

Rapid review of the literature on zoonoses in the context of One Health in the Selva Maya region

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Editorial

In recent years, the global human community has begun to understand what scientists and environmental activists have been spelling out for decades: that the harm we are doing to ecosystems globally is threatening the very foundation of human life. We are starting to experience the effects of climate change; as increasingly extreme and destructive weather events strike and with the world in the grip of the COVID-19 pandemic, there is more and more talk in the media about the link between the destruction of ecosystems, biodiversity loss and health emergencies caused by infectious disease epidemics and pandemics. With the realisation that human life and health depend on the health of the planet, ecosystems, plants and animals comes a growing understanding that it is no longer enough to try to solve environmental problems in an isolated way with piecemeal technological solutions; we need approaches that take this interdependence into account and that bring about a fundamental change in our relationship with the elements that form the basis of life on our planet.

This can only be achieved by acting in a much more holistic and interdisciplinary way. Institutions responsible for conservation cannot protect habitats and biodiversity without changes being made in agriculture and trade, and nor can doctors protect our health without cooperation from other sectors. The One Health concept takes into account the interdependence of ecosystem, animal and human health. The approach relies on intersectoral collaboration on human health, animal health, conservation, agriculture, the economy and trade, civil society, the private sector, academia and others to find and implement sustainable solutions and make the changes required to protect and restore ecosystem, animal and human health all at once.

The Selva Maya is the largest tropical rainforest in Mesoamerica and is shared by Belize, Guatemala and Mexico. It is home to a rich biodiversity spread across various ecosystems that are under serious threat, and this marks it out as a place where future epidemics and pandemics could originate. For this reason, with the support of the project Strengthening the regional strategic and operational cooperation for the protection of the Selva Maya (Selva Maya project), financed by the German Federal Ministry for Economic Cooperation and Development (BMZ) and implemented by the Deutsche Gesellschaft für Internationale Zusammenarbeit (GIZ) GmbH, efforts are being undertaken to build multisectoral cooperation to establish the One Health approach in this region. Activities under this approach will include the creation of an intersectoral platform based on the regional cooperation that already exists in the conservation sector, risk monitoring with better coordination among the different spheres, risk reduction efforts and the implementation of awareness and communication processes aimed at local people and various other sectors.

The One Health approach in the Selva Maya requires information on the specific risks in the region, in addition to a commitment to building cooperation among a wide variety of sectors and an overall understanding of the ways in which they are related to each other. To this end, the project supports proposals for scientific research to increase knowledge of these risks, particularly in relation to zoonoses.

The first step in planning this support is this rapid review of the literature on zoonotic risks in the Selva Maya region, which describes and analyses the current state of knowledge on

existing zoonoses and on potential risks of zoonoses as yet unknown in the region. We are now very pleased to share the findings of the review. It is, as its name implies, a rapid analysis carried out to provide direction to the project and not a systematic scientific review. However, we are confident that the information will be of great value to the German co-operation Selva Maya project and regional and national institutions and organisations that will be involved in implementing the One Health approach in the region.

Finally, I would like to thank the author, Andrea Rasche, and the Selva Maya project team for the work they have carried out and also the Pandemic Dialogue project, financed by the German Federal Foreign Office, for its support. I wish every success to all those contributing to the One Health approach in the Selva Maya region and elsewhere in bringing about the transformative changes needed for its successful implementation.

Klaus Peter Schnellbach
Director, Selva Maya project
GIZ

Introduction

The impact of zoonoses

A zoonosis is a disease that can be transmitted from animals to humans and vice versa. They are mainly caused by viruses, bacteria, parasites, prions and fungi. In terms of global human health, zoonoses are a major group of infectious diseases. More than 60% of emerging infectious diseases (EIDs) are zoonoses, most of them (more than 75%) originate in wildlife (Jones, Patel et al. 2008). New infectious diseases are clearly on the rise and have tripled every decade since 1980 (Smith, Goldberg et al. 2014). Some examples are Ebola virus disease, Zika virus disease, HIV (human immunodeficiency virus) infection, influenza, Lyme disease, ehrlichiosis and, as a particularly relevant and topical example, COVID-19 caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). There are also a significant number of endemic zoonotic diseases that pose a constant threat to people living in affected areas. Endemic zoonoses are constantly transmitted between animals (host) and people but are not normally transmitted from one person to another. Examples include toxoplasmosis, Chagas disease, leishmaniasis and rabies.

What are zoonoses and how prevalent are they?

Zoonoses are diseases transmitted from animals to humans



They account
for:

60%
of all infectious diseases
in humans

75%
of all EIDs

Importance of zoonoses for human health

The negative effects of zoonoses are far-reaching. In addition to high morbidity and mortality in both humans and animals, they can also have considerable economic repercussions as a result of lost labour productivity, a decline in travel and tourism, an impact on livestock and animal products, and restrictions on international trade (Pan American Health Organization – PAHO 2003).

Zoonoses can be transmitted in different ways, including by direct contact between animals and people; indirect contact when animals and people share a contaminated area; transmission by vectors, such as ticks and insects; and transmission through contaminated food or water.

“The likelihood of zoonotic outbreaks is increased considerably by the exploitation and destruction of natural habitats as they lead to close interaction between humans and wild animals.”

Globalisation, including travel and trade, means that an emerging zoonotic disease can spread extremely quickly, as the current pandemic has demonstrated (Cordoba-Aguilar, Ibarra-Cerdeña et al. 2021).

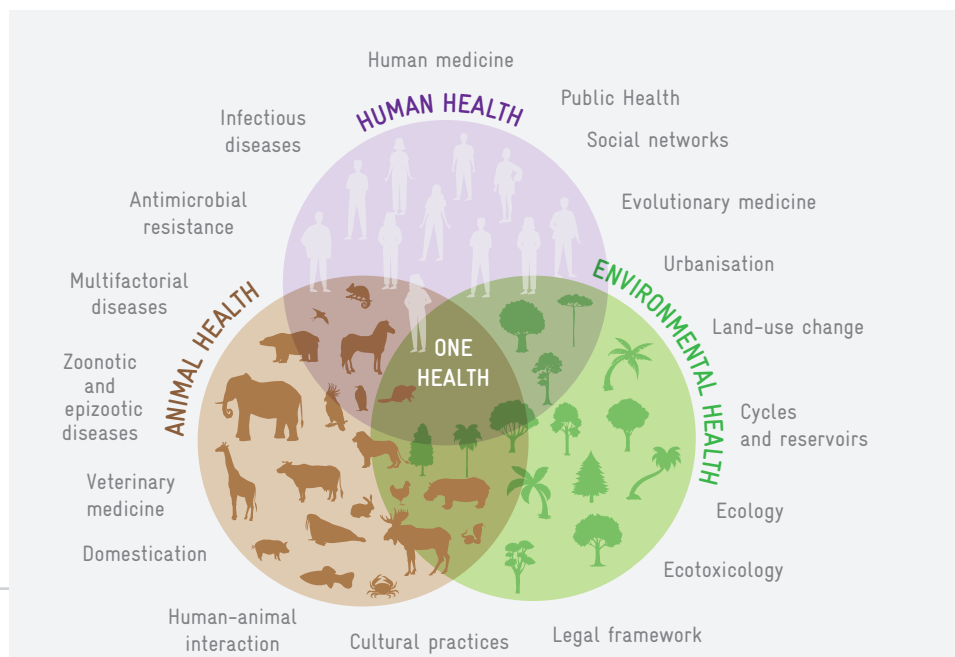
The One Health concept

Concerns about the rise in EIDs prompted the launch of the One Health concept at the beginning of the 21st century.

“One Health is a global strategy for a transdisciplinary approach that addresses human, animal and ecosystem health all at once.”

These three issues are inextricably linked and mutually influence each other. Humans are increasingly disrupting natural wildlife habitats, including protected natural areas, and this has a negative impact on the health of ecosystems and wildlife and also leads to increased threats to human health, such as zoonotic diseases, as mentioned above.

One Health factors need to be studied using an interdisciplinary approach involving not only ecology, human and veterinary medicine and epidemiology, but also other fields, such as sociology and ethnology. However, in recent years, research on the One Health issue has largely focused on emerging zoonoses originating in domestic or wild animals (Destoumieux-Garzon, Mavingui et al. 2018).



Disciplines associated with One Health

One Health in the Selva Maya

The conservation of ecosystems is especially important in the context of the One Health approach. Changes to the landscape due to human use of the land (deforestation, agriculture and the introduction of livestock) have far-reaching adverse consequences in terms of what One Health aims to achieve. Such changes can negatively impact ecosystem health and biodiversity by causing pollution, disrupting food webs, shifting ecosystem properties and introducing non-native species. They can also alter host-pathogen interactions, cause changes in animal behaviour and affect immune systems. In addition, the spread of vectors (living organisms capable of transmitting diseases or parasites from one animal to another, such as biting insects and ticks) is altered by anthropogenic influences (Gottdenker, Streicker et al. 2014).

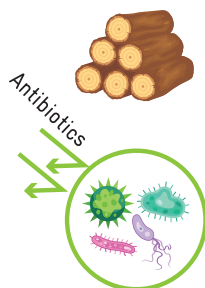
“EID risk is elevated in forested tropical regions experiencing land-use changes and where wildlife biodiversity is high (Allen, Murray et al. 2017).”

From this perspective, ecosystem protection takes on a new meaning. Mesoamerica is a biodiversity hotspot, globally recognised as one of the world’s most biodiverse regions (Myers, Mittermeier et al. 2000) but also one of the most threatened. Around 80% of the region’s vegetation has been converted to agriculture, a development that seriously threatens biodiversity. The Selva Maya region has the largest contiguous tropical forest area in Central America spanning more than 10 million hectares in Mexico, Guatemala and Belize. It includes four million hectares of land with different levels of protection (national parks, forest reserves and biosphere reserves; see <https://selvamaya.info>). However, the region faces a variety of threats, such as wildfires, illegal logging, illegal plant and wildlife trafficking, land-use change and pesticide use (<https://selvamaya.info>). Habitat degradation, greater contact with wildlife and the consumption of wild meat increase the likelihood of zoonotic outbreaks in the region.

What factors contribute to the emergence of zoonoses? (Diseases transmitted from animals to humans)

Deforestation
and land-use
change

Antimicrobial
resistance



Intensive
agriculture and
livestock



Illegal and
unregulated
wildlife trade



Climate change

Factors contributing to the transmission of diseases from animals to humans

Evaluating the extent to which ecosystem disruption affects human and animal health is a huge challenge. One important aspect is observing and predicting the transfer of pathogens between animals and humans, in other words, researching zoonoses.

“ In addressing zoonotic risks, it is important to promote intersectoral dialogue and raise awareness to ensure that people are informed about the impact that human influence and contact with wildlife can have on ecosystems. ”

Objectives of the state-of-the-art study

This document aims to provide an overview of the current state of knowledge of known zoonoses and potential future zoonotic risks in the Selva Maya and surrounding area. To this end, scientific articles on zoonoses and wildlife diseases were examined. Based on the literature review, a report was drawn up summarising and evaluating current knowledge on the subject in the region, identifying knowledge gaps and providing suggestions for future studies. Three experts on zoonoses in the region were consulted.

State-of-the-art study on zoonotic risks in the Selva Maya region

Zoonoses in Central America

There are a wide variety of zoonotic pathogens in Central America although most of them have not been investigated in major epidemiological studies. Zoonotic pathogens can be bacteria, viruses, parasites and, less commonly, fungi and prions. As mentioned above, there are a large number of endemic zoonoses that are repeatedly transmitted to humans. There are also pandemic zoonoses circulating in Central America although they did not necessarily originate in the region (for example, those caused by SARS-CoV-2 and Zika virus). Diseases that originated in animals but have been circulating for a long time in humans, such as HIV or malaria, have not been included in this study. New zoonotic pathogens may also emerge in the future. The risks are unclear and cannot be associated with a particular pathogen. However, by analysing the pathogens that occur in related species in the animal kingdom, it is possible to evaluate the risk of transmission between host species and identify those carrying pathogens that were previously unknown. Studies of this kind led to the detection of various coronaviruses in bats in different parts of the world, raising fears about a coronavirus pandemic even before SARS-CoV-2 appeared. Other examples are the detection of new influenza A viruses in bats in Guatemala and other Latin American countries, whose zoonotic potential is still not clear (Tong, Li et al. 2012), and the detection of potentially zoonotic viruses similar to hepatitis B in bats in Panama (Drexler, Geipel et al. 2013). However, whether or not transmission between humans and animals actually occurs, or whether there is a likelihood of a host switch leading to infection in humans, depends on a series of factors. In the case of viruses, for example, it depends on the existence of cell entry receptors, the host-specific immune response, intracellular replication and production mechanisms. It is not therefore possible to predict zoonotic risk by detecting pathogens in host species although the information obtained contributes significantly to pathogen surveillance, especially in areas with a higher incidence of zoonoses, and can help identify areas that may be at risk from future zoonoses.

There follows an overview of zoonoses caused by bacteria, viruses and parasites in Central America. While there are zoonoses transmitted by other agents, such as fungi, which can cause sporotrichosis, for example, the study only covers those caused by bacteria, viruses and parasites as they account for the vast majority. More detailed information on pathogens can be found in *Zoonoses and Communicable Diseases Common to Man and Animals*, published by the Pan American Health Organization (ISBN 92 75 11991 0; PAHO 2003). A review of zoonoses in Yucatán (Mexico) is provided in Reyes-Novelo, Ruíz-Piña et al. 2011, and an analysis of multidisciplinary studies on zoonotic diseases in Pacheco Castro, Lugo Pérez et al. 2013.

“ Whether or not infections are transmitted effectively between species depends on various factors, including cell entry receptors, immune response, cell replication processes, likelihood of contact and presence of the pathogen in the population. ”

Bacteria

In Central America, zoonotic bacteria are transmitted by direct contact with animals, by vectors or through contaminated food.

Bacteria of the *Leptospira* genus are typically transmitted by rodents but can also be transferred by domestic animals, such as farm animals and dogs. Humans are infected through contact with the urine of infected reservoir hosts or indirectly through contact with contaminated environments. Symptoms can range from none to mild (headaches, muscle pain and fever) to severe (pulmonary haemorrhage and meningitis) (Weil's disease) (Soo, Khan et al. 2020). Bacteria of the genera *Rickettsia*, *Borrelia*, *Bartonella* and *Ehrlichia* are transmitted by vectors. *Rickettsia* spp. can be transmitted by lice (causing epidemic typhus), fleas (causing murine typhus) or ticks (causing Rocky Mountain spotted fever) (Parola, Davoust et al. 2005). *Borrelia* spp. is transmitted by ticks and can cause relapsing fever and Lyme disease (Colunga-Salas, Sánchez-Montes et al. 2020). *Bartonella* spp. are also transmitted by vectors, such as fleas, sandflies, mosquitoes and ticks. They are found in different mammalian hosts, including carnivores, ruminants, rodents and bats. *Bartonella* species responsible for human illness are associated with a broad spectrum of clinical symptoms, including blood culture-negative endocarditis and prolonged fever of unknown origin (Stuckey, Chomel et al. 2017). *Ehrlichia* spp. is transmitted by ticks and causes ehrlichiosis, an acute disease characterised by fever in which systemic complications can lead to death (Alcántara-Rodríguez, Sánchez-Montes et al. 2020).

Brucellosis, one of the world's most common zoonoses, is caused by bacteria of the *Brucella* genus. It is transmitted by direct contact with animals (normally farm animals) or contaminated food. It is a disease with unspecific clinical signs affecting different parts of the body and symptoms that generally include fever and can develop into a chronic infection if not treated (Guzmán-Hernández, Contreras-Rodríguez et al. 2016). Another important example is bovine tuberculosis, which can be transmitted through the air, food or through direct contact with animals (Gutiérrez Reyes, García Casanova et al. 2012). Other zoonoses transmitted through food include *Escherichia coli* O157:H7, *Salmonella* spp., *Campylobacter* spp. and *Streptococcus* spp. which can cause gastrointestinal diseases.

Viruses

A large proportion of zoonoses reported in Central America are caused by arboviruses (transmitted by arthropod vectors). Some examples are dengue virus, Zika virus, yellow fever virus, Cache Valley orthobunyavirus, Mayaro virus, West Nile virus, St Louis encephalitis virus, Madariaga virus, Venezuelan equine encephalitis virus and Oropouche virus (Kopp, Gillespie et al. 2013; Fauci and Morens 2016; Sakkas, Bozidis et al. 2018; Palermo, De la Mora-Covarrubias et al. 2019; Waddell, Pachal et al. 2019; Carrera, Cucunuba et al. 2020; Ganjian and Riviere-Cinnamond 2020). These viruses belong to the families *Peribunyaviridae*, *Togaviridae* and *Flaviviridae*. In addition to arboviruses, there is also the

zoonotic virus influenza A (*Orthomyxoviridae* family) which, for example, caused the 2009-2010 influenza A (H1N1) pandemic (Chowell, Echevarria-Zuno et al. 2011). The rabies virus (*Rhabdoviridae* family) can be transmitted by both wild animals and domestic animals although the risk of infection in domestic animals has been significantly reduced, largely as a result of extensive vaccination campaigns (Belotto, Leanes et al. 2005). Rodents can transmit members of the *Hantaviridae* family, which can cause severe illness in humans, such as hantavirus pulmonary syndrome (HPS) (Vigueras-Galván, López-Pérez et al. 2019). Some genotypes of the hepatitis E virus (*Hepeviridae* family) are also zoonotic and can be transmitted through pork, for example (Fierro, Realpe et al. 2016). There are occasional reports of rotavirus A (*Reoviridae* family) strains of animal origin although the zoonotic potential of this virus has not yet been described (Dóro, Farkas et al. 2015).

Parasites

Zoonotic parasites include some protozoa, such as *Trypanosoma cruzi*, *Leishmania* spp., *Toxoplasma gondii* and *Plasmodium* spp. *T. cruzi* is found in various mammals and can be transmitted by triatomine bugs; in humans, it causes Chagas disease (PAHO 2003), which has an acute and a chronic phase. During the acute phase, symptoms are absent or mild although rare and severe symptoms can also develop. If left untreated, it can become chronic and lead to cardiac or gastrointestinal complications (<https://www.cdc.gov/parasites/chagas/>, last accessed on 22 April 2021). *Leishmania* spp. are transmitted by phlebotomine sandflies, and the disease can take various forms, the main ones being cutaneous, visceral (severe but rare) and mucocutaneous. They are also found in various mammals (WHO 2009). *Trypanosoma* spp. and *Leishmania* spp. are both trypanosomatids (Trypanosomatida order) and are distinguished by having a single flagellum. *T. gondii* and *Plasmodium* spp. belong to a different phylum called Apicomplexa and are intracellular parasites. The definitive hosts of *T. gondii* are cats and other felines, and intermediate hosts can be humans and other vertebrates. Transmission to humans is usually through contaminated food (meat or vegetables and leafy greens that have not been properly washed), contaminated water or contact with cat faeces. Toxoplasmosis is usually a mild disease in humans but can pose a serious risk to a fetus if infected during pregnancy and lead to severe illness in immunosuppressed individuals. *Plasmodium* spp. are transmitted by mosquitoes of the genus *Anopheles* and can cause malaria. There are also zoonoses caused by multicellular parasites, such as diseases caused by worms from the phylum Nematoda (causing filariasis, trichinellosis and gnathostomiasis) and the class Cestoda (causing hymenolepiasis, taeniasis, cysticercosis and echinococcosis) (PAHO 2003).

Zoonoses in the Selva Maya and surrounding area

In order to provide an overview of zoonoses and wildlife diseases in the Selva Maya region, the PubMed international database, developed and maintained by the National Center for Biotechnology Information (NCBI, last accessed in February 2021), was searched for scientific articles on the subject. The search terms used were 'zoonosis' or 'wildlife diseases' combined with different place names: Mexico, Guatemala and Belize and the areas Selva Maya, Maya Biosphere, Yucatán, Campeche, Quintana Roo, Calakmul, Laguna del Tigre, Rio Bravo and Montes Azules. Common search engines (such as Google) were also used to find literature on the subject in Spanish. In addition to this work, three experts in zoonoses in the Selva Maya region were consulted about the current state of research in this field and

asked to provide bibliographic recommendations. This study does not have the same scope as a systematic literature review. Its aim is to provide an overview of existing studies and then illuminate and evaluate this first impression. The table at the end of the document provides a summary of the zoonotic pathogens found in the literature.

Urban and rural studies

Many of the studies examined refer to zoonoses in urban and rural areas, with a focus on domestic animals, and almost all of them are on Mexico. Many studies report zoonotic pathogens in cats and dogs. For example, a serology study found zoonotic parasites (*T. gondii* and nematodes) in dogs and humans in rural Yucatán, Mexico (Ortega-Pacheco, Torres-Acosta et al. 2015), and intestinal parasite infestations in the same area were correlated with zoonotic risk factors, such as the age and physical condition of the dogs studied (Rodríguez-Vivas, Gutierrez-Ruiz et al. 2011). In a similar study, the eggs of zoonotic intestinal nematodes were found in the faeces of dogs in public parks in Mérida, Yucatán (Medina-Pinto, Rodríguez-Vivas et al. 2018). Antibodies against various pathogens (*T. cruzi*, *T. gondii* and *Leptospira interrogans*) were found in free-roaming domestic dogs and cats in a rural community (Mayapan) in Yucatán (Ortega-Pacheco, Guzmán-Marín et al. 2017), and domestic cats were identified as important reservoirs of *T. cruzi* in Yucatán (Jiménez-Coello, Acosta-Viana et al. 2012). Serological and molecular testing detected *T. gondii* in dogs in Yucatán (Valenzuela-Moreno, Rico-Torres et al. 2020) and a wide variety of *T. gondii* strains in cats in Quintana Roo (Valenzuela-Moreno, Rico-Torres et al. 2019). *Rickettsia typhi* was detected by molecular testing (polymerase chain reaction – PCR) in dogs in Yucatán (Martínez-Ortiz, Torres-Castro et al. 2016).

In summary, dogs and cats pose a risk in terms of endemic zoonotic diseases caused by parasites and bacteria. There are fewer studies on other domestic and farm animals. One study identified pigs as an important reservoir of *T. cruzi* in Yucatán (Jiménez-Coello, Acosta-Viana et al. 2012), and antibodies against *L. interrogans* were found in cattle and pigs in rural communities in Yucatán (Cárdenas-Marrufo, Vado-Solís et al. 2011).

“Dogs, cats and other domestic animals pose a risk in terms of endemic zoonotic diseases caused by parasites and bacteria.”

In addition to these studies on domestic animals, there have been others on rodents in urban and rural areas. Some rodent species can be defined as synanthropic (undomesticated species that live in close association with humans), owing to intrusive behaviour that brings them into close proximity with people, facilitating the transmission of pathogens. In Mérida, *T. cruzi*, *Hymenolepis diminuta* and *L. interrogans* were detected in the house mouse (*Mus musculus*) and the black rat (*Rattus rattus*) (Panti-May, de Andrade et al. 2017). Molecular evidence was also found of *L. interrogans* in *R. rattus* and *M. musculus* and in an endemic rodent species, *Heteromys gaumeri*, in a rural community in Yucatán (Torres-Castro, Cruz-Camargo et al. 2018). In rural areas in Yucatán, three different species of hymenolepidid cestodes were detected in children and synanthropic house mice and black rats (Panti-May, Servián et al. 2020). A new *Bartonella* species was isolated from Yucatán deer mice (*Peromyscus yucatanicus*) in rural areas near Mérida (Schulte Fishedick, Stuckey et al. 2016). There have been practically no studies on wild animals in urban areas other

than rodents. The only one found was a serology study on bats reporting the detection of antibodies against flaviviruses in Mérida (Machain-Williams, López-Urbe et al. 2013). Apart from studies on domestic animals and synanthropic rodents and bats, there are also reports of zoonotic pathogens in humans. A study of zoonotic foodborne bacteria (*Salmonella* spp. and *Campylobacter* spp.) in humans in a rural area in Yucatán, combined with animal and food (meat) surveillance for both pathogens, revealed that in spite of high levels of food contamination in this community, the impact on human health was generally low, presumably owing to the fact that food was properly prepared and the population had access to safe water and health care (Zaidi, Campos et al. 2012). By contrast, cutaneous leishmaniasis had a relatively high impact on human health in rural Calakmul, Campeche, with a prevalence of up to 12.3% in the population over a two-year period (Hernández-Rivera, Hernández-Montes et al. 2015).

There are clinical case reports on single zoonotic events where the source of infection is unclear. For example, two reports describe cases of *Lagochilascaris minor* in three patients in Campeche, Yucatán (Barrera-Perez, Manrique-Saide et al. 2012) and one person in Quintana Roo (González-Solís, Elías-Gutiérrez et al. 2019). *R. typhi* was detected in a patient in Campeche and in two patients in Yucatán (Dzul-Rosado, González-Martínez et al. 2013; Blum-Domínguez, Sánchez-Montes et al. 2019). In addition, in Guatemala, a zoonotic group A rotavirus (strain G8P[14]) was detected during routine rotavirus surveillance (Gautam, Mijatovic-Rustempasic et al. 2015).

No cases of rabies caused by domestic animals have been reported in Yucatán since 1998, thanks to vaccination campaigns. However, several cases of rabies transmitted by wild animals have been described. Rabies was detected in a girl bitten by a skunk in 2001 (Ortega-Pacheco and Jiménez-Coello 2017), and another girl was infected in 2006, probably by a vampire bat (Gómez-Carro, L. Ortiz-Alcaraz et al. 2006).

In summary, the review found studies on domestic animals (mostly dogs and cats) and synanthropic wild animals (mostly rodents) and case reports on infections in the human population. Most zoonotic pathogens reported in animals were endemic zoonoses caused by parasites and bacteria (*T. cruzi*, *T. gondii* and *L. interrogans*).

Wildlife

There were relatively few studies on zoonoses in wildlife, and they were predominantly concerned with bats and rodents. Research on bats included bacterial studies that detected haemotropic *Mycoplasma* spp. (for example, haemoplasmas) and *Bartonella* spp. in Belize (Archaeological Reserve and Ka'Kabish) (Becker, Bergner et al. 2018; Becker, Speer et al. 2020). Virology studies identified molecular evidence of dengue virus in bats in Campeche and Chiapas (Mexico) and a wide variety of coronaviruses in Campeche (Anthony, Ojeda-Flores et al. 2013; Sotomayor-Bonilla, Chaves et al. 2014).

Studies on rodent zoonoses included the molecular detection of *Leptospira* sp. in rodents in the wild in Yucatán (Torres-Castro, Cruz-Camargo et al. 2018). Another study on antibodies in wild rodents captured near La Libertad, Campeche, indicated the occurrence of leishmaniasis in the animals (Canto-Lara, Van Wynsberghe et al. 1999).

“ While there are a significant number of studies on zoonoses in urban and rural settings, there are few on wildlife zoonoses. ”

Evidence of *T. cruzi* DNA was found in bats, rodents and marsupials, showing that *T. cruzi* remains in the wildlife cycle (Lopez-Cancino, Tun-Ku et al. 2015). Molecular testing also found Venezuelan equine encephalitis virus in bats and rodents in Calakmul and Montes Azules, Mexico (Sotomayor-Bonilla, Abella-Medrano et al. 2017).

Apart from these studies on bats and rodents, there are also individual studies on other wild animals. For example, antibodies against *L. interrogans* were found in crocodylians in Quintana Roo (Pérez-Flores, Charruau et al. 2017), and the influenza A virus was found by molecular detection in wild pigs (*Sus scrofa*) in fragmented forest areas in Campeche (Maya-Badillo, Ojeda-Flores et al. 2020).

In summary, various pathogens were found in wild animals although few studies have been carried out in this area. Those that do exist focus on rodents and bats, which are the natural reservoirs of a wide range of pathogens (Luis, Hayman et al. 2013).

Vector studies

Vector surveillance studies can also serve as a useful tool for estimating zoonotic risk in a particular area.

The above-mentioned study on Venezuelan equine encephalitis virus, for example, not only detected the virus in hosts, but also showed the presence of certain species of mosquitoes in the same area (Calakmul and Montes Azules) that could act as vectors (Sotomayor-Bonilla, Abella-Medrano et al. 2017). The observation of previously unknown species is also important, such as the new *Anopheles* species detected in Quintana Roo (*Anopheles veruslanei*), which is a potential vector (Chan-Chable, Martínez-Arce et al. 2018).

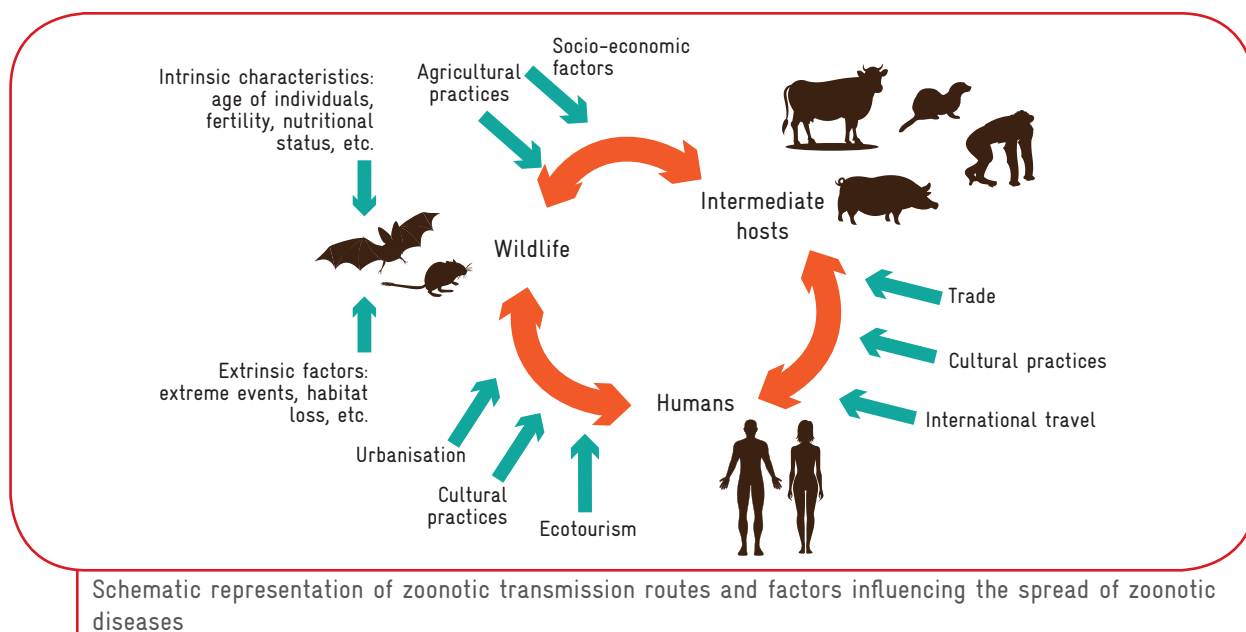
Ticks can also act as vectors. In Yucatán, a study examined the diversity of tick species collected from humans, wildlife and domestic animals (Rodríguez-Vivas, Apanaskevich et al. 2016), and a study on tick parasitism in crocodylians in Quintana Roo showed that, while ticks do not represent a major threat to these animals, habitat fragmentation and cattle expansion could increase tick parasitism and maybe trigger an increase in tick-borne diseases (Charruau, Pérez-Flores et al. 2016).

Leishmania spp. and *Trypanosoma* spp. are examples of parasites transmitted by vectors. Two studies in Calakmul evaluated the importance of different phlebotomine species as potential vectors in the transmission of parasites that cause leishmaniasis (Pech-May, Escobedo-Ortegón et al. 2010; Pech-May, Peraza-Herrera et al. 2016). A study in Guatemala and Belize on *T. cruzi* showed that the feeding sources of *Triatoma dimidiata*, a major cave-dwelling vector of this parasite, were linked to the human use of caves (Stevens, Monroy et al. 2014), and a study that researched *T. dimidiata* infestation dynamics in different rural areas of Guatemala showed very high colonisation rates in highly deforested tropical dry forest regions (Penados, Pineda et al. 2020).

There are few studies available on vectors in the region. Large-scale studies carried out in the future could provide valuable input for research on zoonoses under the One Health concept.

Anthropogenic impacts on wildlife health

Wildlife can be threatened by infectious diseases transmitted by humans (zoonoses) or by other animals (non-zoonotic cross-species transmission). An example of a zoonotic transfer of this kind is the transmission of the parasite *Giardia duodenalis* from humans to black howler monkeys (*Alouatta pigra*) in Belize (Vitazkova and Wade 2006). With increasing human intrusion into wildlife habitats, transmission from domestic animals could also be a serious concern. An example of this is equine infectious anaemia (EIA) virus (*Lentivirus* genus of the *Retroviridae* family), a horse disease that has been considered a potential risk for Baird's tapirs (*Tapirus bairdii*). An analysis of antibodies against EIA virus in horses in the Maya Biosphere Reserve in Guatemala found that 40% of horses were seropositive (Lepe-López, García-Anleu et al. 2018). In view of this finding and observation of the use of horses in the reserve, it can be concluded that it represents a potential threat to tapir populations (Lepe-López, García-Anleu et al. 2018). Another example involves carnivore species. Evidence has been found of two-way transmission between domestic and wild species for carnivore protoparvovirus 1 in Mexico's Janos Biosphere Reserve (López-Pérez, Moreno et al. 2019). If untreated, this virus can cause severe disease and high mortality rates.



“ Rabies is another example of a virus transmitted from wild animals, specifically vampire bats, to domestic animals, particularly cattle (Ellison, Gilbert et al. 2014). ”

Threatened animal species can, of course, also be affected by zoonoses that put specific populations at risk. For example, a serology study in Belize on West Indian manatees (*Trichechus manatus manatus*), listed as an endangered species by the International Union for Conservation of Nature (IUCN), identified antibodies against various potentially zoonotic pathogenic agents, including parasites, bacteria and viruses (*Leptospira* spp., *T. gondii*, viruses from the *Morbillivirus* genus) in the animals studied (Sulzner, Kreuder Johnson et al. 2012).

Anthropogenic impacts can also lead to dietary shifts in wild animals and therefore alter pathogen load. A study on vampire bats in Belize showed that habitat fragmentation affected their diet. Bats living in a small forest fragment had more homogenous diets, indicative of feeding on livestock, compared with those living in intact habitats, and this probably led to shifts in microbiota heterogeneity (Ingala, Becker et al. 2019).

Other examples of threats to wildlife include the fungus *Batrachochytrium dendrobatidis* (Bd) and ranaviruses (RV) which cause high mortality among amphibians (Duffus, Waltzek et al. 2015; Scheele, Pasmans et al. 2019). It is suspected that anthropogenic influences that result in altered habitats, for example, higher water temperatures, increase the risk of infection. Contact between wild and captive amphibians through international trade also increases the threat to these animals (Brunner, Storfer et al. 2015). A study on the interaction of Bd and RV with macroparasite chiggers (Acariformes) in Mexican amphibians found that rates of infection with Bd and RV were not increased by chiggers (Jacinto-Maldonado, García-Peña et al. 2020). However, the role of other parasites in Bd and RV infection is not known. As summarised by the authors, there have been many reports of Bd in Mexico, but as yet none of RV in wild animals, except in captive frogs. Contact between native and exotic species through international trade could increase the risk of infection spreading in wild species (summarised in Jacinto-Maldonado, García-Peña et al. 2020).

In summary, the threat faced by wildlife from infectious diseases is complex and influenced by humans in various ways, including the direct transmission of pathogens, domestic animals, habitat disruption and the introduction of exotic species in the ecosystem, as shown by a number of examples in the Selva Maya and surrounding area.

Risk factors for zoonoses

The likelihood of a zoonotic event occurring is influenced by various factors, as established in the One Health concept. Some risk factors are described in studies on the Selva Maya region. Some studies on the transmission of leishmaniasis provide examples of cultural factors. In a study carried out in Yucatán, rodents and sandflies were found to be infected between November and March, which is when people were out working in the fields and exposed. There was an increase in infection in gum harvesters and farm workers working within a 10 km radius of the villages, while the risk of infection in the villages themselves was relatively low (Andrade-Narváez, Canto-Lara et al. 2003). Another example is the greater risk of cave-dwelling vectors (*T. dimidiata*) becoming infected with *T. cruzi* owing to human cultural practices, such as swimming, hunting and worshipping (Stevens, Monroy et al. 2014). Sex and social structures can also be a risk factor, as shown in a study on the level of knowledge of Chagas disease and triatomines, which found that women in the Calakmul area knew less about vectors and the risks of the disease (Valdez-Tah, Huicochea-Gómez et al. 2015). Household factors can also influence risk, as shown in a study on the infestation dynamics of *T. dimidiata* in Guatemala. It found that walls in poor condition (with cracks where vectors can accumulate), dirt floors and clutter inside the home can increase the risk of *T. dimidiata* infestation (Penados, Pineda et al. 2020).

“Some studies show that sex and social structures can be a risk factor for zoonoses; for example, women in some communities know less about vectors and the spread of disease.”

It has been shown that poor sanitary conditions in areas shared by humans and hosts can increase the risk of transmission of rickettsiae. Waste disposal sites and dirty backyards can attract animals such as rodents and opossums, which are involved in the *R. typhi* infection cycle (Dzul-Rosado, González-Martínez et al. 2013). In urban areas (Maxcanú, Yucatán), the presence of a family fruit and vegetable garden and ectoparasites in the home were risk factors for infection with rickettsia (Torres-Castro, Reyes-Novelo et al. 2020). Socio-economic aspects, such as marginalisation, livestock raising, education, poverty and access to health care were also found to play an important role (Dzul-Rosado, González-Martínez et al. 2013).

The illegal exploitation of wildlife, such as poaching, can increase the risk of zoonoses. A participatory epidemiology study carried out in the Selva Maya region showed that people were driven to poaching by poverty and a lack of employment opportunities. They hunted mainly larger species, including deer and peccaries, although some other smaller species were also sometimes hunted, such as armadillos, lowland pacas (*Cuniculus paca*) and birds (curassows and dusky-legged guans, for example) (Mérida Ruíz, Guerra Centeno et al. 2016). In this regard, it would be especially useful to examine the risk of zoonoses in species that are commonly hunted.

Habitat fragmentation can also increase pathogen infestations, as shown in the study referred to above, which found that it is associated with dietary shifts and microbiota variability in common vampire bats (Ingala, Becker et al. 2019). Forest fragmentation can also lead to behavioural changes in wild animals, for example causing primates to descend to the ground to travel from one forest patch to another and increasing the risk of infection for them, as has been observed for *Giardia* sp. cysts (Vitazkova and Wade 2006). Another risk factor is humans having direct contact with animals, for example, through hand-feeding, as observed in black howler monkeys in the Baboon Sanctuary in Belize (Vitazkova and Wade 2006).

“Zoonotic risk can be increased by illegal exploitation of wildlife, such as poaching, and compounded by socio-economic factors. A participatory epidemiology study carried out in the Selva Maya region showed that people were driven to poaching by poverty and a lack of employment opportunities.”

Educating the population about these issues is also vitally important. A survey on rabies showed that people in two rural communities in Guatemala had little awareness of the danger of bats transmitting rabies, in spite of the fact that they were exposed to frequent contact with these animals (Moran, Juliao et al. 2015). Another example is a survey on *T. dimidiata*, a vector for Chagas disease, which showed that the population had very little knowledge

of the potential danger of *T. dimidiata*. Studies of this kind can reveal significant gaps in the population's knowledge and serve as a basis for public information campaigns (Pacheco Castro, Lugo Pérez et al. 2013).

In general, regional examples corroborate the complexity of risk factors for human and animal health. The interaction between different components highlights the benefits of the One Health approach.

Strategies to reduce zoonotic risk

Risk reduction strategies have been identified in some regional studies. One example is a study for the design of a community-based surveillance programme for influenza in rural areas in Guatemala, which identified a number of challenges for the implementation of such a programme, including knowledge and language gaps between scientific and local players. (Cerón, Ortiz et al. 2016). Community-based surveillance has great potential for the early detection of zoonotic diseases if a common basis can be established through awareness-raising and education.

In the area of vector control, a study on *T. dimidiata* in Guatemala showed that molecular testing of vector blood sources can serve as an early indicator to understand which vector control methods effectively reduce feeding on humans (Pellecer, Dorn et al. 2013).

A vector surveillance study in Belize and Mexico showed that barcoding, that is, the sequencing of specific genomic regions, can be used to identify vectors. This method was used in a study carried out to determine the diversity of Culicidae mosquitoes in Belize and Mexico (Chan-Chable, Martínez-Arce et al. 2019). It helps in investigating the presence and distribution of vector species and identifying new vectors of specific pathogens.

“ Vaccination campaigns can help reduce zoonotic transmission from domestic animals. ”

Vaccination campaigns can help reduce zoonotic transmission from domestic animals, for example, vaccination against leptospirosis for the main vectors (cattle, pigs and dogs) (Soo, Khan et al. 2020). It is also conceivable that vaccination strategies could be developed for wild animals. Research is being carried out on ways to vaccinate South American vampire bats for rabies. A potential solution is viral vector vaccines that spread autonomously through bat populations (Griffiths, Bergner et al. 2020).

Pathogen surveillance studies on wild and domestic animals can help evaluate zoonotic risk. One example of wildlife surveillance is a study carried out on the prevalence of rabies in vampire bats in Guatemala (Ellison, Gilbert et al. 2014). Free-roaming animals, such as dogs, cats, horses, cattle and pigs, can be a source of pathogens for humans and wildlife and warrant special attention. There are various studies on this subject, as mentioned above, but they are generally local and isolated with small sample sizes.

In summary, there are a variety of different strategies for reducing zoonotic risk, including pathogen surveillance in human and animal populations, vector control, vaccination campaigns and public information campaigns. However, approaches to implementing these strategies in the Selva Maya region are still lacking.

Discussion

Review of the literature on zoonoses and infectious diseases in wildlife in the Selva Maya region

The studies presented here show some of the research carried out on zoonotic diseases and infectious diseases in wildlife in the Selva Maya region. The review found a significantly higher number of studies for Mexico than for Guatemala and Belize. The focus was on endemic zoonoses, especially human diseases, such as Chagas disease, leishmaniasis, leptospirosis, rickettsiosis and their vectors. These diseases represent a constant threat to human health in the region. Virology studies were fewer in number and only covered some of the viruses present in Central America. Very few studies addressed the question of future zoonoses, such as research on new pathogens found in wild animals.

Most of the studies were on domestic animals mainly in populated areas, showing the impact on humans of zoonotic diseases in domestic animals. These studies also provided an insight into potential risks for wild animals coming into contact with domestic animals. There were, however, fewer studies focusing directly on wildlife, aimed, for example, at detecting new pathogens or determining the diversity of pathogens in wild animals.

“ While studies on domestic animals help in evaluating the risks for wild animals that come into contact with organisms associated with humans, more research focusing directly on wild animals and aimed at determining the presence and diversity of new pathogens is needed to assess future risks. ”

Most of the studies were relatively limited in scope with small sample sizes. They were mainly serology studies and therefore focused on detecting the presence of antibodies against a specific pathogen. The main purpose of such studies is to estimate the prevalence with which a pathogen infects a specific cohort of animals or people (seroprevalence). The advantage is that the detection of antibodies can also be used to identify previous infections. However, they are not suitable, in principle, for identifying unknown pathogens; this is done by analysing genetic material. To obtain information on DNA sequences, more complex studies are generally required, which are costlier because they involve taking samples, transportation, laboratory testing, evaluation and analysis. Examples of studies of this kind included the detection of a new influenza A virus in bats (*Sturnira lilium*) in southern Guatemala in 2012. (Tong, Li et al. 2012), the detection of new atypical genotypes of *T. gondii* (Valenzuela-Moreno, Rico-Torres et al. 2019; Valenzuela-Moreno, Rico-Torres et al. 2020), the genetic analysis of *T. cruzi* in various mammal hosts (Lopez-Cancino, Tun-Ku

et al. 2015) and the detection of a new *Bartonella* species in rodents (Schulte Fischedick, Stuckey et al. 2016).

The literature review carried out revealed that there were no large-scale studies addressing the One Health issue in the region. There were, however, a few studies that examine the subject. For example, some studies on vectors analysed anthropogenic impacts on the incidence of zoonotic diseases or potential risk factors, including cultural factors. Some of the studies and ideas could be further developed and efforts in this area intensified through collaboration between different fields of research.

The review found few studies that addressed the risk of reverse zoonotic transmission from humans to wild animals, referred to as spillback, or the risk of infections transmitted by animals introduced by humans, such as domestic animals and exotic species.

It should be taken into account that this work must be continued to provide a complete picture of the research available on zoonoses in the region. More thorough searches for specific pathogens or groups of pathogens, for example, would undoubtedly throw up more studies. This review focused mainly on zoonoses and their impact on the population. For a deeper insight into One Health in the Selva Maya region, more detailed research could be conducted on other aspects of anthropogenic influences, for example, the introduction of invasive species and the resulting spread of infectious diseases, or the impact of stress caused by ecosystem disruption on animal health. This knowledge can also be expanded by looking at studies carried out in other Central American countries or in similar ecosystems in other parts of the world. An analysis of such studies would contribute to building a better understanding of ecological and anthropogenic changes and the ways in which they influence the One Health system. Certain issues, such as global warming, the effects of zoonoses in Central America and the impact of habitat fragmentation and construction projects could also be studied in greater depth. In addition to the literature review, it would also be useful to consult the different entities and individuals involved, including government institutions, non-governmental organisations (NGOs), park rangers and people living in the vicinity of nature reserves.

Potential future studies and new approaches

As mentioned above, there is a need for large-scale studies on unknown pathogens in wild animals in the region, especially those considered to be important zoonotic hosts, such as small mammals (particularly bats and rodents) and primates. The problem is that such studies require considerable effort and resources. Capturing wild animals and laboratory testing methods (PCR testing, for example) can be very costly, and the analysis work required is very demanding (large-scale sequencing, for example). Cooperation among different institutions and areas of research is vitally important as savings can be made by pooling resources. For example, samples can be taken from animals captured for ecological purposes. It is also useful to take different types of samples (blood, swabs, faeces, etc.), so that different pathogens can be investigated, and to involve people working on other fields of research, for example by including studies on vectors in the different areas,.

“Cooperation among different institutions and areas of research is vitally important, particularly in processes that involve capturing and sampling wild animals to investigate their pathogens.”

A more in-depth analysis of the potential risks for humans will require monitoring groups of people who are in direct contact with wild animals (for example, hunters, vets, park rangers and community wardens in protected natural areas) or who have frequent contact with different animals (for example, vets). Subsistence hunting is a major problem in the region, and a multidisciplinary pilot study looked at which animals were hunted and how the meat was cooked (Mérida Ruíz, Guerra Centeno et al. 2016). The purpose of the study was to identify possible sources of infection. Extending such a study to examine the pathogens found in the animals hunted would be a useful addition.

The monitoring of cohorts of patients, for example, those with a fever of unknown origin or diarrhoea (detection of a zoonotic rotavirus in Guatemala through routine surveillance (Gautam, Mijatovic-Rustempasic et al. 2015), can also contribute to the early detection of new pathogenic agents in humans.

Monitoring domestic, peridomestic and synanthropic animals is also very important because they can increase transfers between animals and humans. Monitoring enables threats to both animals and humans to be identified.

Animals that have been granted protected status should also be monitored for early detection of potential threats to them. There are a number of approaches for researching anthropogenic influence (for example, habitat fragmentation) on wildlife health. This important aspect can be researched at different levels (emergence of pathogens, pathogen ecology, vectors). Research on anthropogenic influence and the One Health aspect could also be extended to include non-infectious threats to wildlife, such as environmental contamination. A local example is a study conducted on vampire bats in Belize which found that those feeding on domestic animals had higher levels of mercury (Becker, Chumchal et al. 2017). Sometimes, the mechanisms for avoiding the risk of infection are highly complex. For example, black howler monkeys in Belize are at greater risk of being infected by a trematode parasite (*Controrchis* spp.) when they feed on trumpet trees (*Cecropia peltata*). *C. peltata* is a pioneer tree species that typically occurs in disturbed areas, highlighting the important link between habitat disturbance and parasitism in wild mammals (Kowalzik, Pavelka et al. 2010).

Vector-host ecology studies can also indicate if pathogens switch species frequently. Such a study was conducted on *T. cruzi* in different host and vector populations in Guatemala, in which genetic analyses showed clear evidence of parasite-host switches (Pennington, Messenger et al. 2015). Past host switches can also be detected in genetic analyses of pathogenic agents, such as evolutionary biological analyses of viruses (for example, rotaviruses in Costa Rica) (Simsek, Corman et al. 2021). It is crucially important to have information on the diversity of pathogens in wildlife as it helps to rapidly identify possible zoonotic sources for emerging pathogens. Long before the start of the current pandemic caused by SARS-CoV-2, it was known that bats harbour a wide range of potentially zoonotic coronaviruses. This facilitated rapid identification of the origin of the virus (Lu, Zhao et al. 2020). By identifying potential zoonotic sources, the risk of future pandemics can be reduced.

The One Health approach has not yet been studied in any great depth.

“In the future, interdisciplinary studies could be carried out to examine the interaction between ecology, animal health and human health in greater depth. They could focus, for example, on analysing ecosystem disruption and its effect on the interaction between pathogens and their hosts, identifying and studying pathogen host switches and the factors contributing to them, investigating potential vectors of infectious diseases and the influence of environmental factors on their distribution.”

It is also important to look at social factors, for example, the knowledge people have of zoonoses, particularly those in contact with wild animals.

In summary, large-scale interdisciplinary studies focusing on potential new zoonoses and threats to wildlife would be of great value for the Selva Maya region. It is important to ensure the protection and sustainable management of nature reserves, incorporating the One Health approach. The interaction between the environment and animal and human health needs to be investigated more thoroughly, and in addition to efforts to research and understand these interrelationships, it is also vitally important to educate society about One Health, raising awareness not only about the risks of contact with wildlife, but also about the adverse consequences of disrupting ecosystems.

Table 1: Zoonotic pathogens detected in domestic and wild animals in the Selva Maya region (included in this study)

	Pathogen	Place	Animal	Method of detection
Bacteria	<i>Leptospira sp.</i>	Yucatán, Quintana Roo, Mexico;	Dogs, cats, cattle, pigs, rodents, crocodylians	Serology, direct detection (immunofluorescent imprints), molecular detection
	<i>Rickettsia typhi</i>	Yucatán, Campeche, Mexico	Dogs	Molecular detection, human case reports
	<i>Bartonella sp.</i>	Yucatán, Mexico; Belize	Rodents, bats	Molecular detection
	<i>Mycoplasma spp.</i>	Belize	Bats	Molecular detection
	<i>Salmonella spp.</i>	Yucatán, Mexico	Unknown	Human case reports
	<i>Campylobacter spp.</i>	Yucatán, Mexico	Unknown	Human case reports
Parasites	<i>Toxoplasma gondii</i>	Yucatán, Quintana Roo, Mexico	Dogs, cats	Serology, molecular detection
	<i>Leishmania spp.</i>	Campeche, Mexico	Rodents	Serology, molecular detection, vector analysis
	<i>Trypanosoma cruzi</i>	Yucatán, Mexico, Guatemala, Belize	Dogs, cats, pigs, rodents, bats, marsupials	Serology, human case reports, vector analysis
	<i>Lagochilascaris minor</i>	Campeche, Quintana Roo, Mexico	Unknown	Human case reports
	Nematodes	Yucatán, Mexico	Dogs	Direct detection (eggs)

	Pathogen	Place	Animal	Method of detection
	<i>Hymenolepis spp.</i>	Yucatán, Mexico	Rodents	Direct detection (eggs), molecular detection
Viruses	Flavivirus	Yucatán, Mexico	Bats	Serology
	<i>Rabies virus</i>	Yucatán, Mexico	Bats, skunks	Human case reports
	<i>Dengue virus</i>	Campeche, Chiapas, Mexico	Bats	Molecular detection
	Coronavirus	Campeche, Mexico	Bats	Molecular detection
	<i>Venezuelan equine encephalitis virus</i>	Campeche, Mexico	Bats, rodents	Molecular detection
	<i>Influenza A virus</i>	Campeche, Mexico	Wild pigs	Molecular detection
	<i>Group A rotavirus</i>	Guatemala	Unknown	Human case reports

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