent the introduction and spread of IAS and associated zoonoses including enhanced monitoring and surveillance linking to integrated early warning systems. Consider opportunities for involving citizens in surveillance activities.
- Build interdisciplinary capacity, expertise and coordination for pathogens. Consulting and informing institutions responsible for establishing regulations (intergovernmental organizations, European Commission, governments of EU member countries)

- Develop collaborations through adoption of One Health initiatives (incorporating EcoHealth and Planetary Health) to improve representation of zoonoses within legislation, policy and management frameworks (9).

Key research priorities

- Improve the collation and dissemination of information relevant for monitoring and surveillance of disease transmission over time (prevalence and abundance of pathogens and vectors of disease) including development of standard terminology and classification within cross-sectoral open-access databases. Foster the inclusion of pathogens in IAS datasets and address geographic and taxonomic biases in studies on zoonotic pathogen transmission dynamics.
- Extend datasets to link population genetic structure of IAS and associated pathogens (co-phylogeography) including transcriptomics. Furthermore, consider Importance of immuno-competence and immuno-genetics linked to longitudinal population dynamics studies.
- Embrace innovative approaches, including molecular tools, to improve mechanistic understanding of pathogen transmission dynamics. As an example combining high-throughput sequence typing with networks tools and statistical modelling is a promising approach for characterizing transmission cycles of multi-host pathogens in complex ecological settings.
- Extend expert-elicitation approaches underpinned by available evidence to develop horizon scanning and risk assessment frameworks that are appropriate for pathogens.
- Improve modelling approaches, underpinned by robust data, to derive predictions on future risk of IAS and zoonotic pathogens accounting for scenarios of global environmental change.
- Adoption of system approaches, including network theory that integrates ecological and social systems, to increase understanding of the changing dynamics of pathogens in response to global environmental change. Build on existing frameworks for studying the consequences of eco-evolutionary novelty, specifically the consequences of introduction or species (IAS and pathogens) that lack ecological analogues in their recipient environments (10).

Acknowledgements

Bibliography

1.   Klohe K, Amuasi J, Kaducu JM, Haavardsson I, Bogatyreva E, Onarheim KH, et al. The 2017 Oslo conference report on neglected tropical diseases and emerging/re-emerging infectious diseases - focus on populations underserved. Infect Dis Poverty. 2019 May 28;8(1):40.

2.   Haydon DT, Cleaveland S, Taylor LH, Laurenson MK. Identifying reservoirs of infection: a conceptual and practical challenge. Emerging Infect Dis. 2002 Dec;8(12):1468–1473.

3.   Pyšek P, Hulme PE, Simberloff D, Bacher S, Blackburn TM, Carlton JT, et al. Scientists' warning on invasive alien species. Biol Rev Camb Philos Soc. 2020 Jun 25;

4.   Schindler S, Staska B, Adam M, Rabitsch W, Essl F. Alien species and public health impacts in Europe: a literature review. NEOBIOTA. 2015 Sep 15;27:1–23.

5.   Seebens H, Blackburn TM, Dyer EE, Genovesi P, Hulme PE, Jeschke JM, et al. Global rise in emerging alien species results from increased accessibility of new source pools. Proc Natl Acad Sci USA. 2018 Mar 6;115(10):E2264–E2273.

6.   Seebens H, Blackburn TM, Dyer EE, Genovesi P, Hulme PE, Jeschke JM, et al. No saturation in the accumulation of alien species worldwide. Nat Commun. 2017 Feb 15;8:14435.

7.   Hulme PE. Invasive species challenge the global response to emerging diseases. Trends Parasitol. 2014 Jun;30(6):267–270.

8.   Dunn AM, Hatcher MJ. Parasites and biological invasions: parallels, interactions, and control. Trends Parasitol. 2015 May;31(5):189–199.

9.   Roy HE, Hesketh H, Purse BV, Eilenberg J, Santini A, Scalera R, et al. Alien Pathogens on the Horizon: Opportunities for Predicting their Threat to Wildlife. Conserv Lett. 2016 Aug;2016.

10.   Nuñez MA, Pauchard A, Ricciardi A. Invasion Science and the Global Spread of SARS-CoV-2. Trends Ecol Evol (Amst). 2020 May 19;35(8):642–645.

11.   Saul W-C, Jeschke JM. Eco-evolutionary experience in novel species interactions. Ecol Lett. 2015 Mar;18(3):236–245.

12.   Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, et al. Global trends in emerging infectious diseases. Nature. 2008 Feb 21;451(7181):990–993.

13.   Halliday J, Daborn C, Auty H, Mtema Z, Lembo T, Bronsvoort BMD, et al. Bringing together emerging and endemic zoonoses surveillance: shared challenges and a common solution. Philos Trans R Soc Lond B, Biol Sci. 2012 Oct 19;367(1604):2872–2880.

14.   Halliday JEB, Allan KJ, Ekwem D, Cleaveland S, Kazwala RR, Crump JA. Endemic zoonoses in the tropics: a public health problem hiding in plain sight. Vet Rec. 2015 Feb 28;176(9):220–225.

15.   Grace D, Gilbert J, Randolph T, Kang'ethe E. The multiple burdens of zoonotic disease and an Ecohealth approach to their assessment. Trop Anim Health Prod. 2012 Sep;44 Suppl 1:S67–73.

16.   Jones BA, Grace D, Kock R, Alonso S, Rushton J, Said MY, et al. Zoonosis emergence linked to agricultural intensification and environmental change. Proc Natl Acad Sci USA. 2013 May 21;110(21):8399–8404.

17.   Dzingirai V, Bukachi S, Leach M, Mangwanya L, Scoones I, Wilkinson A. Structural drivers of vulnerability to zoonotic disease in Africa. Philos Trans R Soc Lond B, Biol Sci. 2017 Jul 19;372(1725).

18.   Estrada-Peña A, Ostfeld RS, Peterson AT, Poulin R, de la Fuente J. Effects of environmental change on zoonotic disease risk: an ecological primer. Trends Parasitol. 2014 Apr;30(4):205–214.

19.   Johnson CK, Hitchens PL, Pandit PS, Rushmore J, Evans TS, Young CCW, et al. Global shifts in mammalian population trends reveal key predictors of virus spillover risk. Proc Biol Sci. 2020 Apr 8;287(1924):20192736.

20.   Wood JLN, Leach M, Waldman L, Macgregor H, Fooks AR, Jones KE, et al. A framework for the study of zoonotic disease emergence and its drivers: spillover of bat pathogens as a case study. Philos Trans R Soc Lond B, Biol Sci. 2012 Oct 19;367(1604):2881–2892.

21.   Enserink M. Coronavirus rips through Dutch mink farms, triggering culls. Science. 2020 Jun 12;368(6496):1169.

22.   Molenaar RJ, Vreman S, Hakze-van der Honing RW, Zwart R, de Rond J, Weesendorp E, et al. Clinical and Pathological Findings in SARS-CoV-2 Disease Outbreaks in Farmed Mink (Neovison vison). Vet Pathol. 2020 Jul 14;57(5):653–657.

23.   Guo Q, Li M, Wang C, Fang Z, Wang P, Tan J, et al. Host and infectivity prediction of Wuhan 2019 novel coronavirus using deep learning algorithm. BioRxiv. 2020 Jan 24;

24.   Plowright RK, Parrish CR, McCallum H, Hudson PJ, Ko AI, Graham AL, et al. Pathways to zoonotic spillover. Nat Rev Microbiol. 2017 Aug;15(8):502–510.

25.   Zhu G-L, Tang Y-Y, Limpanont Y, Wu Z-D, Li J, Lv Z-Y. Zoonotic parasites carried by invasive alien species in China. Infect Dis Poverty. 2019 Jan 9;8(1):2.

26.   Puckett EE, Park J, Combs M, Blum MJ, Bryant JE, Caccone A, et al. Global population divergence and admixture of the brown rat (Rattus norvegicus). Proc Biol Sci. 2016 Oct 26;283(1841).

27.   Wells K, O'Hara RB, Morand S, Lessard J-P, Ribas A. The importance of parasite geography and spillover effects for global patterns of host-parasite associations in two invasive species. Diversity and Distributions. 2015 Apr;21(4):477–486.

28.   Kosoy M, Bai Y. Bartonella bacteria in urban rats: A movement from the jungles of southeast asia to metropoles around the globe. Front Ecol Evol. 2019 Mar 28;7.

29.   Moseley M, Rahelinirina S, Rajerison M, Garin B, Piertney S, Telfer S. Mixed Leptospira Infections in a Diverse Reservoir Host Community, Madagascar, 2013-2015. Emerging Infect Dis. 2018;24(6):1138–1140.

30.   Yssouf A, Lagadec E, Bakari A, Foray C, Stachurski F, Cardinale E, et al. Colonization of Grande Comore Island by a lineage of Rhipicephalus appendiculatus ticks. Parasit Vectors. 2011 Mar 17;4:38.

31.   Ronai I, Tufts DM, Diuk-Wasser MA. Aversion of the invasive Asian longhorned tick to the white-footed mouse, the dominant reservoir of tick-borne pathogens in the U.S.A. Med Vet Entomol. 2020 Apr 6;

32.   Lounibos LP. Invasions by insect vectors of human disease. Annu Rev Entomol. 2002;47:233–266.

33.   Schaffner F, Medlock JM, Van Bortel W. Public health significance of invasive mosquitoes in Europe. Clin Microbiol Infect. 2013 Aug;19(8):685–692.

34.   Martinet J-P, Ferté H, Failloux A-B, Schaffner F, Depaquit J. Mosquitoes of North-Western Europe as Potential Vectors of Arboviruses: A Review. Viruses. 2019 Nov 14;11(11).

35.   Wilke ABB, Benelli G, Beier JC. Beyond frontiers: On invasive alien mosquito species in America and Europe. PLoS Negl Trop Dis. 2020 Jan 9;14(1):e0007864.

36.   Ciocchetta S, Prow NA, Darbro JM, Frentiu FD, Savino S, Montarsi F, et al. The new European invader Aedes (Finlaya) koreicus: a potential vector of chikungunya virus. Pathog Glob Health. 2018 May 8;112(3):107–114.

37.   Tsetsarkin KA, Vanlandingham DL, McGee CE, Higgs S. A single mutation in chikungunya virus affects vector specificity and epidemic potential. PLoS Pathog. 2007 Dec;3(12):e201.

38.   Schaffner F, Kaufmann C, Hegglin D, Mathis A. The invasive mosquito Aedes japonicus in Central Europe. Med Vet Entomol. 2009 Dec;23(4):448–451.

39.   Kraemer MUG, Reiner RC, Brady OJ, Messina JP, Gilbert M, Pigott DM, et al. Past and future spread of the arbovirus vectors Aedes aegypti and Aedes albopictus. Nat Microbiol. 2019 Mar 4;4(5):854–863.

40.   Benedict MQ, Levine RS, Hawley WA, Lounibos LP. Spread of the tiger: global risk of invasion by the mosquito Aedes albopictus. Vector Borne Zoonotic Dis. 2007;7(1):76–85.

41.   Montarsi F, Martini S, Michelutti A, Da Rold G, Mazzucato M, Qualizza D, et al. The invasive mosquito Aedes japonicus japonicus is spreading in northeastern Italy. Parasit Vectors. 2019 Mar 26;12(1):120.

42.   Petrić D, Bellini R, Scholte E-J, Rakotoarivony LM, Schaffner F. Monitoring population and environmental parameters of invasive mosquito species in Europe. Parasit Vectors. 2014 Apr 16;7:187.

43.   Clements K, Giménez L, Jones DL, Wilson J, Malham SK. Epizoic barnacles act as pathogen reservoirs on shellfish beds. J Shellfish Res. 2013 Aug;32(2):533–538.

44.   Majoros G, Fehér Z, Deli T, Földvári G. Establishment of Biomphalaria tenagophila snails in Europe. Emerging Infect Dis. 2008 Nov;14(11):1812–1814.

45.   Mulero S, Rey O, Arancibia N, Mas-Coma S, Boissier J. Persistent establishment of a tropical disease in Europe: the preadaptation of schistosomes to overwinter. Parasit Vectors. 2019 Jul 29;12(1):379.

46.   Cleveland CA, Swanepoel L, Box EK, De Nicola A, Yabsley MJ. Rickettsia species in ticks collected from wild pigs (Sus scrofa) and Philippine deer (Rusa marianna) on Guam, Marianna Islands, USA. Acta Trop. 2019 Jun;194:89–92.

47. Duscher GG, Hodžić A, Hufnagl P, Wille-Piazzai W, Schötta A-M, Markowicz MA, et al. Adult Hyalomma marginatum tick positive for Rickettsia aeschlimannii in Austria, October 2018. Euro Surveill. 2018 Nov;23(48).

48. Chamot E, Chatelanat P, Humair L, Aeschlimann A, Bowessidjaou J. [5 cases of Mediterranean boutonneuse fever in Switzerland]. Ann Parasitol Hum Comp. 1987;62(5):371–379.

49. Vezzani D, Eiras DF, Wisnivesky C. Dirofilariasis in Argentina: historical review and first report of Dirofilaria immitis in a natural mosquito population. Vet Parasitol. 2006 Mar 31;136(3-4):259–273.

50. Vezzani D, Mesplet M, Eiras DF, Fontanarrosa MF, Schnittger L. PCR detection of Dirofilaria immitis in Aedes aegypti and Culex pipiens from urban temperate Argentina. Parasitol Res. 2011 Apr;108(4):985–989.

51. Silaghi C, Beck R, Capelli G, Montarsi F, Mathis A. Development of Dirofilaria immitis and Dirofilaria repens in Aedes japonicus and Aedes geniculatus. Parasit Vectors. 2017 Feb 20;10(1):94.

52. Cancrini G, Frangipane di Regalbono A, Ricci I, Tessarin C, Gabrielli S, Pietrobelli M. Aedes albopictus is a natural vector of Dirofilaria immitis in Italy. Vet Parasitol. 2003 Dec;118(3-4):195–202.

53. Komar N, Dohm DJ, Turell MJ, Spielman A. Eastern equine encephalitis virus in birds: relative competence of European starlings (Sturnus vulgaris). Am J Trop Med Hyg. 1999 Mar;60(3):387–391.

54. Yang F, Chan K, Marek PE, Armstrong PM, Liu P, Bova JE, et al. Cache Valley Virus in Aedes japonicus japonicus Mosquitoes, Appalachian Region, United States. Emerging Infect Dis. 2018;24(3):553–557.

55. Wagner S, Mathis A, Schönenberger AC, Becker S, Schmidt-Chanasit J, Silaghi C, et al. Vector competence of field populations of the mosquito species Aedes japonicus japonicus and Culex pipiens from Switzerland for two West Nile virus strains. Med Vet Entomol. 2018;32(1):121–124.

56. Schönenberger AC, Wagner S, Tuten HC, Schaffner F, Torgerson P, Furrer S, et al. Host preferences in host-seeking and blood-fed mosquitoes in Switzerland. Med Vet Entomol. 2016 Mar;30(1):39–52.

57. Lounibos LP, Kramer LD. Invasiveness of Aedes aegypti and Aedes albopictus and Vectorial Capacity for Chikungunya Virus. J Infect Dis. 2016 Dec 15;214(suppl 5):S453–S458.

58. Paupy C, Kassa Kassa F, Caron M, Nkoghé D, Leroy EM. A chikungunya outbreak associated with the vector Aedes albopictus in remote villages of Gabon. Vector Borne Zoonotic Dis. 2012 Feb;12(2):167–169.

59. McTighe SP, Vaidyanathan R. Vector competence of Aedes albopictus from Virginia and Georgia for chikungunya virus isolated in the Comoros Islands, 2005. Vector Borne Zoonotic Dis. 2012 Oct;12(10):867–871.

60. Faraji A, Egizi A, Fonseca DM, Unlu I, Crepeau T, Healy SP, et al. Comparative host feeding patterns of the Asian tiger mosquito, Aedes albopictus, in urban and suburban Northeastern USA and implications for disease transmission. PLoS Negl Trop Dis. 2014 Aug 7;8(8):e3037.

61. Tsetsarkin KA, Chen R, Weaver SC. Interspecies transmission and chikungunya virus emergence. Curr Opin Virol. 2016 Feb;16:143–150.

62. Dennett JA, Bala A, Wuithiranyagool T, Randle Y, Sargent CB, Guzman H, et al. ASSOCIATIONS BETWEEN TWO MOSQUITO POPULATIONS AND WEST NILE VIRUS IN HARRIS COUNTY, TEXAS, 2003–06[1]. J Am Mosq Control Assoc. 2007 Sep;23(3):264–275.

63. Clements MF, Gidwani K, Kumar R, Hostomska J, Dinesh DS, Kumar V, et al. Measurement of recent exposure to Phlebotomus argentipes, the vector of Indian visceral Leishmaniasis, by using human antibody responses to sand fly saliva. Am J Trop Med Hyg. 2010 May;82(5):801–807.

64. Stockdale-Walden HD, Slapcinsky J, Qvarnstrom Y, McIntosh A, Bishop HS, Rosseland B. Angiostrongylus cantonensis in Introduced Gastropods in Southern Florida. J Parasitol. 2015 Apr;101(2):156–159.

65. Heneberg P, Rojas A, Bizos J, Kocková L, Malá M, Rojas D. Focal Philophthalmus gralli infection possibly persists in Melanoides tuberculata over two years following the definitive hosts' removal. Parasitol Int. 2014 Dec;63(6):802–807.

66. Literák I, Heneberg P, Sitko J, Wetzel EJ, Cardenas Callirgos JM, Čapek M, et al. Eye trematode infection in small passerines in Peru caused by Philophthalmus lucipetus, an agent with a zoonotic potential spread by an invasive freshwater snail. Parasitol Int. 2013 Aug;62(4):390–396.

67. Coelho P. Updated distribution and range expansion of the gastropod invader Melanoides tuberculata (Müller, 1774) in Brazilian waters. Bioinvasions Rec. 2018;7(4):405–409.

68. Gruwell JA, Fogarty CL, Bennett SG, Challet GL, Vanderpool KS, Jozan M, et al. Role of peridomestic birds in the transmission of St. Louis encephalitis virus in southern California. J Wildl Dis. 2000 Jan;36(1):13–34.

69. Arrigo NC, Adams AP, Watts DM, Newman PC, Weaver SC. Cotton rats and house sparrows as hosts for North and South American strains of eastern equine encephalitis virus. Emerging Infect Dis. 2010 Sep;16(9):1373–1380.

70. Lee D-H, Park J-K, Youn H-N, Lee Y-N, Lim T-H, Kim M-S, et al. Surveillance and isolation of HPAI H5N1 from wild Mandarin Ducks (Aix galericulata). J Wildl Dis. 2011 Oct;47(4):994–998.

71. Mase M, Imada T, Sanada Y, Etoh M, Sanada N, Tsukamoto K, et al. Imported parakeets harbor H9N2 influenza A viruses that are genetically closely related to those transmitted to humans in Hong Kong. J Virol. 2001 Apr;75(7):3490–3494.

72. Naguib MM, Verhagen JH, Mostafa A, Wille M, Li R, Graaf A, et al. Global patterns of avian influenza A (H7): virus evolution and zoonotic threats. FEMS Microbiol Rev. 2019 Nov 1;43(6):608–621.

73. Chilvers BL, Cowan PE, Waddington DC, Kelly PJ, Brown TJ. The prevalence of infection of Giardia spp. and Cryptosporidium spp. in wild animals on farmland, southeastern North Island, New Zealand. Int J Environ Health Res. 1998 Mar;8(1):59–64.

74. Feare CJ, Sanders MF, Blasco R, Bishop JD. Canada goose (Branta canadensis) droppings as a potential source of pathogenic bacteria. J R Soc Promot Health. 1999 Sep;119(3):146–155.

75. Dickx V, Kalmar ID, Tavernier P, Vanrompay D. Prevalence and genotype distribution of Chlamydia psittaci in feral Canada geese (Branta canadensis) in Belgium. Vector Borne Zoonotic Dis. 2013 Jun;13(6):382–384.

76. Gedye KR, Fremaux M, Garcia-Ramirez JC, Gartrell BD. A preliminary survey of Chlamydia psittaci genotypes from native and introduced birds in New Zealand. N Z Vet J. 2018 May;66(3):162–165.

77. Pisanu B, Laroucau K, Aaziz R, Vorimore F, Le Gros A, Chapuis J-L, et al. Chlamydia avium' ' detection from a ring-necked parakeet (psittacula krameri) in france. Journal of Exotic Pet Medicine. 2018 Feb;0(0):68–74.

78. Mauel MJ, Miller DL, Frazier KS. Bacterial Pathogens Isolated from Cultured Bullfrogs (Rana Castesbeiana). Journal of Veterinary …. 2002;

79. Li K, Clausen JH, Murrell KD, Liu L, Dalsgaard A. Risks for fishborne zoonotic trematodes in tilapia production systems in Guangdong province, China. Vet Parasitol. 2013 Nov 15;198(1-2):223–229.

80. Shamsi S, Turner A, Wassens S. Description and genetic characterization of a new Contracaecum larval type (Nematoda: Anisakidae) from Australia. J Helminthol. 2018 Mar;92(2):216–222.

81. Kuhn T, García-Màrquez J, Klimpel S. Adaptive radiation within marine anisakid nematodes: a zoogeographical modeling of cosmopolitan, zoonotic parasites. PLoS One. 2011 Dec 13;6(12):e28642.

82. Carlson JC, Franklin AB, Hyatt DR, Pettit SE, Linz GM. The role of starlings in the spread of Salmonella within concentrated animal feeding operations. J Appl Ecol. 2011 Apr;48(2):479–486.

83. Erbeck DH, Nunn SA. Chlamydiosis in Pen-Raised Bobwhite Quail (Colinus virginianus) and Chukar Partridge (Alectoris chukar) with High Mortality. Avian Dis. 1999 Oct;43(4):798.

84. Briceño C, Surot D, González-Acuña D, Martínez FJ, Fredes F. Parasitic survey on introduced monk parakeets (Myiopsitta monachus) in Santiago, Chile. Rev Bras Parasitol Vet. 2017 Jun;26(2):129–135.

85. Madani SA, Peighambari SM. PCR-based diagnosis, molecular characterization and detection of atypical strains of avian Chlamydia psittaci in companion and wild birds. Avian Pathol. 2013 Feb;42(1):38–44.

86. Nemeth NM, Bosco-Lauth AM, Sciulli RH, Gose RB, Nagata MT, Bowen RA. Serosurveillance for Japanese encephalitis and West Nile viruses in resident birds in Hawai'i. J Wildl Dis. 2010 Apr;46(2):659–664.

87. Miles JA. The ecology of Whataroa virus, an alphavirus, in South Westland, New Zealand. J Hyg (Lond). 1973 Dec;71(4):701–713.

88. TIZARD IR, HARMESON J, LAI CH. PREVALENCE OF SERUM ANTIBODIES TO TOXOPLASMA-GONDII IN ONTARIO MAMMALS. Canadian Journal of Comparative Medicine-Revue Canadienne De Medecine Comparee. 1978;42(2):177–183.

89.   Miranda JMS, Rocha KS, Monteiro LH, Baia IWM. Presence of anti-Leptospira spp. antibodies in captive yellow-spotted river turtles (Podocnemis unifilis) in the Eastern Amazon. Ciência Rural. 2020;

90.   Feng AYT, Himsworth CG. The secret life of the city rat: a review of the ecology of urban Norway and black rats (Rattus norvegicus and Rattus rattus). Urban Ecosyst. 2014 Mar;17(1):149–162.

91.   Pépin M, Dupinay T, Zilber AL, McElhinney LM. Of rats and pathogens: pathogens transmitted by urban rats with an emphasis on hantaviruses. CAB Rev. 2016;

92.   Jiménez RR, Barquero-Calvo E, Abarca JG, Porras LP. *Salmonella* Isolates in the Introduced Asian House Gecko (*Hemidactylus frenatus*) with Emphasis on*Salmonella* Weltevreden, in Two Regions in Costa Rica. Vector-Borne and Zoonotic Diseases. 2015 Sep;15(9):550–555.

93.   Callaway Z, Thomas A, Melrose W, Buttner P, Speare R. Salmonella Virchow and Salmonella Weltevreden in a random survey of the Asian house gecko, Hemidactylus frenatus, in houses in northern Australia. Vector Borne Zoonotic Dis. 2011 Jun;11(6):621–625.

94.   Mitura A, Niemczuk K, Zaręba K, Zając M, Laroucau K, Szymańska-Czerwińska M. Free-living and captive turtles and tortoises as carriers of new Chlamydia spp. PLoS One. 2017 Sep 26;12(9):e0185407.

95.   Gong S, Wang F, Shi H, Zhou P, Ge Y, Hua L, et al. Highly pathogenic Salmonella Pomona was first isolated from the exotic red-eared slider (Trachemys scripta elegans) in the wild in China: Implications for public health. Sci Total Environ. 2014 Jan 15;468-469:28–30.

96.   Marin C, Ingresa-Capaccioni S, González-Bodi S, Marco-Jiménez F, Vega S. Free-living turtles are a reservoir for Salmonella but not for Campylobacter. PLoS One. 2013 Aug 7;8(8):e72350.

97.   Roy HE, Bacher S, Essl F, Adriaens T, Aldridge DC, Bishop JDD, et al. Developing a list of invasive alien species likely to threaten biodiversity and ecosystems in the European Union. Glob Change Biol. 2018 Dec 12;

98.   Bigler WJ, Hoff GL, Hemmert WH, Tomas JA, Janowski HT. Trends of brucellosis in Florida. An epidemiologic review. Am J Epidemiol. 1977 Mar;105(3):245–251.

99.   CLARK RK, JESSUP DA, HIRD DW, RUPPANNER R, MEYER ME. SEROLOGIC SURVEY OF CALIFORNIA WILD HOGS FOR ANTIBODIES AGAINST SELECTED ZOONOTIC DISEASE AGENTS. J Am Vet Med Assoc. 1983;183(11):1248–1251.

100.   Musser JMB, Schwartz AL, Srinath I, Waldrup KA. Use of serology and bacterial culture to determine prevalence of Brucella spp. In feral Swine (sus scrofa) in proximity to a beef cattle herd positive for Brucella suis and Brucella abortus. J Wildl Dis. 2013 Apr;49(2):215–220.

101.   Bevins SN, Pedersen K, Lutman MW, Gidlewski T, Deliberto TJ. Consequences Associated with the Recent Range Expansion of Nonnative Feral Swine. Bioscience. 2014 Apr 1;64(4):291–299.

102.   Eales KM, Norton RE, Ketheesan N. Brucellosis in northern Australia. Am J Trop Med Hyg. 2010 Oct;83(4):876–878.

103.   Ridoutt C, Lee A, Moloney B, Massey P, Charman N, Jordan D. Detection of brucellosis and leptospirosis in feral pigs in New South Wales. Aust Vet J. 2014 Sep;92(9):343–347.

104. Lama JK, Bachoon DS. Detection of Brucella suis, Campylobacter jejuni, and Escherichia coli Strains in Feral Pig (Sus scrofa) Communities of Georgia. Vector Borne Zoonotic Dis. 2018 Apr 26;18(7):350–355.

105. Carr AN, Milleson MP, Hernández FA, Merrill HR, Avery ML, Wisely SM. Wildlife Management Practices Associated with Pathogen Exposure in Non-Native Wild Pigs in Florida, U.S. Viruses. 2018 Dec 26;11(1).

106. Muller L, Poudyal N, Applegate RD, Yoest C. Control efforts and serologic survey of pseudorabies and brucellosis in wild pigs of Tennessee. Human-Wildlife Interactions. 2019;13(1):167–175.

107. Jay-Russell MT, Bates A, Harden L, Miller WG, Mandrell RE. Isolation of Campylobacter from feral swine (Sus scrofa) on the ranch associated with the 2006 Escherichia coli O157:H7 spinach outbreak investigation in California. Zoonoses Public Health. 2012 Aug;59(5):314–319.

108. Cooper A, Goullet M, Mitchell J, Ketheesan N, Govan B. Serological evidence of Coxiella burnetii exposure in native marsupials and introduced animals in Queensland, Australia. Epidemiol Infect. 2012 Jul;140(7):1304–1308.

109. Atwill ER, Sweitzer RA, Pereira MG, Gardner IA, Van Vuren D, Boyce WM. Prevalence of and associated risk factors for shedding Cryptosporidium parvum oocysts and Giardia cysts within feral pig populations in California. Appl Environ Microbiol. 1997 Oct;63(10):3946–3949.

110. Rodriguez-Rivera LD, Cummings KJ, McNeely I, Suchodolski JS, Scorza AV, Lappin MR, et al. Prevalence and diversity of cryptosporidium and giardia identified among feral pigs in texas. Vector Borne Zoonotic Dis. 2016 Oct 20;16(12):765–768.

111. Castellaw AH, Chenney EF, Varela-Stokes AS. Tick-borne disease agents in various wildlife from Mississippi. Vector Borne Zoonotic Dis. 2011 Apr;11(4):439–442.

112. Clavijo A, Nikooienejad A, Esfahani MS, Metz RP, Schwartz S, Atashpaz-Gargari E, et al. Identification and analysis of the first 2009 pandemic H1N1 influenza virus from U.S. feral swine. Zoonoses Public Health. 2013 Aug;60(5):327–335.

113. Hall JS, Minnis RB, Campbell TA, Barras S, Deyoung RW, Pabilonia K, et al. Influenza exposure in United States feral swine populations. J Wildl Dis. 2008 Apr;44(2):362–368.

114. Irwin MJ, Massey PD, Walker B, Durrheim DN. Feral pig hunting: a risk factor for human brucellosis in north-west NSW? N S W Public Health Bull. 2009 Dec;20(11-12):192–194.

115. Heise-Pavlov PM, Heise-Pavlov SR. Feral pigs in tropical lowland rainforest of northeastern Australia: ecology, zoonoses and management. Wildlife Biology. 2003;9:21–27.

116. Baroch JA, Gagnon CA, Lacouture S, Gottschalk M. Exposure of feral swine (Sus scrofa) in the United States to selected pathogens. Canadian Journal of Veterinary Research-Revue Canadienne De Recherche Veterinaire. 2015;79(1):74–78.

117. Brandão LNS, Rosa JMA, Kramer B, Sousa ATHI de, Trevisol IM, Silva VS, et al. Detection of Toxoplasma gondii infection in feral wild boars (Sus scrofa) through indirect hemagglutination and PCR. Cienc Rural. 2019 Mar 14;49(3).

118. Sandfoss M, DePerno C, Patton S, Flowers J, Kennedy-Stoskopf S. Prevalence of antibody to Toxoplasma gondii and Trichinella spp. in feral pigs (Sus scrofa) of eastern North Carolina. J Wildl Dis. 2011 Apr;47(2):338–343.

119. Dubey JP, Rollor EA, Smith K, Kwok OCH, Thulliez P. Low Seroprevalence of Toxoplasma gondii in Feral Pigs from a Remote Island Lacking Cats. J Parasitol. 1997 Oct;83(5):839.

120. Diderrich V, New JC, Noblet GP, Patton S. Serologic survey of Toxoplasma gondii antibodies in free-ranging wild hogs (Sus scrofa) from the Great Smoky Mountains National Park and from sites in South Carolina. J Eukaryot Microbiol. 1996 Oct;43(5):122S.

121. Hill DE, Dubey JP, Baroch JA, Swafford SR, Fournet VF, Hawkins-Cooper D, et al. Surveillance of feral swine for Trichinella spp. and Toxoplasma gondii in the USA and host-related factors associated with infection. Vet Parasitol. 2014 Oct 15;205(3-4):653–665.

122. Hidalgo A, Villanueva J, Becerra V, Soriano C, Melo A, Fonseca-Salamanca F. Trichinella spiralis Infecting Wild Boars in Southern Chile: Evidence of an Underrated Risk. Vector Borne Zoonotic Dis. 2019 Mar 5;19(8):625–629.

123. Nockler K. Prevalence and importance of Trichinella in Germany. Wiener Tierarztliche Monatsschrift. 2005;92(12):301–307.

124. Comeaux JM, Curtis-Robles R, Lewis BC, Cummings KJ, Mesenbrink BT, Leland BR, et al. Survey of Feral Swine (Sus scrofa) Infection with the Agent of Chagas Disease (Trypanosoma cruzi) in Texas, 2013-14. J Wildl Dis. 2016 Jul;52(3):627–630.

125. Karamon J, Samorek-Pieróg M, Moskwa B, Różycki M, Bilska-Zając E, Zdybel J, et al. Intestinal helminths of raccoon dogs (Nyctereutes procyonoides) and red foxes (Vulpes vulpes) from the Augustów Primeval Forest (north-eastern Poland). J Vet Res. 2016 Sep 1;60(3):273–277.

126. Laurimaa L, Süld K, Davison J, Moks E, Valdmann H, Saarma U. Alien species and their zoonotic parasites in native and introduced ranges: The raccoon dog example. Vet Parasitol. 2016 Mar 30;219:24–33.

127. Al-Sabi MNS, Chriél M, Jensen TH, Enemark HL. Endoparasites of the raccoon dog (Nyctereutes procyonoides) and the red fox (Vulpes vulpes) in Denmark 2009-2012 - A comparative study. Int J Parasitol Parasites Wildl. 2013 Dec;2:144–151.

128. Bružinskaitė-Schmidhalter R, Šarkūnas M, Malakauskas A, Mathis A, Torgerson PR, Deplazes P. Helminths of red foxes (Vulpes vulpes) and raccoon dogs (Nyctereutes' ' procyonoides) in Lithuania. Parasitology. 2012 Jan;139(1):120–127.

129. Duscher T, Hodžić A, Glawischnig W, Duscher GG. The raccoon dog (Nyctereutes procyonoides) and the raccoon (Procyon lotor)-their role and impact of maintaining and transmitting zoonotic diseases in Austria, Central Europe. Parasitol Res. 2017 Apr;116(4):1411–1416.

130. Härtwig V, von Loewenich FD, Schulze C, Straubinger RK, Daugschies A, Dyachenko V. Detection of Anaplasma phagocytophilum in red foxes (Vulpes vulpes) and raccoon dogs (Nyctereutes procyonoides) from Brandenburg, Germany. Ticks Tick Borne Dis. 2014 Apr;5(3):277–280.

131. Schwarz S, Sutor A, Staubach C, Mattis R, Tackmann K, Conraths FJ. Estimated prevalence of Echinococcus multilocularis in raccoon dogs Nyctereutes procyonoides in northern Brandenburg, Germany. Curr Zool. 2011 Oct 1;57(5):655–661.

132. Maas M, van den End S, van Roon A, Mulder J, Franssen F, Dam-Deisz C, et al. First findings of Trichinella spiralis and DNA of Echinococcus multilocularis in wild raccoon dogs in the Netherlands. Int J Parasitol Parasites Wildl. 2016 Dec;5(3):277–279.

133. Laurimaa L, Süld K, Moks E, Valdmann H, Umhang G, Knapp J, et al. First report of the zoonotic tapeworm Echinococcus multilocularis in raccoon dogs in Estonia, and comparisons with other countries in Europe. Vet Parasitol. 2015 Sep 15;212(3-4):200–205.

134. Schulze C, Heuner K, Myrtennäs K, Karlsson E, Jacob D, Kutzer P, et al. High and novel genetic diversity of Francisella tularensis in Germany and indication of environmental persistence. Epidemiol Infect. 2016 Jun 30;144(14):3025–3036.

135. Kuehn A, Schulze C, Kutzer P, Probst C, Hlinak A, Ochs A, et al. Tularaemia seroprevalence of captured and wild animals in Germany: the fox (Vulpes vulpes) as a biological indicator. Epidemiol Infect. 2013 Apr;141(4):833–840.

136. Schwarz S, Sutor A, Mattis R, Conraths FJ. [The raccoon roundworm (Baylisascaris procyonis)--no zoonotic risk for Brandenburg?]. Berl Munch Tierarztl Wochenschr. 2015 Feb;128(1-2):34–38.

137. Robardet E, Picard-Meyer E, Dobroštana M, Jaceviciene I, Mähar K, Muižniece Z, et al. Rabies in the baltic states: decoding a process of control and elimination. PLoS Negl Trop Dis. 2016 Feb 5;10(2):e0004432.

138. Maciulskis P, Lukauskas K, Sederevicius A, Kiudulas V, Pockevicius A. Epidemiology of enzootic rabies in Lithuania. Medycyna Weterynaryjna-Veterinary Medicine-Science and Practice. 2006;62(7):769–772.

139. Zienius D, Bagdonas J, Dranseika A. Epidemiological situation of rabies in Lithuania from 1990 to 2000. Vet Microbiol. 2003 May;93(2):91–100.

140. Lyczak A, Tomasiewicz K, Krawczuk G, Modrzewska R. Epizootic situation and risk of rabies exposure in Polish population in 2000, with special attention to Lublin province. Annals of Agricultural and Environmental Medicine. 2001;8(2):131–135.

141. Ostrowska JD, HermanowskaSzpakowicz T. Rabies and its prevention in people. Medycyna Weterynaryjna. 1997;53(3):144–147.

142. Lis H. Rabies of animals, in Poland. Medycyna Weterynaryjna. 1996;52(3):170–172.

143. Zienius D, Sajute K, Žilinskas H, Stankevicius A. Phylogenetic Analysis of the Rabies Virus N-coding Region in Lithuanian Rabies Isolates. Acta Vet Brno. 2009;78(2):273–280.

144. Malakauskas A, Paulauskas V, Järvis T, Keidans P, Eddi C, Kapel CMO. Molecular epidemiology of Trichinella spp. in three Baltic countries: Lithuania, Latvia, and Estonia. Parasitol Res. 2007 Mar;100(4):687–693.

145. Osten-Sacken N, Solarczyk P. Trichinella spiralis in road-killed raccoon dogs (Nyctereutes procyonoides) in western Poland. Ann Parasitol. 2016;62(1):77–79.

146. Deksne G, Segliņa Z, Jahundoviča I, Esīte Z, Bakasejevs E, Bagrade G, et al. High prevalence of Trichinella spp. in sylvatic carnivore mammals of Latvia. Vet Parasitol. 2016 Nov 15;231:118–123.

147. Mayer-Scholl A, Reckinger S, Schulze C, Nöckler K. Study on the occurrence of Trichinella spp. in raccoon dogs in Brandenburg, Germany. Vet Parasitol. 2016 Nov 15;231:102–105.

148. Cybulska A, Kornacka A, Moskwa B. The occurrence and muscle distribution of Trichinella britovi in raccoon dogs (Nyctereutes procyonoides) in wildlife in the Głęboki Bród Forest District, Poland. Int J Parasitol Parasites Wildl. 2019 Aug;9:149–153.

149. Laurimaa L, Davison J, Süld K, Plumer L, Oja R, Moks E, et al. First report of highly pathogenic Echinococcus granulosus genotype G1 in dogs in a European urban environment. Parasit Vectors. 2015 Mar 26;8:182.

150. Lagadec E, Gomard Y, Le Minter G, Cordonin C, Cardinale E, Ramasindrazana B, et al. Identification of Tenrec ecaudatus, a Wild Mammal Introduced to Mayotte Island, as a Reservoir of the Newly Identified Human Pathogenic Leptospira mayottensis. PLoS Negl Trop Dis. 2016 Aug 30;10(8):e0004933.

151. Kaewmongkol G, Kaewmongkol S, Fleming PA, Adams PJ, Ryan U, Irwin PJ, et al. Zoonotic Bartonella species in fleas and blood from red foxes in Australia. Vector Borne Zoonotic Dis. 2011 Dec;11(12):1549–1553.

152. Jenkins DJ, Fraser A, Bradshaw H, Craig PS. DETECTION OF echinococcus granulosus COPROANTIGENS IN AUSTRALIAN CANIDS WITH NATURAL OR EXPERIMENTAL INFECTION. Journal of Parasitology. 2000 Feb;86(1):140–145.

153. Dybing NA, Jacobson C, Irwin P, Algar D, Adams PJ. Leptospira Species in Feral Cats and Black Rats from Western Australia and Christmas Island. Vector Borne Zoonotic Dis. 2017 Mar 6;17(5):319–324.

154. Peterson DR, Cooney MK, Beasley RP. Prevalence of antibody to Toxoplasma among Alaskan natives: relation to exposure to the felidae. J Infect Dis. 1974 Dec;130(6):557–563.

155. Davis AA, Lepczyk CA, Haman KH, Morden CW, Crow SE, Jensen N, et al. Toxoplasma gondii Detection in Fecal Samples from Domestic Cats (Felis catus) in Hawaiʻi. Pac Sci. 2018 Oct;72(4):501–511.

156. Gholipour H, Busquets N, Fernández-Aguilar X, Sánchez A, Ribas MP, De Pedro G, et al. Influenza A Virus Surveillance in the Invasive American Mink (Neovison vison) from Freshwater Ecosystems, Northern Spain. Zoonoses Public Health. 2017;64(5):363–369.

157. Ramírez-Pizarro F, Silva-de la Fuente C, Hernández-Orellana C, López J, Madrid V, Fernández Í, et al. Zoonotic pathogens in the american mink in its southernmost distribution. Vector Borne Zoonotic Dis. 2019 Jul 17;19(12):908–914.

158. Kołodziej-Sobocińska M, Dvorožňáková E, Hurníková Z, Reiterová K, Zalewski A. Seroprevalence of Echinococcus spp. and Toxocara spp. in Invasive Non-native American Mink. Ecohealth. 2020 Mar;17(1):13–27.

159. Barros M, Sáenz L, Lapierre L, Nuñez C, Medina-Vogel G. High prevalence of pathogenic Leptospira in alien American mink (Neovison vison) in Patagonia. Rev chil hist nat. 2014 Dec;87(1):19.

160. Ribas MP, Almería S, Fernández-Aguilar X, De Pedro G, Lizarraga P, Alarcia-Alejos O, et al. Tracking Toxoplasma gondii in freshwater ecosystems: interaction with the invasive American mink (Neovison vison) in Spain. Parasitol Res. 2018 Jul;117(7):2275–2281.

161. Horimoto T, Maeda K, Murakami S, Kiso M, Iwatsuki-Horimoto K, Sashika M, et al. Highly pathogenic avian influenza virus infection in feral raccoons, Japan. Emerging Infect Dis. 2011 Apr;17(4):714–717.

162. Al-Sabi MNS, Chriél M, Hansen MS, Enemark HL. Baylisascaris procyonis in wild raccoons (Procyon lotor) in Denmark. Vet Parasitol Reg Stud Reports. 2015 Dec;1-2:55–58.

163. Rentería-Solís Z, Birka S, Schmäschke R, Król N, Obiegala A. First detection of Baylisascaris procyonis in wild raccoons (Procyon lotor) from Leipzig, Saxony, Eastern Germany. Parasitol Res. 2018 Oct;117(10):3289–3292.

164. Bauer C. Baylisascariosis (Baylisascaris procyonis) - a rare parasitic zoonosis in Europe. Berliner Und Munchener Tierarztliche Wochenschrift. 2011;124(11-12):465–472.

165. Xie Y, Zhou X, Li M, Liu T, Gu X, Wang T, et al. Zoonotic*Baylisascaris procyonis* Roundworms in Raccoons, China. Emerging Infect Dis. 2014 Dec;20(12):2170–2172.

166. Karamon J, Kochanowski M, Cencek T, Bartoszewicz M, Kusyk P. Gastrointestinal helminths of raccoons (Procyon lotor) in western Poland (Lubuskie province) - with particular regard to Baylisascaris procyonis. Bulletin of the Veterinary Institute in Pulawy. 2014 Dec 1;58(4):547–552.

167. Davidson RK, Øines Ø, Hamnes IS, Schulze JE. Illegal wildlife imports more than just animals-- Baylisascaris procyonis in raccoons (Procyon lotor) in Norway. J Wildl Dis. 2013 Oct;49(4):986–990.

168. Sato H, Kamiya H, Furuoka H. Epidemiological aspects of the first outbreak of Baylisascaris procyonis larva migrans in rabbits in Japan. Journal of Veterinary Medical Science. 2003;65(4):453–457.

169. Küchle M, Knorr HL, Medenblik-Frysch S, Weber A, Bauer C, Naumann GO. Diffuse unilateral subacute neuroretinitis syndrome in a German most likely caused by the raccoon roundworm, Baylisascaris procyonis. Graefes Arch Clin Exp Ophthalmol. 1993;231(1):48–51.

170. Asakawa M, Matoba Y, Yamada D, Kamiyama T. Review of the parasitological state of feral raccoons captured in Nopporo National Park and its proximity, Hokkaido. Journal of Rakuno Gakuen University Natural Science. 2000;25(1):1–8.

171. Lee K, Iwata T, Nakadai A, Kato T, Hayama S, Taniguchi T, et al. Prevalence of Salmonella, Yersinia and Campylobacter spp. in feral raccoons (Procyon lotor) and masked palm civets (Paguma larvata) in Japan. Zoonoses Public Health. 2011 Sep;58(6):424–431.

172. Inoue K, Kabeya H, Fujita H, Makino T, Asano M, Inoue S, et al. Serological survey of five zoonoses, scrub typhus, Japanese spotted fever, tularemia, Lyme disease, and Q fever, in feral raccoons (Procyon lotor) in Japan. Vector Borne Zoonotic Dis. 2011 Jan;11(1):15–19.

173. Leśniańska K, Perec-Matysiak A, Hildebrand J, Buńkowska-Gawlik K, Piróg A, Popiołek M. Cryptosporidium spp. and Enterocytozoon bieneusi in introduced raccoons (Procyon lotor)- first evidence from Poland and Germany. Parasitol Res. 2016 Dec;115(12):4535–4541.

174. Nowakiewicz A, Zięba P, Ziółkowska G, Gnat S, Muszyńska M, Tomczuk K, et al. Free-Living Species of Carnivorous Mammals in Poland: Red Fox, Beech Marten, and Raccoon as a Potential Reservoir of Salmonella, Yersinia, Listeria spp. and Coagulase-Positive Staphylococcus. PLoS One. 2016 May 12;11(5):e0155533.

175. Stolte M, Odening K, Walter G. The raccoon as intermediate host of three Sarcocystis species in Europe. Journal of the Helminthological Society of Washington. 1996;63(1):145–149.

176. Sato H, Suzuki K, Osanai A, Kamiya H, Furuoka H. Identification and characterization of the threadworm, Strongyloides procyonis, from feral raccoons (Procyon lotor) in Japan. J Parasitol. 2006 Feb;92(1):63–68.

177. Baumeister S, Pohlmeyer K, Kuschfeldt S, Stoye M. On the prevalence of Echinococcus multilocularis and other metacestodes and cestodes in the muskrat (Ondatra zibethicus Link, 1795) in Lower Saxony. Deutsche Tierarztliche Wochenschrift. 1997;104(10):448–452.

178. Sinski E, Bednarska M, Bajer A. The role of wild rodents in ecology of cryptosporidiosis in Poland. Folia Parasitologica. 1998;45(2):173–174.

179. Boussinesq M, Bresson S, Liance M, Houin R. [A new natural intermediate host of Echinococcus multilocularis in France: the muskrat (Ondatra zibethicus L.)]. Ann Parasitol Hum Comp. 1986;61(4):431–434.

180. Umhang G, Richomme C, Boucher J-M, Guedon G, Boué F. Nutrias and muskrats as bioindicators for the presence of Echinococcus multilocularis in new endemic areas. Vet Parasitol. 2013 Oct 18;197(1-2):283–287.

181. Karanis P, Opiela K, Renoth S, Seitz HM. Possible contamination of surface waters with Giardia spp through muskrats. Zentralblatt Fur Bakteriologie-International Journal of Medical Microbiology Virology Parasitology and Infectious Diseases. 1996;284(2-3):302–306.

182. Vahlenkamp M, Müller T, Tackmann K, Löschner U, Schmitz H, Schreiber M. The muskrat (Ondatra zibethicus) as a new reservoir for puumala-like hantavirus strains in Europe. Virus Res. 1998 Oct;57(2):139–150.

183. Lataste-Dorolle C, Fiocre B. [Muskrats, Ondatra (Fiber zibethicus, Linnaeus), carriers in France of various leptospirian serotypes: isolation of the 1st French strain related to the Hebdomadis serogroup]. Bull Soc Pathol Exot Filiales. 1969;62(2):312–20.

184. Lim SR, Lee D-H, Park SY, Lee S, Kim HY, Lee M-S, et al. Wild Nutria (Myocastor coypus) Is a Potential Reservoir of Carbapenem-Resistant and Zoonotic Aeromonas spp. in Korea. Microorganisms. 2019 Jul 30;7(8).

185. Asakawa M, Sato M, Sone K, Tatsuzawa S, Oda S. Further helminthological survey on alien rodents, coypu (Myocastor coypus: Myocastoridae) in Aichi and Hyogo Prefectures, Japan. Journal of Rakuno Gakuen University Natural Science. 2009;33(2):291–292.

186. Nardoni S, Angelici MC, Mugnaini L, Mancianti F. Prevalence of Toxoplasma gondii infection in Myocastor coypus in a protected Italian wetland. Parasit Vectors. 2011 Dec 23;4:240.

187. Diagne C, Galan M, Tamisier L, d Ambrosio J, Dalecky A, Bâ K, et al. Ecological and sanitary impacts of bacterial communities associated to biological invasions in African commensal rodent communities. Sci Rep. 2017 Nov 3;7(1):14995.

188. Chakma S, Picard J, Duffy R, Constantinoiu C, Gummow B. A Survey of Zoonotic Pathogens Carried by Non-Indigenous Rodents at the Interface of the Wet Tropics of North Queensland, Australia. Transbound Emerg Dis. 2017 Feb;64(1):185–193.

189. Diagne CA, Charbonnel N, Henttonen H, Sironen T, Brouat C. Serological survey of zoonotic viruses in invasive and native commensal rodents in senegal, west africa. Vector Borne Zoonotic Dis. 2017 Sep 5;17(10):730–733.

190. Dahmana H, Granjon L, Diagne C, Davoust B, Fenollar F, Mediannikov O. Rodents as hosts of pathogens and related zoonotic disease risk. Pathogens. 2020 Mar 10;9(3).

191. Hancke D, Suárez OV. Helminth Diversity in Synanthropic Rodents from an Urban Ecosystem. Ecohealth. 2017 Apr 17;14(3):603–613.

192. Benavidez KM, Guerra T, Torres M, Rodriguez D, Veech JA, Hahn D, et al. The prevalence of Leptospira among invasive small mammals on Puerto Rican cattle farms. PLoS Negl Trop Dis. 2019 May 20;13(5):e0007236.

193. Correa JP, Bucarey SA, Cattan PE, Landaeta-Aqueveque C, Ramírez-Estrada J. Renal carriage of Leptospira species in rodents from Mediterranean Chile: The Norway rat (Rattus norvegicus) as a relevant host in agricultural lands. Acta Trop. 2017 Dec;176:105–108.

194. Galal L, Sarr A, Cuny T, Brouat C, Coulibaly F, Sembène M, et al. The introduction of new hosts with human trade shapes the extant distribution of Toxoplasma gondii lineages. PLoS Negl Trop Dis. 2019 Jul 11;13(7):e0007435.

195. Tatard C, Garba M, Gauthier P, Hima K, Artige E, Dossou DKHJ, et al. Rodent-borne Trypanosoma from cities and villages of Niger and Nigeria: A special role for the invasive genus Rattus? Acta Trop. 2017 Jul;171:151–158.

196. Nakamura M, Takahashi K, Taira K, Taira M, Ohno A, Sakugawa H, et al. Hepatitis E virus infection in wild mongooses of Okinawa, Japan: Demonstration of anti-HEV antibodies and a full-genome nucleotide sequence. Hepatol Res. 2006 Mar;34(3):137–140.

197. Takeuchi-Storm N, Al-Sabi MNS, Thamsborg SM, Enemark HL. *Alaria alata* Mesocercariae among Feral Cats and Badgers, Denmark. Emerging Infect Dis. 2015 Oct;20(10):1872–1874.

198. Adams WH, Emmons RW, Brooks JE. The changing ecology of murine (endemic) typhus in Southern California. Am J Trop Med Hyg. 1970 Mar;19(2):311–318.

199. Cuervo PF, Cataldo SD, Fantozzi MC, Deis E, Isenrath GD, Viberti G, et al. Liver fluke (Fasciola hepatica) naturally infecting introduced European brown hare (Lepus europaeus) in northern Patagonia: phenotype, prevalence and potential risk. Acta Parasitol. 2015 Sep;60(3):536–543.

200. Whitehouse CA, Keirstead N, Taylor J, Reinhardt JL, Beierschmitt A. Prevalence of hypermucoid Klebsiella pneumoniae among wild-caught and captive vervet monkeys (Chlorocebus aethiops sabaeus) on the island of St. Kitts. J Wildl Dis. 2010 Jul;46(3):971–976.

201. Jensen K, Alvarado-Ramy F, González-Martínez J, Kraiselburd E, Rullán J. B-virus and free-ranging macaques, Puerto Rico. Emerging Infect Dis. 2004 Mar;10(3):494–496.

202. Wisely SM, Sayler KA, Anderson CJ, Boyce CL, Klegarth AR, Johnson SA. Macacine Herpesvirus 1 Antibody Prevalence and DNA Shedding among Invasive Rhesus Macaques, Silver Springs State Park, Florida, USA. Emerging Infect Dis. 2018;24(2):345–351.

203. Basso W, Rütten M, Deplazes P, Grimm F. Generalized Taenia crassiceps cysticercosis in a chinchilla (Chinchilla lanigera). Vet Parasitol. 2014 Jan 17;199(1-2):116–120.

204. Shiokawa K, Llanes A, Hindoyan A, Cruz-Martinez L, Welcome S, Rajeev S. Peridomestic small Indian mongoose: An invasive species posing as potential zoonotic risk for leptospirosis in the Caribbean. Acta Trop. 2019 Feb;190:166–170.

205. Schlottau K, Hoffmann B, Homeier-Bachmann T, Fast C, Ulrich RG, Beer M, et al. Multiple detection of zoonotic variegated squirrel bornavirus 1 RNA in different squirrel species suggests a possible unknown origin for the virus. Arch Virol. 2017 Sep;162(9):2747–2754.

206. Millins C, Magierecka A, Gilbert L, Edoff A, Brereton A, Kilbride E, et al. An Invasive Mammal (the Gray Squirrel, Sciurus carolinensis) Commonly Hosts Diverse and Atypical Genotypes of the Zoonotic Pathogen Borrelia burgdorferi Sensu Lato. Appl Environ Microbiol. 2015 Jul;81(13):4236–4245.

207. Romeo C, Lecollinet S, Caballero J, Isla J, Luzzago C, Ferrari N, et al. Are tree squirrels involved in the circulation of flaviviruses in Italy? Transbound Emerg Dis. 2018 Oct;65(5):1372–1376.

208. Tappe D, Schmidt-Chanasit J, Rauch J, Allartz P, Herden C. Immunopathology of Fatal Human Variegated Squirrel Bornavirus 1 Encephalitis, Germany, 2011-2013. Emerging Infect Dis. 2019;25(6):1058–1065.

209. Jacquot M, Abrial D, Gasqui P, Bord S, Marsot M, Masseglia S, et al. Multiple independent transmission cycles of a tick-borne pathogen within a local host community. Sci Rep. 2016 Aug 8;6:31273.

210. Reeves WK, Durden LA, Dasch GA. A Spotted Fever Group *Rickettsia* from an Exotic Tick Species, *Amblyomma exornatum* (Acari: Ixodidae), in a Reptile Breeding Facility in the United States. ME. 2006 Sep 1;43(5):1099–1101.

211. Reeves WK, Easterbrook JD, Loftis AD, Glass GE. Serologic evidence for Rickettsia typhi and an ehrlichial agent in Norway rats from Baltimore, Maryland, USA. Vector Borne Zoonotic Dis. 2006;6(3):244–247.

212. Chikweto A, Bhaiyat MI, Macpherson CNL, Deallie C, Pinckney RD, Richards C, et al. Existence of Angiostrongylus cantonensis in rats (Rattus norvegicus) in Grenada, West Indies. Vet Parasitol. 2009 May 26;162(1-2):160–162.

213. Julius RS, Schwan EV, Chimimba CT. Helminth composition and prevalence of indigenous and invasive synanthropic murid rodents in urban areas of Gauteng Province, South Africa. J Helminthol. 2017 Sep 4;1–10.

214. Easterbrook JD, Kaplan JB, Vanasco NB, Reeves WK, Purcell RH, Kosoy MY, et al. A survey of zoonotic pathogens carried by Norway rats in Baltimore, Maryland, USA. Epidemiol Infect. 2007 Oct;135(7):1192–1199.

215. Smith HM, Reporter R, Rood MP, Linscott AJ, Mascola LM, Hogrefe W, et al. Prevalence study of antibody to ratborne pathogens and other agents among patients using a free clinic in downtown Los Angeles. J Infect Dis. 2002 Dec 1;186(11):1673–1676.

216. Rothenburger JL, Himsworth CG, La Perle KMD, Leighton FA, Nemeth NM, Treuting PM, et al. Pathology of wild Norway rats in Vancouver, Canada. J Vet Diagn Invest. 2019 Mar;31(2):184–199.

217. HARVEY DA, MACNEILL AC. A SURVEY OF ZOONOTIC DISEASES AND ARTHROPOD VECTORS ISOLATED FROM LIVE-TRAPPED NORWAY RATS (RATTUS-NORVEGICUS) IN THE MUNICIPALITY OF RICHMOND, BRITISH-COLUMBIA. Canadian Journal of Public Health-Revue Canadienne De Sante Publique. 1984;75(5):374–378.

218. YANAGIHARA R. HANTAVIRUS INFECTION IN THE UNITED-STATES - EPIZOOTIOLOGY AND EPIDEMIOLOGY. Reviews of Infectious Diseases. 1990;12(3):449–457.

219. Burek KA, Rossi CA, Leduc JW, Yuill TM. Serologic and virologic evidence of a Prospect Hill-like hantavirus in Wisconsin and Minnesota. Am J Trop Med Hyg. 1994 Sep;51(3):286–294.

220. Kabrane-Lazizi Y, Fine JB, Elm J, Glass GE, Higa H, Diwan A, et al. Evidence for widespread infection of wild rats with hepatitis E virus in the United States. Am J Trop Med Hyg. 1999 Aug;61(2):331–335.

221. Dybing NA, Jacobson C, Irwin P, Algar D, Adams PJ. Challenging the dogma of the "Island Syndrome": a study of helminth parasites of feral cats and black rats on Christmas Island. Australasian Journal of Environmental Management. 2018 Jan 2;25(1):99–118.

222. Stokes VL, Spratt DM, Banks PB, Pech RP, Williams RL. Occurrence of Angiostrongylus species (Nematoda) in populations of Rattus rattus and Rattus fuscipes in coastal forests of south-eastern Australia. Aust J Zool. 2007;55(3):177.

223. Wallace GD, Rosen L. Studies on eosinophilic meningitis. i. observations on the geographic distribution of angiostrongylus cantonensis in the pacific area and its prevalence in wild rats. Am J Epidemiol. 1965 Jan;81:52–62.

224. Fratini S, Natali C, Zanet S, Iannucci A, Capizzi D, Sinibaldi I, et al. Assessment of rodenticide resistance, eradication units, and pathogen prevalence in black rat populations from a Mediterranean biodiversity hotspot (Pontine Archipelago). Biol Invasions. 2020 Apr;22(4):1379–1395.

225. Moreno Salas L, Espinoza-Carniglia M, Lizama Schmeisser N, Torres LG, Silva-de la Fuente MC, Lareschi M, et al. Fleas of black rats (Rattus rattus) as reservoir host of Bartonella spp. in Chile. PeerJ. 2019 Aug 1;7:e7371.

226. Billeter SA, Borchert JN, Atiku LA, Mpanga JT, Gage KL, Kosoy MY. Bartonella species in invasive rats and indigenous rodents from Uganda. Vector Borne Zoonotic Dis. 2014 Mar;14(3):182–188.

227. Brook CE, Bai Y, Yu EO, Ranaivoson HC, Shin H, Dobson AP, et al. Elucidating transmission dynamics and host-parasite-vector relationships for rodent-borne Bartonella spp. in Madagascar. Epidemics. 2017 Mar 16;20:56–66.

228. Peavy CA, Lane RS, Kleinjan JE. Role of small mammals in the ecology of Borrelia burgdorferi in a peri-urban park in north coastal California. Exp Appl Acarol. 1997 Aug;21(8):569–584.

229. Berentsen AR, Vogt S, Guzman AN, Vice DS, Pitt WC, Shiels AB, et al. Capillaria hepatica infection in black rats (Rattus rattus) on Diego Garcia, British Indian Ocean Territory. J Vet Diagn Invest. 2015 Mar;27(2):241–244.

230. Cassan C, Diagne CA, Tatard C, Gauthier P, Dalecky A, Bâ K, et al. Leishmania major and Trypanosoma lewisi infection in invasive and native rodents in Senegal. PLoS Negl Trop Dis. 2018 Jun 29;12(6):e0006615.

231. Dietrich M, Gomard Y, Lagadec E, Ramasindrazana B, Le Minter G, Guernier V, et al. Biogeography of Leptospira in wild animal communities inhabiting the insular ecosystem of the western Indian Ocean islands and neighboring Africa. Emerg Microbes Infect. 2018 Apr 4;7(1):57.

232. Blasdell KR, Morand S, Perera D, Firth C. Association of rodent-borne Leptospira spp. with urban environments in Malaysian Borneo. PLoS Negl Trop Dis. 2019 Feb 27;13(2):e0007141.

233. Glass GE, Livingstone W, Mills JN, Hlady WG, Fine JB, Biggler W, et al. Black Creek Canal Virus infection in Sigmodon hispidus in southern Florida. Am J Trop Med Hyg. 1998 Nov;59(5):699–703.

234. Costa DGC, Marvulo MFV, Silva JSA, Santana SC, Magalhães FJR, Filho CDFL, et al. Seroprevalence of Toxoplasma gondii in domestic and wild animals from the Fernando de Noronha, Brazil. J Parasitol. 2012 Jun;98(3):679–680.

235. Dobigny G, Poirier P, Hima K, Cabaret O, Gauthier P, Tatard C, et al. Molecular survey of rodent-borne Trypanosoma in Niger with special emphasis on T. lewisi imported by invasive black rats. Acta Trop. 2011 Mar;117(3):183–188.

236. Dobigny G, Gauthier P, Houéménou G, Dossou HJ, Badou S, Etougbétché J, et al. Spatio-temporal survey of small mammal-borne Trypanosoma lewisi in Cotonou, Benin, and the potential risk of human infection. Infect Genet Evol. 2019 Jul 22;75:103967.

237. Dietrich G, Montenieri JA, Panella NA, Langevin S, Lasater SE, Klenk K, et al. Serologic evidence of west nile virus infection in free-ranging mammals, Slidell, Louisiana, 2002. Vector Borne Zoonotic Dis. 2005;5(3):288–292.

238. Puthiyakunnon S, Boddu S, Li Y, Zhou X, Wang C, Li J, et al. Strongyloidiasis--an insight into its global prevalence and management. PLoS Negl Trop Dis. 2014 Aug 14;8(8):e3018.

239. Allan BF, Dutra HP, Goessling LS, Barnett K, Chase JM, Marquis RJ, et al. Invasive honeysuckle eradication reduces tick-borne disease risk by altering host dynamics. Proc Natl Acad Sci USA. 2010 Oct 26;107(43):18523–18527.

240. Civitello DJ, Flory SL, Clay K. Exotic Grass Invasion Reduces Survival of *Amblyomma americanum* and *Dermacentor variabilis* Ticks (Acari: Ixodidae). J Med Entomol. 2008 Sep 1;45(5):867–872.

241. Mackay AJ, Muturi EJ, Ward MP, Allan BF. Cascade of ecological consequences for West Nile virus transmission when aquatic macrophytes invade stormwater habitats. Ecol Appl. 2016 Jan;26(1):219–232.

242. Hoyer IJ, Blosser EM, Acevedo C, Thompson AC, Reeves LE, Burkett-Cadena ND. Mammal decline, linked to invasive Burmese python, shifts host use of vector mosquito towards reservoir hosts of a zoonotic disease. Biol Lett. 2017 Oct;13(10).

243. Swei A, Briggs CJ, Lane RS, Ostfeld RS. Impacts of an introduced forest pathogen on the risk of Lyme disease in California. Vector Borne Zoonotic Dis. 2012 Aug;12(8):623–632.

244. Fuehrer H-P, Auer H, Leschnik M, Silbermayr K, Duscher G, Joachim A. Dirofilaria in Humans, Dogs, and Vectors in Austria (1978-2014)-From Imported Pathogens to the Endemicity of Dirofilaria repens. PLoS Negl Trop Dis. 2016 May 19;10(5):e0004547.

245. Dunbar M, Lu S, Chin B, Huh L, Dobson S, Al-Rawahi GN, et al. Baylisascariasis: A young boy with neural larva migrans due to the emerging raccoon round worm. Ann Clin Transl Neurol. 2019;6(2):397–400.

246. Pace A, Dipineto L, Aceto S, Censullo MC, Valoroso MC, Varriale L, et al. Diagnosis of Centrocestus formosanus Infection in Zebrafish (Danio rerio) in Italy: A Window to a New Globalization-Derived Invasive Microorganism. Animals (Basel). 2020 Mar 9;10(3).

247. Kuchta R, Esteban J-G, Brabec J, Scholz T. Misidentification of diphyllobothrium species related to global fish trade, Europe. Emerging Infect Dis. 2014 Nov;20(11):1955–1957.

248. Torgerson PR, Devleesschauwer B, Praet N, Speybroeck N, Willingham AL, Kasuga F, et al. World health organization estimates of the global and regional disease burden of 11 foodborne parasitic diseases, 2010: A data synthesis. PLoS Med. 2015 Dec 3;12(12):e1001920.

249. Kurth A, Straube M, Kuczka A, Dunsche AJ, Meyer H, Nitsche A. Cowpox virus outbreak in banded mongooses (Mungos mungo) and jaguarundis (Herpailurus yagouaroundi) with a time-delayed infection to humans. PLoS One. 2009 Sep 3;4(9):e6883.

250. Higgins R, Messier S, Daignault D, Lorange M. Arcobacter butzleri isolated from a diarrhoeic non-human primate. Lab Anim. 1999 Jan;33(1):87–90.

251. Stam F, Römkens TEH, Hekker TAM, Smulders YM. Turtle-associated human salmonellosis. Clin Infect Dis. 2003 Dec 1;37(11):e167–9.

252. Soares RM, de Souza SLP, Silveira LH, Funada MR, Richtzenhain LJ, Gennari SM. Genotyping of potentially zoonotic Giardia duodenalis from exotic and wild animals kept in captivity in Brazil. Vet Parasitol. 2011 Aug 25;180(3-4):344–348.

253. Fevre EM. Animal movements and the spread of infectious diseases. Trends Microbiol. 2006 Mar;14(3):125–131.

254. Mihalca AD. Ticks imported to Europe with exotic reptiles. Vet Parasitol. 2015 Sep 30;213(1-2):67–71.

255. Scalera R. Report on alien pathogens and pathogens spread by invasive alien species in Europe. Convention on the Conservation of European wildlife and natural habitats. European Commission; 2019 p. 25. Report No.: T-PVS/Inf(2019)18.

256. Schaffner F, Bellini R, Petrić D, Scholte E-J, Zeller H, Rakotoarivony LM. Development of guidelines for the surveillance of invasive mosquitoes in Europe. Parasit Vectors. 2013 Jul 18;6:209.

257. Goka K, Okabe K, Takano A. Recent cases of invasive alien mites and ticks in Japan: why is a regulatory framework needed? Exp Appl Acarol. 2013 Feb;59(1-2):245–261.

258. United Nations Environment Programme and International Livestock Research Institute. Preventingthe Next Pandemic: Zoonotic diseases and how to break the chain oftransmission. . Nairobi, Kenya: UNEP & ILRI; 2020 p. 82.

259. Mulder AC, Kroneman A, Franz E, Vennema H, Tulen AD, Takkinen J, et al. HEVnet: a One Health, collaborative, interdisciplinary network and sequence data repository for enhanced hepatitis E virus molecular typing, characterisation and epidemiological investigations. Euro Surveill. 2019 Mar;24(10).

260. Babo Martins S, Rushton J, Stärk KDC. Economics of zoonoses surveillance in a "One Health" context: an assessment of Campylobacter surveillance in Switzerland. Epidemiol Infect. 2017 Jan 23;145(6):1148–1158.

261. Ogden NH, Wilson JRU, Richardson DM, Hui C, Davies SJ, Kumschick S, et al. Emerging infectious diseases and biological invasions: a call for a One Health collaboration in science and management. R Soc Open Sci. 2019 Mar 13;6(3):181577.

262. Wardeh M, Risley C, McIntyre MK, Setzkorn C, Baylis M. Database of host-pathogen and related species interactions, and their global distribution. Sci Data. 2015 Sep 15;2:150049.

263. Mazza G, Tricarico E, editors. Invasive species and human health. Wallingford: CABI; 2018.

264. Ogden NH, AbdelMalik P, Pulliam J. Emerging infectious diseases: prediction and detection. Can Commun Dis Rep. 2017 Oct 5;43(10):206–211.

265. Roy HE, Peyton J, Aldridge DC, Bantock T, Blackburn TM, Britton R, et al. Horizon scanning for invasive alien species with the potential to threaten biodiversity in Great Britain. Glob Change Biol. 2014 Dec;20(12):3859–3871.

266. D'hondt B, Vanderhoeven S, Roelandt S, Mayer F, Versteirt V, Adriaens T, et al. Harmonia + and Pandora +: risk screening tools for potentially invasive plants, animals and their pathogens. Biol Invasions. 2015 Jun;17(6):1869–1883.

267. Han BA, Schmidt JP, Bowden SE, Drake JM. Rodent reservoirs of future zoonotic diseases. Proc Natl Acad Sci USA. 2015 Jun 2;112(22):7039–7044.

268. Evans MV, Dallas TA, Han BA, Murdock CC, Drake JM. Data-driven identification of potential Zika virus vectors. Elife. 2017 Feb 28;6.

269. Bodin Ö, Alexander SM, Baggio J, Barnes ML, Berardo R, Cumming GS, et al. Improving network approaches to the study of complex social–ecological interdependencies. Nat Sustain. 2019 Jul;2(7):551–559.

270. Dee LE, Allesina S, Bonn A, Eklöf A, Gaines SD, Hines J, et al. Operationalizing network theory for ecosystem service assessments. Trends Ecol Evol (Amst). 2017;32(2):118–130.

271. Wardeh M, Sharkey KJ, Baylis M. Integration of shared-pathogen networks and machine learning reveals the key aspects of zoonoses and predicts mammalian reservoirs. Proc Biol Sci. 2020 Feb 12;287(1920):20192882.

Appendix 1. Summary of studies in which pathogen / parasite prevalence and roles in transmission were compared between IAS (and other alien species) and native hosts

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
Insecta	Diptera: Culicidae	*Aedes aegypti*	Yellow fever mosquito	*Ae. triseriatus*	Eastern tree hole mosquito	Eastern equine encephalitis	Virus	IAS ~ native	United States (Massachussets)	(53)
Insecta	Diptera: Culicidae	*Aedes albopictus*	Asian tiger mosquito	*Ae. triseriatus*	Eastern tree hole mosquito	Eastern equine encephalitis	Virus	IAS ~ native	United States (Massachussets)	(53)
Insecta	Diptera: Culicidae	*Aedes japonicus japonicus*	Rock pool mosquito	*Ae. triseriatus*	Eastern tree hole mosquito	Cache Valley virus	Virus	IAS ~ native	United States (Virginia)	(54)
Aves	Columbiformes : Columbidae	*Columba livia*	Pigeon	*Carpodacus mexicanus*	House finches	St. Louis encephalitis (SLE)	Virus	IAS > native	United States (California)	(68)
Aves	Columbiformes : Columbidae	*Columba livia*	Pigeon	*Carpodacus mexicanus*	House finches	Western equine encephalomyelitis (WEE)	Virus	IAS > native	United States (California)	(68)
Aves	Galliformes: Phasianidae	*Alectoris chukar*	chukar partridge	*Colinus virginianus*	Bobwhite quail	Chlamydia psittaci	Bacteria	IAS ~ native	United States (Kentucky)	(83)
Aves	Passeriformes: Passeridae	*Passer domesticus*	House sparrow	*Carpodacus mexicanus*	House finches	St. Louis encephalitis (SLE)	Virus	IAS ~ native	United States (California)	(68)
Aves	Passeriformes: Passeridae	*Passer domesticus*	House sparrow	*Carpodacus mexicanus*	House finches	Western equine encephalomyelitis (WEE)	Virus	IAS ~ native	United States (California)	(68)
Mammalia	Artiodactyla: Suidae	*Sus scrofa*	feral swine	*Isoodon macrourus*	Northern brown bandicoot	Coxiella burnetii	Bacteria	IAS ~ native	Australia	(108)
Mammalia	Carnivora: Canidae	*Canis lupus dingo*	dingo	*Isoodon macrourus*	Northern brown bandicoot	Coxiella burnetii	Bacteria	IAS < native	Australia	(108)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Alaria alata	Intestinal helminths	IAS ~ native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Alaria alata; Brachylaima tokudai; Cryptocotyle spp.; Dipylidium caninum; Echinococcus multilocularis; Mesocestoides spp.; Mesorchis denticulatus; Pygidiopsis summa; Taenia spp.; Toxocara	Platyhelminthes	Multiple pathogens and varies with pathogens	Denmark	(127)

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
						canis; Trichinella spp.; Uncinaria stenocephala				
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Alaria alata; Capillaria plica; Capillaria putorii Crenosoma vulpis; Echinococcus multilocularis; Eucoleus aerophilus; Mesocestoides spp.; Taenia polyacantha, T. crassiceps; Toxocara canis; Trichinella spp.; Uncinaria stenocephala	Nematoda; Platyhelminthes	Multiple pathogens and varies with pathogen	Lithuania	(128)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Anaplasma phagocytophilum	Bacteria	IAS > native	Germany	(130)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Apophallus spp.	Intestinal helminths	IAS > native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Echinoccocus multilocularis	Intestinal helminths	IAS < native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Echinococcus multilocularis	Tapeworm	IAS < native	Germany	(131)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Echinococcus multilocularis	Tapeworm	IAS < native	Estonia	(133)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Francisella tularensis	Bacteria	IAS < native	Germany	(135)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	hookworms	Intestinal helminths	IAS > native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Mesocestoides spp.	Intestinal helminths	IAS < native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Rabies	Virus	IAS ~ native	Lithuania	(138)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Rabies	Virus	IAS < native	Lithuania	(139)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Rabies	Virus	IAS < native	Poland	(140)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Martes martes*	Pine marten	Rabies	Virus	IAS > native	Poland	(140)

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Rabies	Virus	IAS > native	Poland	(141)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Rabies	Virus	IAS < native	Poland	(142)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	rabies (Genotype 1, RABV)	Virus	IAS ~ native	Lithuania	(143)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Taenia spp.	Intestinal helminths	IAS < native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Toxicara/Toxicaris	Intestinal helminths	IAS < native	Poland	(125)
Mammalia	Carnivora: Canidae	*Nyctereutes procyonoides*	Raccoon dog	*Vulpes vulpes*	Red fox	Trichinella	Roundworm	IAS ~ native	Lithuania, Lativa, Estonia	(144)
Mammalia	Carnivora: Canidae	*Vulpes vulpes*	Red fox	*Isoodon macrourus*	Northern brown bandicoot	Coxiella burnetii	Bacteria	IAS > native	Australia	(108)
Mammalia	Carnivora: Felidae	*Felis catus*	Feral cat	*Isoodon macrourus*	Northern brown bandicoot	Coxiella burnetii	Bacteria	IAS > native	Australia	(108)
Mammalia	Rodentia: Muridae	*Gerbillus nigeriae*	Nigerian gerbil	*Various*		Borrelia crocidurae	Bacteria	IAS ~ native	Senegal	(190)
Mammalia	Rodentia: Muridae	*Mus musculus*	House mouse	*Various*		Hepatozoon canis	Protozoa	IAS > native	Senegal	(190)
Mammalia	Rodentia: Muridae	*Mus musculus*	House mouse	*Various*		Leptospira	Bacteria	IAS > native	Madagascar	(29)
Mammalia	Rodentia: Muridae	*Mus musculus*	House mouse	*Abrothrix olivaceus*	Olive grass mouse	Leptospira spp;	Bacteria	IAS > native	Chile	(193)
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Cricetomys gambianus*	Gambian pouch rat	Trypanosoma lewis	Protozoa	IAS > native	Niger; Nigeria	(195)
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Mastomys coucha*	Southern multimammate mouse	Aspiculuris tetraptera; Eucoleus sp.; Heterakis spumosa; Mastophorus muris; Nippostrongylus brasiliensis; Protospirura sp.; Strongyloides ratti; Syphacia obvelata; Syphacia muris; Trichuris sp.; Trichosomoides crassicauda; Hymenolepis diminuta; Hymenolepis nana;	Nematoda; Platyhelminthes	IAS > native	South Africa	(213)

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
						Inermicapsifer madagascariensis; Hydatigera taeniaeformis				
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Various*		Hantavirus	Virus	IAS > native	United States (Minnesota, Winsconsin)	(219)
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Mastomys coucha*	Southern multimammate mouse	Hymenolepis diminuta; Hymenolepis nana;	Nematoda; Platyhelminthes	IAS > native	South Africa	
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Various*		Leptospira	Bacteria	IAS > native	Madagascar	(29)
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Abrothrix olivaceus*	Olive grass mouse	Leptospira spp;	Bacteria	IAS > native	Chile	(193)
Mammalia	Rodentia: Muridae	*Rattus norvegicus*	Norway rat	*Cricetomys gambianus*	Gambian pouch rat	Trypanosoma lewis	Protozoa	IAS > native	Niger; Nigeria	(195)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Cricetomys gambianus*	Gambian pouch rat	Trypanosoma lewis	Protozoa	IAS < native	Niger; Nigeria	(195)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Mastomys coucha*	Southern multimammate mouse	Aspiculuris tetraptera; Eucoleus sp.; Heterakis spumosa; Mastophorus muris; Nippostrongylus brasiliensis; Protospirura sp.; Strongyloides ratti; Syphacia obvelata; Syphacia muris; Trichuris sp.; Trichosomoides crassicauda; Hymenolepis diminuta; Hymenolepis nana; Inermicapsifer madagascariensis; Hydatigera taeniaeformis; Moniliformis moniliformis	Nematoda; Platyhelminthes; Acanthocephala	IAS > native	South Africa	(213)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Arvicanthis niloticus*		Bartonella spp.	Bacteria	Uganda	Also Cricetomys gambianus	(226)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Borrelia burgorferi	Bacteria	IAS > native	United States (California)	(228)

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Mastomys coucha*	Southern multimammate mouse	Hymenolepis diminuta; Hymenolepis nana;	Nematoda; Platyhelminthes; Acanthocephala	IAS > native	South Africa	(213)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Leishmania spp.	Trypanosome	IAS > native	Senegal	(230)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Leptospira	Bacteria	IAS > native	Madagascar	(29)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Leptospira	Bacteria	IAS > native	La Réunion, Mauritius, Seychelles, South Africa, Swaziland, Mozambique, and Madagascar	(231)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Sundamys muelleri*	Müller's giant Sunda rat	Leptospira spp;	Bacteria	IAS > native	Malayian Borneo	(232)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Sin Nombre Virus	Virus	IAS < native	United States (Florida)	(233)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Bubulcus ibis*	Cattle egret	Toxoplasma gondii	Protozoa	IAS < native	Brazil (islands)	(234)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Cricetomys gambianus*	Gambian pouch rat	Trypanosoma lewis	Protozoa	IAS < native	Niger; Nigeria	(195)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Trypanosoma lewisi	Protozoa	IAS > native	Benin	(236)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Trypanosoma lewisi	Protozoa	IAS > native	Senegal	(230)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Various*		Trypanosoma lewisi	Protozoa	IAS > native	Niger	(235)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Sigmodon hispidus*	hispid cotton rat	West Nile Virus	Virus	IAS ~ native	United States (Louisiana)	(237)
Mammalia	Rodentia: Muridae	*Rattus rattus*	Black rat	*Sciurus carolinensis*	Eastern grey squirrel	West Nile Virus	Virus	IAS ~ native	United States (Louisiana)	(237)
Mammalia	Rodentia: Muridae	*Rattus tanezumi*	Tanezumi rat	*Mastomys coucha*	Southern multimammate mouse	Aspiculuris tetraptera; Eucoleus sp.; Heterakis spumosa; Mastophorus muris; Nippostrongylus brasiliensis;	Nematoda; Platyhelminthes	IAS > native	South Africa	(213)

Class	Order: Family	Invasive Alien Species	Common name	Native Species	Common name	Pathogen	Class of pathogen	Outcome	Country of study	Reference
						Protospirura sp.; Strongyloides ratti; Syphacia obvelata; Syphacia muris; Trichuris sp.; Trichosomoides crassicauda; Hymenolepis diminuta; Hymenolepis nana; Inermicapsifer madagascariensis; Hydatigera taeniaeformis				
Mammalia	Rodentia: Muridae	*Rattus tanezumi*	Tanezumi rat	*Mastomys coucha*	Southern multimammate mouse	Hymenolepis diminuta; Hymenolepis nana;	Nematoda; Platyhelminthes	IAS > native	South Africa	(213)
Mammalia	Rodentia: Muridae	*Suncus murinus*	shrew	*Various*		Leptospira	Bacteria	IAS > native	Madagascar	(29)
Mammalia	Rodentia: Sciuridae	*Tamias sibiricus barberi*	Siberian chipmunk	*Myodes glareolus*	Bank voles	Borrelia burgdorferi species complex;	Bacteria	IAS > native	France	(209)

Supplementary Information 1

Table of parasites encompassed in the IAS-parasite interactions, with organism, type of transmission and broad host associations and human health impact in Europe. A = aerosol transmission. C= contact transmission. O = oral transmission through food (F) or (W). V = vector-borne transmission by either flea (F), tick (T), mite (MI), lice (LI), biting flies (BF), *Triatminae* (Tri) or mosquitoes (MOS). Annual Cases is the mean number of cases reported each year to ECDC from 2012-2018 and case fatality rate is mean of case fatality rate per year reported by ECDC from 2012-2018 (where data are available).

Organism	Class	Transmission	Hosts	Cases	Case fatality (%)	References
Aeromonas spp.	Bacteria	O(W)	Fish, Mollusca, Amphibians, Reptiles,Shrimp,Livestock	-	-	1
Alaria alata	Trematode	O(F)	Red fox, wild boar, mustelids	-	-	2
Anaplasma phagocytophilum	Bacteria	V(T)	Ruminants, Rodents, Horse, Rodents, Canines, Felines	-	-	3
Anasakis simplex	Nematode	O(F)	Fish, Cephalopods,Sea mammals and birds	-	-	4
Ancylostoma spp.	Nematode	C	Felines, Canines	-	-	5
Angiostrongylus spp.	Nematode	O(F)	Rodents, Mollusca, Felines, Canids, Mustelids	-	-	6,7
Anoplocephalidae	Cestode	O	Wide host range including mites, reptiles, birds and mammals.	-	-	8
Apophallus spp.	Trematode	O(F)	Molluscs and Fish	-	-	9
Ascaridinae	Nematode	O(F)(W)	Wide host range including Cats, birds, pigs	-	-	10
Aspicularis tetraptera	Nematode	O(F)	Rodents	-	-	11
Babesia spp.	Apicomplexa	V(T)	Dogs, Rodents	-	-	12,13,14
Bartonella spp.	Bacteria	V(F)	Rodents,Felines,Ruminants, Canines	-	-	15

Baylisascaris procyonis	Nematode	O	Racoons	-	-	16
Borrelia burgdorferi	Bacteria	V(T)	Rodents	-	-	17
Borrelia spp.	Bacteria	V(T, LI)	Broad host range	-	-	18,19
Brucella spp.	Bacteria	C;O(F)	Ruminants, Canines,Pigs, Rodents	388	0.73	20
B-virus	Virus	C	Primates	-	-	21
Cache Valley Virus	Virus	V(MOS)	Broad host range including goats, sheep and cattle	-	-	22
Calodium hepatica	Nematode	O	Primarily rodent but wide host range	-	-	23
Campylobacter spp.	Bacteria	O(F)	Poultry, Ruminants, Pigs, Wild birds	233533	0.13	24
Candidatus Rickettsia senegalensis	Bacteria	V(F)		-	-	25
Capillaria hepatica	Nematode	O	Rodents, Carnivores	-	-	26
Centrocestus formosanus	Trematode	O(W)(F)	Wide range of hosts including birds mammals,.fish,Mollusca	-	-	27
Chikungunya virus	Virus	V(MOS)	Primates	-	-	28
Chlamydia spp.	Bacteria	A;C	Broad host range including Birds, Poultry and Livestock	-	-	29,30
Clonorchis sinensis	Trematode	O(W)(F)	Fish, Crustaceae, Mollusca	-	-	31
Coccidia	Apicomplexa	O	Poultry, Livestock, Domestic animals	-	-	32
Coliforms	Bacteria	C	Broad host range	-	-	33
Contracaecum bancrofti	Nematode	O(W)(F)	Fish	-	-	34
Coxiella burnetii	Bacteria	A;O(F)	Ruminants	810	0.69	35
Cryptosporidium spp.	Apicomplexa	O(W)(F)	Broad host range including mammals and birds	11043	0.01	36

Dengue	Virus	V(MOS)	Primates	16*	NA	37
Dicrocoelium dendriticum	Trematode	O	Ants, molluscs, ruminants	-	-	38
Diphyllobothrium spp.	Cestode	O(F)	Fish, Copepods, Cornivores	-	-	39
Diplogonoporus balaenopterae	Cestode	O(F)	Fish, Copepods, Cornivores	-	-	40
Dirofilaria spp.	Nematode	V(MOS)	Canines, Felines	-	-	41,42
Eastern equine encephalitis virus	Virus	V(MOS)	Horses,Birds	-	-	43
Echinococcus spp.	Cestode	O	Ruminants, Canines	815	0.64	44
Echinostomatid spp.	Trematode	O(F)	Birds,Mammals, Reptiles, Fish	-	-	45
Ehrlichia spp.	Bacteria	V(T)	Deer,Canines, Rodents	-	-	46
Entamoeba	Amoeba	C;O(W)	-	-	-	47
Enterococcus spp.	Bacteria	O	Wide host range	-	-	48
Enterocytozoon bieneusi	Fungus	O(W)	Broad host range	-	-	49
Escherichia coli	Bacteria	O(F)	Broad host range including livestock	6311	0.30	50
Eucoleus spp.	Nematode	O	Canine and Feline	-	-	51
Everglades virus	Virus	V(MOS)	Rodents	-	-	52
Fasciola hepatica	Trematode	O(W)(F)	Bovine, Mullosca	-	-	53
Francisella tularensis	Bacteria	V(T,BF,MOS)	Rodents, Squirrels, Rabbits	585	3.05	54
Giardia spp.	Diplomonad	O	Wide range of hosts Including livestock and felines and canines	18242	0.05	55
Gongylonema neoplasticum	Nematode	O	Rodents	-	-	56
Hantavirus	Virus	A;C	Small mammals	1236*	NA	57
Haplorchis pumilio	Trematode	O(F)	Fish,Canines, Felines, Pigs	-	-	58

Hepatitis E	Virus	O(F)	Broad host range including pigs, poultry, ruminants, rodents	-	-	59
Hepatozoon canis	Apicomplexa	V(T)	Dogs, hemotophagius arthropods	-	-	60
Heterakis spumosa	Nematode	O	Rodents	-	-	61
Heterophyidae	Trematode	O(F)	Wide host range fish eating mammals and birds	-	-	62
Hydatigera taeniaeformis	Cestode	O	Felines, rodents	-	-	63
Hymenolepis spp.	Cestode	O(F)	Rodents, Beetles	-	-	64,65
Inermicapsifer madagascariensis	Cestode	O	Rodents, Beetles	-	-	66
Influenza A	Virus	A;C	Wide host range including Birds, Pigs	-	-	67
Japanese encephalitis virus	Virus	V(MOS)	Wild Birds, Pigs, Horses, Bovine	-	-	68
Klebsiella pneumoniae	Bacteria	A	Birds	-	-	69
Leishmania spp.	Trypanosome	V(BF)	Canines, Rodents,	-	-	70
Leptospira spp.	Bacteria	A;C;O(W)	Broad host range including rodents, livestock, pets	725	3.08	71,72
Listeria spp	Bacteria	O(F)	Wide range of host including livestock, canines and rodents	2801	15.91	73
Macacine herpesvirus 1 (McHV-1)	Virus	C	Primates	-	-	74
Mammarenavirus	Virus	A	Rodents	-	-	75
Mastophorus muris	Nematode	O	Rodents	-	-	76
Mesocestoides spp.	Nematode	O	Canines,felines, birds,mites,rodents	-	-	77

Species	Type	Transmission	Hosts			Ref
Molineus spp.	Nematode	O	Felines, Canines	-	-	78
Moniliformis moniliformis	Acanthocephalan	O	Rodents, Felines, Canines, Cockroach	-	-	79
Mycobacterium avium	Bacteria	A	Broad host range including livestock, rodents and birds	-	-	80
Nematospiroides dubius	Nematode	O	Rodents	-	-	81
Nippostrongylus brasiliensis	Nematode	C	Rodents	-	-	82
Orientia tsutsugamushi	Bacteria	V(MI)	Mite	-	-	83
Paragonimus westermani	Platyhelminth	O(F)	Pigs,Crustaceans, Molluscs	-	-	84
Philophthalmus gralli	Platyhelminth	O(W)	Birds, Molluscs	-	-	85
Protospirura spp.	Nematode	O	Rodents, Canines, Insects	-	-	86,87
Pseudorabies virus	Virus	A;O	Swine, Ruminants, Carnivores and Rodents	-	-	88
Pterygodermatites spp.	Nematode	O	Rodents, Canines, Felines	-	-	89,90
Rabies virus	Virus	C	Canines, Racoons, Bats	1.14	100.00	91
Rickettsia aeschlimannii	Bacteria	V(T)	Ticks	-	-	92
Rickettsia conorii	Bacteria	V(T)	Ticks	-	-	93
Rickettsia japonica	Bacteria	V(T)	Rodents	-	-	94
Rickettsia typhi	Bacteria	V(F)	Rodents	-	-	95
Salmonella enterica	Bacteria	O(F)	Birds, Livestock	-	-	96
Salmonella panama	Bacteria	O(F)	Reptiles, Livestock	-	-	97
Salmonella spp.	Bacteria	O(F)	Wide range of hosts Including Livestock, Reptiles and Poultry	90703	0.20	98

Schistosoma mansoni	Trematode	O(W)	Molluscs	-	-	99
Seoul Hantavirus	Virus	A;C	Small mammals	-	-	100
Sin Nombre Virus (Hantavirus)	Virus	A;C	Small mammals	1236*	NA	101
St. Louis encephalitis virus (SLEV)	Virus	V(MOS)	Birds	-	-	102
Staphylococcus spp.	Bacteria	A;C	Poultry, Cattle and Canines	-	-	103
Streptococcus suis	Bacteria	O(F)	Pigs,Poultry, Ruminants, Felines, Canines	-	-	104
Strongyloides spp.	Nematode	C	Rodents, Racoon	-	-	105,106,107
Syphacia spp.	Nematode	O	Rodents	-	-	108,109
Taenia spp.	Cestode	O(F)	Broad host range including Felines, Bovine, Pigs, Canines and Rodents	-	-	111,112,113
Theileria parva	Apicomplexa	V(T)	Buffalo, Cattle	-	-	114
Toxocara spp.	Nematode	O	Felines, Canines,Cats, Rodents, birds, worms, molluscs	-	-	115,116
Toxoplasma spp.	Apicomplexa	O(F)	Wid host range including felines, birds and mammals	199	2.11	117
Trichinella spp.	Nematode	O(F)	Broad host range including birds, mammals and reptiles	189	0.42	118
Trichosomoides crassicauda	Nematode	O	Rodents	-	-	119
Trichostrongylus spp.	Nematode	O(F)	Livestock, Rabbits	-	-	120
Trichuris spp.	Nematode	O	Wide host range including domestic animals	-	-	121

Trypanosoma	Apicomplexa	O;V(GEN,TRI,FL)	Broad host range including rodents, domestic animals and livestock	-	-	122,123,124
Uncinaria stenocephala	Nematodes	O	Canines	-	-	125
Usutu virus (USUV)	Virus	V(MOS)	Birds	-	-	126
Variegated squirrel bornavirus 1 (VSBV-1)	Virus	A	Squirrels	-	-	127
West Nile Virus	Virus	V(MOS)	Birds	383	9.13	128
Western equine encephalomyelitis virus (WEEV)	Virus	V(MOS)	Birds, Horses	-	-	129
Whataroa virus	Virus	V(MOS)	Birds	-	-	130
Yersinia pestis	Bacteria	A;V(FL)	Broad incedental host range but mainly maintained in rodents	-	-	131
Yersinia spp.	Bacteria	A;O(W)(F);V(F)	Broad host range including domestic animals and rodents	6780	0.07	132
Zika virus	Virus	V(MOS)	Primates	-	-	133

References for Appendix 1

1 Igbinosa, I.H., Igumbor, E.U., Aghdasi, F., Tom, M. and Okoh, A.I., 2012. Emerging Aeromonas species infections and their significance in public health. The Scientific World Journal, 2012.

2 Tăbăran, F., Sándor, A.D., Marinov, M., Cătoi, C. and Mihalca, A.D., 2013. Alaria alata infection in European mink. Emerging Infectious Diseases, 19(9), p.1547.

3 Rikihisa, Y., 2011. Mechanisms of obligatory intracellular infection with Anaplasma phagocytophilum. Clinical microbiology reviews, 24(3), pp.469-489.

4 Audicana, M.T. and Kennedy, M.W., 2008. Anisakis simplex: from obscure infectious worm to inducer of immune hypersensitivity. Clinical microbiology reviews, 21(2), pp.360-379.

5 Scharf, C., 2017. Dermoscopy Findings in Infectious and Parasitic Diseases. In The Microbiology of Skin, Soft Tissue, Bone and Joint Infections (pp. 303-313). Academic Press.

6 Barratt, J., Chan, D., Sandaradura, I., Malik, R., Spielman, D., Lee, R., Marriott, D., Harkness, J., Ellis, J. and Stark, D., 2016. Angiostrongylus cantonensis: a review of its distribution, molecular biology and clinical significance as a human pathogen. Parasitology, 143(9), pp.1087-1118.

7 Valente, R., Robles, M.D.R., Navone, G.T. and Diaz, J.I., 2018. Angiostrongylus spp. in the Americas: geographical and chronological distribution of definitive hosts versus disease reports. Memórias do Instituto Oswaldo Cruz, 113(3), pp.143-152.

8 Denegri, G., Bernadina, W. and Perez-Serrano, J., 1998. Anoplocephalid cestodes of veterinary and medical significance: a review. Folia Parasitol (Praha), 45(1), pp.1-8.

9 Tyutin, A.V. and Izvekova, G.I., 2013. Infection of mollusks and fish by the trematode Apophallus muehlingi (Jagerskiold, 1898) and its interrelations with intermediate hosts. Inland water biology, 6(1), pp.52-56.

10 Mota, K.C.P., Grama, D.F., Fava, N.M.N., Úngari, L.P., Faria, E.S.M. and Cury, M.C., 2018. Distribution and risk factors of Ascarididae and other geohelminths in the soil of Uberlandia, Minas Gerais, Brazil. Revista do Instituto de Medicina Tropical de São Paulo, 60.

11 Derothe, J.M., Loubes, C., Orth, A., Renaud, F. and Moulia, C., 1997. Comparison between patterns of pinworm infection (Aspiculuris tetraptera) in wild and laboratory strains of mice, Mus musculus. International journal for parasitology, 27(6), pp.645-651.

12 Yabsley, M.J. and Shock, B.C., 2013. Natural history of zoonotic Babesia: role of wildlife reservoirs. International Journal for Parasitology: Parasites and Wildlife, 2, pp.18-31.

13 Hu, C.M., Humair, P.F., Wallich, R. and Gern, L., 1997. Apodemus sp. rodents, reservoir hosts for Borrelia afzelii in an endemic area in Switzerland. Zentralblatt für Bakteriologie, 285(4), pp.558-564.

14 Alho, A.M., Pita, J., Amaro, A., Amaro, F., Schnyder, M., Grimm, F., Custódio, A.C., Cardoso, L., Deplazes, P. and de Carvalho, L.M., 2016. Seroprevalence of vector-borne pathogens and molecular detection of Borrelia afzelii in military dogs from Portugal. Parasites & vectors, 9(1), pp.1-6.

15 Vayssier-Taussat, M., Le Rhun, D., Bonnet, S. and Cotté, V., 2009. Insights in Bartonella host specificity. Annals of the New York Academy of Sciences, 1166(1), pp.127-132.

16 Sorvillo, F., Ash, L.R., Berlin, O.G.W., Yatabe, J., Degiorgio, C. and Morse, S.A., 2002. Baylisascaris procyonis: an emerging helminthic zoonosis. Emerging infectious diseases, 8(4), p.355.

17 Hyde, J.A., 2017. Borrelia burgdorferi keeps moving and carries on: a review of borrelial dissemination and invasion. Frontiers in immunology, 8, p.114.

19 Fryxell, R.T.T., Steelman, C.D., Szalanski, A.L., Kvamme, K.L., Billingsley, P.M. and Williamson, P.C., 2012. Survey of Borreliae in ticks, canines, and white-tailed deer from Arkansas, USA. Parasites & vectors, 5(1), p.139.

100

de Figueiredo, P., Ficht, T.A., Rice-Ficht, A., Rossetti, C.A. and Adams, L.G., 2015. Pathogenesis and immunobiology of brucellosis: review of Brucella–Host Interactions. The American journal of pathology, 185(6), pp.1505-1517.

20

Jainkittivong, A. and Langlais, R.P., 1998. Herpes B virus infection. Oral Surgery, Oral Medicine, Oral Pathology, Oral Radiology, and Endodontology, 85(4), pp.399-403.

21

Waddell, L., Pachal, N., Mascarenhas, M., Greig, J., Harding, S., Young, I. and Wilhelm, B., 2019. Cache Valley virus: A scoping review of the global evidence. Zoonoses and public health, 66(7), pp.739-758.

22

Fuehrer, H.P., 2014. An overview of the host spectrum and distribution of Calodium hepaticum (syn. Capillaria hepatica): part 2—Mammalia (excluding Muroidea). Parasitology Research, 113(2), pp.641-651.

23

Facciolà, A., Riso, R., Avventuroso, E., Visalli, G., Delia, S.A. and Laganà, P., 2017. Campylobacter: from microbiology to prevention. Journal of preventive medicine and hygiene, 58(2), p.E79.

24

Mediannikov, O., Aubadie-Ladrix, M. and Raoult, D., 2015. Candidatus 'Rickettsia senegalensis' in cat fleas in Senegal. New Microbes and New Infections, 3, pp.24-28.

25

Misdraji, J., 2010. Liver and bile duct infections. Diagnostic Pathology of Infectious Disease, p.255.

26

Pinto HA, Gonçalves NQ, López-Hernandez D, Pulido-Murillo EA, Melo AL. 2018. The life cycle of a zoonotic parasite reassessed: Experimental infection of Melanoides tuberculata (Mollusca: Thiaridae) with Centrocestus formosanus (Trematoda: Heterophyidae). PLoS ONE 13(4): e0194161.

27

Staples, J.E., Breiman, R.F. and Powers, A.M., 2009. Chikungunya fever: an epidemiological review of a re-emerging infectious disease. Clinical infectious diseases, 49(6), pp.942-948.

28

29   Knittler, M.R., Berndt, A., Böcker, S., Dutow, P., Hänel, F., Heuer, D., Kägebein, D., Klos, A., Koch, S., Liebler-Tenorio, E. and Ostermann, C., 2014. Chlamydia psittaci: new insights into genomic diversity, clinical pathology, host–pathogen interaction and anti-bacterial immunity. International Journal of Medical Microbiology, 304(7), pp.877-893.

30   Bachmann, N.L., Polkinghorne, A. and Timms, P., 2014. Chlamydia genomics: providing novel insights into chlamydial biology. Trends in microbiology, 22(8), pp.464-472.

31   Tang, Z.L., Huang, Y. and Yu, X.B., 2016. Current status and perspectives of Clonorchis sinensis and clonorchiasis: epidemiology, pathogenesis, omics, prevention and control. Infectious diseases of poverty, 5(1), p.71.

32   Dubey, J.P. ed., 2019. Coccidiosis in Livestock, Poultry, Companion Animals, and Humans. CRC Press.

34   Shamsi, S., Stoddart, A., Smales, L. and Wassens, S., 2019. Occurrence of Contracaecum bancrofti larvae in fish in the Murray–Darling Basin. Journal of helminthology, 93(5), pp.574-579.

35   Glaser, C. and Christie, L., 2010. Rickettsial and ehrlichial infections. In Handbook of Clinical Neurology (Vol. 96, pp. 143-158). Elsevier.

36   Fayer, R. and Ungar, B.L., 1986. Cryptosporidium spp. and cryptosporidiosis. Microbiological reviews, 50(4), p.458.

37   Valentine, M.J., Murdock, C.C. and Kelly, P.J., 2019. Sylvatic cycles of arboviruses in non-human primates. Parasites & vectors, 12(1), p.463.

38   Ekstam, B., Johansson, B., Dinnétz, P. and Ellström, P., 2011. Predicting risk habitats for the transmission of the small liver fluke, Dicrocoelium dendriticum to grazing ruminants. Geospatial health, pp.125-131.

39   Scholz, T. and Kuchta, R., 2016. Fish-borne, zoonotic cestodes (Diphyllobothrium and relatives) in cold climates: a never-ending story of neglected and (re)-emergent parasites. Food and waterborne parasitology, 4, pp.23-38.

41 McCall, J.W., Varloud, M., Hodgkins, E., Mansour, A., DiCosty, U., McCall, S., Carmichael, J., Carson, B. and Carter, J., 2017. Shifting the paradigm in Dirofilaria immitis prevention: blocking transmission from mosquitoes to dogs using repellents/insecticides and macrocyclic lactone prevention as part of a multimodal approach. Parasites & vectors, 10(2), p.525.

42 McCall, J.W., Varloud, M., Hodgkins, E., Mansour, A., DiCosty, U., McCall, S., Carmichael, J., Carson, B. and Carter, J., 2017. Shifting the paradigm in Dirofilaria immitis prevention: blocking transmission from mosquitoes to dogs using repellents/insecticides and macrocyclic lactone prevention as part of a multimodal approach. Parasites & vectors, 10(2), p.525.

43 Morens, D.M., Folkers, G.K. and Fauci, A.S., 2019. Eastern Equine Encephalitis Virus—Another Emergent Arbovirus in the United States. New England Journal of Medicine, 381(21), pp.1989-1992.

44 McManus, D.P., Zhang, W., Li, J. and Bartley, P.B., 2003. Echinococcosis. The Lancet, 362(9392), pp.1295-1304.

45 Toledo, R. and Fried, B., 2014. Helminth-Trematode: Echinostoma.

47 Skappak, C., Akierman, S., Belga, S., Novak, K., Chadee, K., Urbanski, S.J., Church, D. and Beck, P.L., 2014. Invasive amoebiasis: a review of Entamoeba infections highlighted with case reports. Canadian Journal of Gastroenterology and Hepatology, 28.

48 Torres, C., Alonso, C.A., Ruiz-Ripa, L., León-Sampedro, R., Del Campo, R. and Coque, T.M., 2018. Antimicrobial Resistance in Enterococcus spp. of animal origin. Antimicrobial Resistance in Bacteria from Livestock and Companion Animals, pp.185-227.

49 Guo, Y., Alderisio, K.A., Yang, W., Cama, V., Feng, Y. and Xiao, L., 2014. Host specificity and source of Enterocytozoon bieneusi genotypes in a drinking source watershed. Applied and Environmental Microbiology, 80(1), pp.218-225.

50 Wasteson, Y., 2002. Zoonotic Escherichia coli. Acta Veterinaria Scandinavica, 43(1), pp.1-6.

51   Elhamiani Khatat, S., Rosenberg, D., Benchekroun, G. and Polack, B., 2016. Lungworm Eucoleus aerophilus (Capillaria aerophila) infection in a feline immunodeficiency virus-positive cat in France. Journal of Feline Medicine and Surgery Open Reports, 2(1), p.2055116916651649.

52   Coffey, L.L., Crawford, C., Dee, J., Miller, R., Freier, J. and Weaver, S.C., 2006. Serologic evidence of widespread Everglades virus activity in dogs, Florida. Emerging infectious diseases, 12(12), p.1873.

53   Vázquez, A.A., de Vargas, M., Alba, A., Sanchez, J., Alda, P., Sabourin, E., Vittecoq, M., Alarcón-Elbal, P.M., Pointier, J.P. and Hurtrez-Boussès, S., 2019. Reviewing Fasciola hepatica transmission in the West Indies and novel perceptions from experimental infections of sympatric vs. allopatric snail/fluke combinations. Veterinary parasitology, 275, p.108955.

54   Ellis, J., Oyston, P. C., Green, M., & Titball, R. W. 2002. Tularemia. Clinical microbiology reviews, 15(4), 631–646.

55   Heyworth, M.F., 2016. Giardia duodenalis genetic assemblages and hosts. Parasite, 23.

56   da Costa Cordeiro, H., de Vasconcelos Melo, F.T., Giese, E.G. and Santos, J.N.D., 2018. Gongylonema parasites of rodents: A key to species and new data on Gongylonema neoplasticum. The Journal of parasitology, 104(1), pp.51-59.

57   Ramsden, C., Holmes, E.C. and Charleston, M.A., 2009. Hantavirus evolution in relation to its rodent and insectivore hosts: no evidence for codivergence. Molecular biology and evolution, 26(1), pp.143-153.

58   Anh, N.T.L., Phuong, N.T., Johansen, M.V., Murrell, K.D., Van, P.T., Dalsgaard, A., Thu, L.T. and Thamsborg, S.M., 2009. Prevalence and risks for fishborne zoonotic trematode infections in domestic animals in a highly endemic area of North Vietnam. Acta Tropica, 112(2), pp.198-203.

59   Van der Poel, W.H., 2014. Food and environmental routes of Hepatitis E virus transmission. Current opinion in virology, 4, pp.91-96.

60 Baneth, G.A.D., Samish, M., Alekseev, E., Aroch, I. and Shkap, V., 2001. Transmission of Hepatozoon canis to dogs by naturally-fed or percutaneously-injected Rhipicephalus sanguineus ticks. Journal of Parasitology, 87(3), pp.606-611.

61 Šnábel, V., Utsuki, D., Kato, T., Sunaga, F., Ooi, H.K., Gambetta, B. and Taira, K., 2014. Molecular identification of Heterakis spumosa obtained from brown rats (Rattus norvegicus) in Japan and its infectivity in experimental mice. Parasitology research, 113(9), pp.3449-3455.

62 Taraschewski, H., 1985. Transmission experiments on the host specificity ofHeterophyes species in 16 potential definitive hosts. Zeitschrift für Parasitenkunde, 71(4), pp.505-518.

63 Premaalatha, B., Chandrawathani, P., Tan, P.S., Tharshini, J., Jamnah, O., Ramlan, M. and NOR, I.S., 2016. Taenia taeniaeformis in wild rats.

64 Bogitsh, B.J., Carter, C.E. and Oeltmann, T.N., 2018. Human parasitology. Academic Press.

65 Thompson, R.C.A., 2015. Neglected zoonotic helminths: Hymenolepis nana, Echinococcus canadensis and Ancylostoma ceylanicum. Clinical Microbiology and Infection, 21(5), pp.426-432.

66 Khemiri, H., Jrijer, J., Neifar, L. and Nouira, S., 2017. A survey study on the helminth parasites of two wild jirds, Meriones shawi and M. libycus (Rodentia: Gerbillinae), in Tunisian desert areas. The European Zoological Journal, 84(1), pp.303-310.

67 Yoon, S.W., Webby, R.J. and Webster, R.G., 2014. Evolution and ecology of influenza A viruses. In Influenza Pathogenesis and Control-Volume I (pp. 359-375). Springer, Cham.

68 Mansfield, K.L., Hernández-Triana, L.M., Banyard, A.C., Fooks, A.R. and Johnson, N., 2017. Japanese encephalitis virus infection, diagnosis and control in domestic animals. Veterinary microbiology, 201, pp.85-92.

Davies, Y.M., Cunha, M.P.V., Oliveira, M.G.X., Oliveira, M.C.V., Philadelpho, N., Romero, D.C., Milanelo, L., Guimarães, M.B., Ferreira, A.J.P., Moreno, A.M. and Sá, L.R.M., 2016. Virulence and antimicrobial resistance of Klebsiella pneumoniae isolated from passerine and psittacine birds. Avian Pathology, 45(2), pp.194-201.

69

Bennai, K., Tahir, D., Lafri, I., Bendjaballah-Laliam, A., Bitam, I. and Parola, P., 2018. Molecular detection of Leishmania infantum DNA and host blood meal identification in Phlebotomus in a hypoendemic focus of human leishmaniasis in northern Algeria. PLoS Neglected Tropical Diseases, 12(6), p.e0006513.

70

Evangelista, K.V. and Coburn, J., 2010. Leptospira as an emerging pathogen: a review of its biology, pathogenesis and host immune responses. Future microbiology, 5(9), pp.1413-1425.

71

Nascimento, A.L.T.O.D., Verjovski-Almeida, S., Van Sluys, M.A., Monteiro-Vitorello, C.B., Camargo, L.E.A., Digiampietri, L.A., Harstkeerl, R.A., Ho, P.L., Marques, M.V., Oliveira, M.C. and Setubal, J.C., 2004. Genome features of Leptospira interrogans serovar Copenhageni. Brazilian journal of medical and biological research, 37(4), pp.459-477.

72

Dhama, K., Karthik, K., Tiwari, R., Shabbir, M.Z., Barbuddhe, S., Malik, S.V.S. and Singh, R.K., 2015. Listeriosis in animals, its public health significance (food-borne zoonosis) and advances in diagnosis and control: a comprehensive review. Veterinary Quarterly, 35(4), pp.211-235.

73

74   Magden, E.R., Mansfield, K.G., Simmons, J.H. and Abee, C.R., 2015. Nonhuman primates. In Laboratory animal medicine (pp. 771-930). Academic Press.

75   Hallam, S.J., Koma, T., Maruyama, J. and Paessler, S., 2018. Review of mammarenavirus biology and replication. Frontiers in Microbiology, 9, p.1751.

Lafferty, K.D., Hathaway, S.A., Wegmann, A.S., Shipley, F.S., Backlin, A.R., Helm, J. and Fisher, R.N., 2010. Stomach nematodes (Mastophorus muris) in rats (Rattus rattus) are associated with coconut (Cocos nucifera) habitat at Palmyra Atoll. Journal of Parasitology, 96(1), pp.16-20.

76

77 Zaleśny, G. and Hildebrand, J., 2012. Molecular identification of Mesocestoides spp. from intermediate hosts (rodents) in central Europe (Poland). Parasitology research, 110(2), pp.1055-1061.

78 Balasingam, E., 1963. Experimental infection of dogs and cats with Molineus barbatus Chandler, 1942, with a discussion on the distribution of Molineus spp. Canadian Journal of Zoology, 41(4), pp.599-602.

79 Berenji, F., Fata, A. and Hosseininejad, Z., 2007. A case of Moniliformis moniliformis (Acanthocephala) infection in Iran. The Korean journal of parasitology, 45(2), p.145.

80 Stevenson, K., Alvarez, J., Bakker, D., Biet, F., De Juan, L., Denham, S., Dimareli, Z., Dohmann, K., Gerlach, G.F., Heron, I. and Kopecna, M., 2009. Occurrence of Mycobacterium avium subspecies paratuberculosis across host species and European countries with evidence for transmission between wildlife and domestic ruminants. BMC microbiology, 9(1), p.212.

81 Bryant, V., 1973. The life cycle of Nematospiroides dubius, Baylis, 1926 (Nematoda: Heligmosomidae). Journal of helminthology, 47(3), pp.263-268.

82 Ogilvie, B.M. and Jones, V.E., 1971. Nippostrongylus brasiliensis: a review of immunity and the host/parasite relationship in the rat. Experimental parasitology, 29(1), pp.138-177.

83 Luce-Fedrow, A., Lehman, M.L., Kelly, D.J., Mullins, K., Maina, A.N., Stewart, R.L., Ge, H., John, H.S., Jiang, J. and Richards, A.L., 2018. A review of scrub typhus (Orientia tsutsugamushi and related organisms): then, now, and tomorrow. Tropical medicine and infectious disease, 3(1), p.8.

84 Kim, D.C., 1984. Paragonimus westermani: life cycle, intermediate hosts, transmission to man and geographical distribution in Korea. Arzneimittel-Forschung, 34(9B), pp.1180-1183.

85 Church, M.L., Barrett, P.M., Swenson, J., Kinsella, J.M. and Tkach, V.V., 2013. Outbreak of Philophthalmus gralli in four greater rheas (Rhea americana). Veterinary ophthalmology, 16(1), pp.65-72.

86 Smales, L.R., Harris, P.D. and Behnke, J.M., 2009. A redescription of Protospirura muricola Gedoelst, 1916 (Nematoda: Spiruridae), a parasite of murid rodents. Systematic Parasitology, 72(1), p.15.

87 El-Shehabi, F.S., Abdel-Hafez, S.K. and Kamhawi, S.A., 1999. Prevalence of intestinal helminths of dogs and foxes from Jordan. Parasitology research, 85(11), pp.928-934.

88 Müller, T., Hahn, E.C., Tottewitz, F., Kramer, M., Klupp, B.G., Mettenleiter, T.C. and Freuling, C., 2011. Pseudorabies virus in wild swine: a global perspective. Archives of virology, 156(10), p.1691.

89 Dewi, K., 2010. THE TAXONOMIC STATUS OF PTERYGODERMATITES SPP. AND THE SCANNING ELECTRONMICROSCOPY STUDY OF PTERYGODERMATITES WHARTONI (TUBANGUI, 1931)(NEMATODA: RICTULARIIDAE) FROM INDONESIAN MURIDS. Zoo Indonesia, 19(1).

90 Scioscia, N.P., Beldomenico, P.M. and Denegri, G.M., 2016. New host and distribution expansion for Pterygodermatites (Multipectines) affinis. Helminthologia, 53(1), pp.81-86.

91 Fooks, A., Cliquet, F., Finke, S. et al. 2017. Rabies. Nat Rev Dis Primers 3, 17091 .

92 Mokrani, N., Parola, P., Tebbal, S., Dalichaouche, M., Aouati, A. and Raoult, D., 2008. Rickettsia aeschlimannii infection, Algeria. Emerging infectious diseases, 14(11), p.1814.

93 Socolovschi, C., Gaudart, J., Bitam, I., Huynh, T.P., Raoult, D. and Parola, P., 2012. Why are there so few Rickettsia conorii conorii-infected Rhipicephalus sanguineus ticks in the wild?. PLoS Negl Trop Dis, 6(6), p.e1697.

94 Inokuma, H., Matsuda, H., Sakamoto, L., Tagawa, M. and Matsumoto, K., 2011. Evaluation of Rickettsia japonica pathogenesis and reservoir potential in dogs by experimental inoculation and epidemiologic survey. Clinical and Vaccine Immunology, 18(1), pp.161-166.

95   Peniche-Lara, G., Dzul-Rosado, K., Perez-Osorio, C. and Zavala-Castro, J., 2015. Rickettsia typhi in rodents and R. felis in fleas in Yucatán as a possible causal agent of undefined febrile cases. Revista do Instituto de Medicina Tropical de São Paulo, 57(2), pp.129-132.

96   Bäumler, A.J., Tsolis, R.M., Ficht, T.A. and Adams, L.G., 1998. Evolution of Host Adaptation inSalmonella enterica. Infection and immunity, 66(10), pp.4579-4587.

97   Pulford, C.V., Perez-Sepulveda, B.M., Rodwell, E.V., Weill, F.X., Baker, K.S. and Hinton, J.C., 2019. Salmonella enterica serovar Panama, an understudied serovar responsible for extraintestinal salmonellosis worldwide. Infection and immunity, 87(9), pp.e00273-19.

98   Giannella, R.A., 1996. Chapter 21: Salmonella. Medical microbiology, 4.

99   Johnson, P.T., Lund, P.J., Hartson, R.B. and Yoshino, T.P., 2009. Community diversity reduces Schistosoma mansoni transmission, host pathology and human infection risk. Proceedings of the Royal Society B: Biological Sciences, 276(1662), pp.1657-1663.

102   Diaz, A., Coffey, L.L., Burkett-Cadena, N. and Day, J.F., 2018. Reemergence of St. Louis encephalitis virus in the Americas. Emerging infectious diseases, 24(12), p.2150.

103   Hughes, J.M., Wilson, M.E., Wertheim, H.F., Nghia, H.D.T., Taylor, W. and Schultsz, C., 2009. Streptococcus suis: an emerging human pathogen. Clinical Infectious Diseases, 48(5), pp.617-625.

104   Staats, J.J., Feder, I., Okwumabua, O. and Chengappa, M.M., 1997. Streptococcus suis: past and present. Veterinary research communications, 21(6), pp.381-407.

105   SATO, H., SUZUKI, K., UNI, S. and KAMIYA, H., 2005. Recovery of the everted cystacanth of seven acanthocephalan species of birds from feral raccoons (Procyon lotor) in Japan. Journal of veterinary medical science, 67(12), pp.1203-1206.

106   Sato, H., Suzuki, K., Osanai, A., Kamiya, H. and Furuoka, H., 2006. Identification and characterization of the threadworm, Strongyloides procyonis, from feral raccoons (Procyon lotor) in Japan. Journal of Parasitology, 92(1), pp.63-68.

107   Fisher, M.C. and Viney, M.E., 1998. The population genetic structure of the facultatively sexual parasitic nematode Strongyloides ratti in wild rats. Proceedings of the Royal Society of London. Series B: Biological Sciences, 265(1397), pp.703-709.

108   Stahl, W., 1961. Syphacia muris, the rat pinworm. Science, 133(3452), pp.576-577.

109   Sato, Y., Ooi, H.K., Nonaka, N., Oku, Y. and Kamiya, M., 1995. Antibody production in Syphacia obvelata infected mice. The Journal of parasitology, pp.559-562.

111   Ntoukas, V., Tappe, D., Pfütze, D., Simon, M. and Holzmann, T., 2013. Cerebellar cysticercosis caused by larval Taenia crassiceps tapeworm in immunocompetent woman, Germany. Emerging infectious diseases, 19(12), p.2008.

112   Haby, M.M., Sosa Leon, L.A., Luciañez, A., Nicholls, R.S., Reveiz, L. and Donadeu, M., 2020. Systematic review of the effectiveness of selected drugs for preventive chemotherapy for Taenia solium taeniasis. PLoS neglected tropical diseases, 14(1), p.e0007873.

113   Pritchett-Corning, K.R. and Clifford, C.B., 2012. Parasitic Infections of Laboratory Mice. The Laboratory Mouse, ed. HJ Hedrich, pp.503-518.

114   Olds, C.L., Mason, K.L. and Scoles, G.A., 2018. Rhipicephalus appendiculatus ticks transmit Theileria parva from persistently infected cattle in the absence of detectable parasitemia: implications for East Coast fever epidemiology. Parasites & vectors, 11(1), p.126.

115   Rodan, I. and Sparkes, A.H., 2012. Preventive health care for cats. The Cat, p.151.

116 Despommier, D., 2003. Toxocariasis: clinical aspects, epidemiology, medical ecology, and molecular aspects. Clinical microbiology reviews, 16(2), pp.265-272.

117 Aguirre, A.A., Longcore, T., Barbieri, M., Dabritz, H., Hill, D., Klein, P.N., Lepczyk, C., Lilly, E.L., McLeod, R., Milcarsky, J. and Murphy, C.E., 2019. The one health approach to toxoplasmosis: epidemiology, control, and prevention strategies. EcoHealth, 16(2), pp.378-390.

118 Gottstein, B., Pozio, E. and Nöckler, K., 2009. Epidemiology, diagnosis, treatment, and control of trichinellosis. Clinical microbiology reviews, 22(1), pp.127-145.

119 Otto, G.M., Franklin, C.L. and Clifford, C.B., 2015. Biology and diseases of rats. In Laboratory animal medicine (pp. 151-207). Academic Press.

120 Bundy, D.A., Appleby, L.J. and Brooker, S.J., 2020. Nematodes Limited to the Intestinal Tract (Enterobius vermicularis, Trichuris trichiura, Capillaria philippinensis, and Trichostrongylus spp.). In Hunter's Tropical Medicine and Emerging Infectious Diseases (pp. 834-839). Content Repository Only!.

122 Crisi, P.E., Di Cesare, A. and Boari, A., 2018. Feline troglostrongylosis: current epizootiology, clinical features, and therapeutic options. Frontiers in Veterinary Science, 5, p.126.

123 Noireau, F., Diosque, P. and Jansen, A.M., 2009. Trypanosoma cruzi: adaptation to its vectors and its hosts. Veterinary research, 40(2), pp.1-23.

124 Lee C.M., Armstrong E. 2004. Rodent Trypanosomiasis: A Comparison Between Trypanosoma Lewisi and Trypanosoma Musculi. In: Encyclopedia of Entomology. Springer, Dordrecht.

125 Reinemeyer, C.R., 2016. Formulations and Clinical Uses of Pyrimidine Compounds in Domestic Animals. In Pyrantel Parasiticide Therapy in Humans and Domestic Animals (pp. 67-107). Academic Press.

126 Clé, M., Beck, C., Salinas, S., Lecollinet, S., Gutierrez, S., Van de Perre, P., Baldet, T., Foulongne, V. and Simonin, Y., 2019. Usutu virus: A new threat?. Epidemiology & Infection, 147.

Petzold, J., van den Brand, J.M., Nobach, D., Hoffmann, B., Hoffmann, D., Fast, C., Reusken, C.B., van Run, P.R., Schlottau, K., Beer, M. and Herden, C., 2019. Distribution of zoonotic variegated squirrel bornavirus 1 in naturally infected variegated and Prevost's squirrels. Scientific reports, 9(1), pp.1-10.

Londono-Renteria, B. and Colpitts, T.M., 2016. A brief review of West Nile virus biology. In West Nile Virus (pp. 1-13). Humana Press, New York, NY.

Bergren, N.A., Haller, S., Rossi, S.L., Seymour, R.L., Huang, J., Miller, A.L., Bowen, R.A., Hartman, D.A., Brault, A.C. and Weaver, S.C., 2020. "Submergence" of Western equine encephalitis virus: Evidence of positive selection argues against genetic drift and fitness reductions. PLoS pathogens, 16(2), p.e1008102.

Tompkins, D.M., Paterson, R., Massey, B. and Gleeson, D.M., 2010. Whataroa virus four decades on: emerging, persisting, or fading out?. Journal of the Royal Society of New Zealand, 40(1), pp.1-9.

Gage, K.L. and Kosoy, M.Y., 2005. Natural history of plague: perspectives from more than a century of research. Annu. Rev. Entomol., 50, pp.505-528.

Percival, S.L. and Williams, D.W., 2014. Yersinia. In Microbiology of Waterborne Diseases (pp. 249-259). Academic Press.

Vorou, R., 2016. Zika virus, vectors, reservoirs, amplifying hosts, and their potential to spread worldwide: what we know and what we should investigate urgently. International Journal of Infectious Diseases, 48, pp.85-90.