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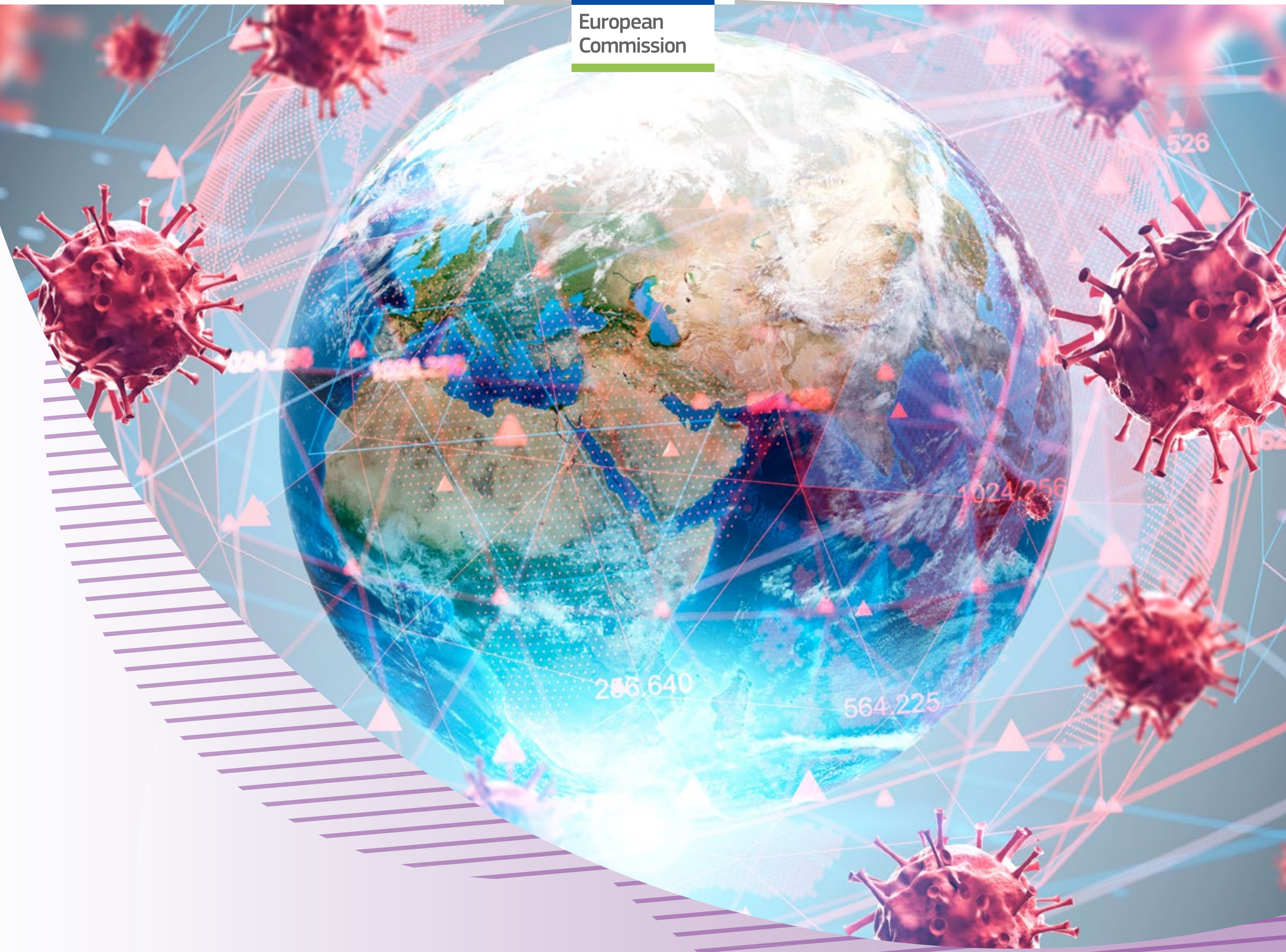

Science for Environment Policy

FUTURE BRIEF:
COVID-19 and the environment: links, impacts and lessons learned

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COVID-19 and the environment: links, impacts and lessons learned

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Science for Environment Policy Future Brief 26:

COVID-19 and the environment: links, impacts and lessons learned

Contents

1. Introduction

Since early 2020, the disease caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), known as COVID-19 (first detected at the end of 2019), has hit societies worldwide, unsparingly, causing massive impacts on people's lives: our health, activities, livelihoods, societies and economies. However, over the course of the pandemic, COVID-19 is not the only crisis our human and planetary systems have been dealing with. While the pandemic has been progressing, the world has simultaneously been undergoing other existing crises: those of biodiversity loss, loss of environmental health and rapid climate changes, associated with resource use, land-use changes and ongoing emission of carbon into the atmosphere. A growing world population and encroachment into areas of high biodiversity and microbial diversity, often in search of food, minerals or for farming purposes has meant that habitats and species are increasingly under pressure from human activities (IPBES, 2020).

Viral epidemic or pandemic spreading around the world (©Getty Images/ libre de droit, public domain)

The same factors threatening wildlife are leading to increased pathogen emergence; degrading biodiversity undermines the web of life and increases the risk of disease spillover (transmission of disease from one species to another). Chapter 2 presents the current state of scientific knowledge as regards possible links between the spread of diseases, including the spread of COVID-19, and environmental factors. While the impacts on people's lives have been enormous, there have also been significant effects on the environment – the most well-evidenced of these is discussed in Chapter 3.

The costs of implementing more sustainable practices worldwide are far outweighed by the losses – monetary and non-monetary – that pandemics and wildlife epidemics will cost cumulatively, if a business-as-usual approach is maintained. The longer-term responses to this pandemic (some of which are discussed in Chapter 4) offer a unique and unrepeatable opportunity for transformative change. Designing a 'green economic recovery' from COVID-19 may also offer protection against future outbreaks.

The European roadmap to sustainability, the 'European Green Deal', has transformation at its heart, and via the EU Biodiversity Strategy for 2030, aims to protect and restore ecosystems. To implement this approach, governments worldwide now need to work together to form a cohesive approach to avoid entering into an era of pandemics and to decrease the likelihood of future pandemics, including through maintaining and restoring environmental health.

> **"Making nature healthy again is key to our physical and mental wellbeing and is an ally in the fight against climate change and disease outbreaks. It is at the heart of our growth strategy, the European Green Deal, and is part of a European recovery that gives more back to the planet than it takes away."**
>
> Ursula von der Leyen, President of the European Commission (EU, 2020)

The rapid global spread and health impacts of the virus that causes COVID-19 have alerted the world to society's vulnerability to zoonotic disease pandemics – where new pathogens are transmitted from wildlife to humans (Plowright *et al*., 2021). The 20th century saw numerous major pandemics including the 'Spanish' flu of 1918-19, the 'Asian' flu (H2N2) of 1957, and the 'Hong Kong' flu of 1968 (the geographical designations do not necessarily indicate places of origin). The frequency of these events is increasing; COVID-19 is not the first zoonotic epidemic or pandemic of the 21st century to affect multiple countries. Before COVID-19 came: severe acute respiratory syndrome (SARS), beginning in 2002, 'swine flu' in 2009, Middle East Respiratory Syndrome (MERS) in 2012, and Ebola virus disease in 2013 (Gössling, Scott and Hall, 2020).

1.1 What are coronaviruses?

Coronaviruses are viruses in the order *Nidovirales. Nidovirales* infect vertebrates and invertebrates, and the coronaviruses are a subfamily (*Orthocoronavirinae*) in the *Coronaviridae* family that infect birds and mammals (Gorbalenya *et al*., 2020). There are seven types of coronavirus known to infect humans. These all originated following human infection from another animal species, which acted either as a reservoir host (such as bats) or intermediate host (such as Asian palm civets). According to the European Centre for Disease Prevention and Control (ECDC, 2021a), four human-infective coronaviruses cause "mild-to-moderate disease", while three others cause "more severe and even fatal disease" and have only become recognised in the past two decades (see Table 1).

These three more dangerous coronaviruses have each caused significant outbreaks. Firstly, 2002 saw the SARS outbreak, caused by the SARS-CoV virus. SARS was first reported in China, is thought to have originated from bats and been transmitted to humans by civets (*Paguma larvata*) acting as an intermediate host. SARS had a mortality rate of 11% (Li *et al*., 2020). In 2012, the MERS-CoV virus led to the first outbreak of MERS, which emerged in Saudi Arabia. MERS-CoV has its ancestry among bats, but is now transmitted among camels – in which it causes mild symptoms – and from camels to people, with a fatality rate among people of over one-third (Killerby *et al*., 2020). MERS-CoV has since emerged in other countries both sporadically and in clusters. In late 2019, SARS-CoV-2 caused the current global pandemic: an outbreak of the associated disease COVID-19 was first reported in China. While the initial animal-to-human transmission pathway for SARS-CoV-2 remains unclear, the virus is presently suspected to have originated from Chinese horseshoe bats or, less likely, pangolins, as coronaviruses related to SARS-CoV-2 – but not similar enough to confirm origin – have been found in both species (WHO, 2021a; Boni *et al*., 2020; Nga *et al*., 2022; Chan and Zhan, 2022). The role of any other intermediate host or hosts, however, is yet to be confirmed.

Table 1: Taxonomy of coronaviruses, including species that cause disease in humans. Table adapted from ECDC (2021a) with additional information sourced from Li *et al*. (2020).

Order: Nidovirales				
Family: Coronaviridae				
Sub-family	**Genus**	**Sub-genus**	**Species**	**Strain**
Orthocoronavirinae	Alphacoronavirus (infects mammals)	Duvinacoronavirus	Human coronavirus 229E	
		Sertacovirus	Human coronavirus NL63	
	Betacoronavirus (infects mammals)	Embecovirus	Human coronavirus HKU1	
			Betacoronavirus 1	HCoV-OC43
		Merbecovirus	Middle East respiratory syndrome-related coronavirus	MERS-CoV
		Sarbecovirus	Severe acute respiratory syndrome–related coronavirus	SARS-CoV
				SARS-CoV-2
	Deltacoronavirus (infects mammals and birds)			
	Gammacoronavirus (infects birds)			

Table legend:

Mild-to-moderate disease

Severe-to-fatal disease

1.2 Coronavirus outbreaks

Spread chiefly via respiratory droplets from infected people, including aerosols, and less commonly through contact with contaminated surfaces, SARS (caused by the SARS-CoV virus) was the “first severe and readily transmissible new disease to emerge in the 21st century and showed a clear capacity to spread along the routes of international air travel”, says the World Health Organization (2021c). The virus has an incubation period of up to 10 days and causes fever, malaise, muscle pain, and mild respiratory symptoms, in some cases progressing to severe respiratory illness, shortness of breath and hypoxemia (low blood oxygen). There is currently no cure or vaccine for SARS, and the 2002-2004 outbreak was brought under control in Asia and Canada via quarantine and screening measures. The virus killed about 10% of those infected (774 of 8,098 infections), with older people (65+) more at risk and accounting for over half of SARS-associated deaths (NHS, 2019). There have been no reported cases of SARS since 2004 (NIAID, 2020).

Middle East Respiratory Syndrome (MERS, caused by the MERS-CoV virus) causes fever, cough, and potential atypical pneumonia, has no current vaccine, and is spread via cough droplets. Again, older people are more susceptible to severe presentation with the illness, as are those with weakened immune systems and/or chronic illness. Cases have been reported from 27 countries since the initial 2012 outbreak in Saudi Arabia, and two further outbreaks have occurred in South Korea (2015) and Saudi Arabia (2018). Overall, over one-third of those known to have contracted MERS have died (940 of 2,589 infections; ECDC, 2021b), although – as with all coronaviruses – mild cases of MERS may have been overlooked, inflating the relative case fatality percentage. Like SARS, there is no specific treatment for the disease, and MERS was – and is, when it emerges – controlled using public health interventions, monitoring, and respiratory treatment.

COVID-19 (the disease caused by the SARS-CoV-2 virus) is spread in a similar way to MERS and SARS. Most people contracting COVID-19 will experience fever, a dry cough, and fatigue, with other symptoms including aches and pains, a sore throat, headaches, and a loss of taste or smell. This can progress to difficulty breathing and severe respiratory distress, especially in vulnerable patients. It is highly transmissible; six months following the virus’ discovery, over 10 million people had been infected and over 500,000 had died (NIAID, 2020). By January 2022, over 290 million cases had been confirmed, with 5.5 million deaths (WHO, 2022). Case fatality rates as of this date average around 1 to 2% in high-income countries with good diagnostic capability. South Africa, Brazil and Russia have reported rates between 2.5-3%; Mexico 7.5% (JHU, n.d.). Determining the true infection fatality rate is difficult because of changes in case ages, co-morbidities, treatments, and diagnostic capacities by country and through time. However, in countries most hit, like Peru, more than 1 in 200 people have died of COVID-19 (O’Driscoll *et al.*, 2020; MINSA, 2021). Successful vaccination programmes and new treatments, meanwhile, plus the emergence of different dominant variants, mean these statistics are rapidly changing.

SARS, MERS, and SARS-CoV-2 infection can all present as asymptomatic, increasing their potential to be a global public health issue as they can be transmitted before the infection is known. In contrast to SARS-CoV and MERS-CoV, however, SARS-CoV-2 has a high likelihood of asymptomatic expression, estimated at 35% (Sah *et al.*, 2021), meaning that infection rates may be far higher than confirmed cases.

The COVID-19 outbreak has prompted unprecedented, stringent and widespread preventative measures, with local and national restrictions on going outdoors (including curfews), travel, work, activity, and socialising; halting of international travel; and rapid development and rollout of a vaccination programme. Mass public testing has also been promoted.

1.3 Viral structure

Coronaviruses are positive-sense, single-stranded viruses composed of ribonucleic acid (RNA), and have the largest genome of all known RNA viruses (Li *et al.*, 2020). The descriptors of 'positive-sense' and 'single-stranded' refer to the way in which these viruses store information, and how this information is translated into a sequence of amino acids for replication; positive-strand RNA virus material can be directly turned into protein within a host cell.

Their spherical structure comprises a string of nucleoproteins connected to genomic RNA, itself wrapped ('enveloped') in a lipid membrane protein studded by 'spike' proteins. These spikes, which are critical for the virus successfully bonding with and entering a host cell, somewhat resemble a crown (or, in Latin, a '*corona*') – hence the virus' name. Coronavirus virions are roughly 60-140 nanometres in diameter, and made up of four main structural proteins: spike (S), membrane (M), envelope (E), and nucleocapsid (N), all of which hold different functions and enable the virus to store material within its viral envelope, bind to host cells, and replicate within the human (or mammalian or avian) body.

Figure 1: The spike protein on SARS-CoV-2 attaches to the ACE2 receptor in human and animal hosts.
Source: Kateryna Kon / Shutterstock

1.4 Evolution of SARS-CoV-2 worldwide

SARS-CoV-2 was initially identified in Wuhan, China, in December 2019 and consensus is that this is where the virus emerged. It may have been introduced in the EU as early as December 2019, although this was not known at the time – RNA fragments of the virus were detected retrospectively via analysis of sewage samples gathered from northern Italy (ECDC, 2021a; La Rosa *et al.*, 2021a; Nadeau *et al.*, 2021). Since then, the virus has spread to every continent on the planet via human-to-human transmission – even Antarctica, where 36 people tested positive at a research station in December 2020.

As the virus has been transmitted in huge numbers, it has undergone genetic mutations, giving rise to a number of new 'variants' of the virus. Some variants have demonstrated increased transmissibility, associated disease severity, or immune evasion ('escape') after vaccination, and have therefore been classified as a global public health concern and labelled 'variants of interest, concern, or under monitoring'. According to the World Health Organization (2021b), in order to be a variant, the virus must display genetic changes that are "predicted or known to affect virus characteristics such as transmissibility, disease severity, immune escape, diagnostic or therapeutic escape" and affect how the virus presents itself clinically or epidemiologically, while presenting a potential threat to global public health. As of January 2022, there are four global variants of concern in the EU, and three further variants of interest (ECDC, 2022; see Table 2).

Table 2: Coronavirus variants of concern and interest. The date of initial documentation does not correlate to when the variant was deemed of concern (for instance, the Lambda variant was first spotted in Peru in Dec 2020 but designated a variant of interest in June 2021).

Variants of concern		Variants of interest	
Beta	Initially documented in South Africa, September 2020	**Mu**	Initially documented in Colombia, January 2021
Gamma	Initially documented in Brazil, November 2020	**Lambda**	Initially documented in Peru, December 2020
Delta	Initially documented in India, October 2020	**Lineage AY.4.2** **(no label assigned as yet)**	Initially documented in the UK, June 2021
Omicron	Initially documented in South Africa and Botswana, November 2021		

2. Possible links between the emergence and spread of COVID-19 and environmental factors

The increasing frequency of epidemics and pandemics since 2000 has been linked to global change factors such as land use change causing encroachment onto wild areas, global wildlife trade, live wildlife markets, intensive agricultural practices, climate change, global tourism and poor air quality (IPBES, 2020; Mallapaty, 2020a; Gössling, Scott and Hall, 2020). The likelihood of pandemics emerging is increased by the same global environmental changes driving biodiversity loss and climate change, including land-use change, agricultural expansion and intensification, wildlife trade and consumption – all of which increase human–wildlife contact (IPBES, 2020; Rulli *et al.*, 2021).

Novel diseases like COVID-19 frequently start where environmental degradation in biodiversity hotspots, such as tropical rainforests, leads to new human and animal interactions (Jones *et al.*, 2008; Austin, 2021). Some researchers highlight how trade inequalities, which cause exploitation of both people and the environment in poor nations, increase the likelihood of such degradation. Patterns of consumption in the Global North are in this way linked to the emergence of zoonotic diseases (*ibid.*).

This chapter presents what is known about the environmental drivers that have been linked to COVID-19's emergence and rapid spread (IPBES, 2020). Case studies will highlight systemic environmental links common across large-scale, historical disease outbreaks – including other recent wildlife and human epidemics, or pandemics, that have likely emerged in a similar way to COVID-19. It is important for the public to understand how environmental degradation is implicated in disease outbreak. Knowledge is the basis of human behavioural changes that nudge people towards better environmental stewardship – benefitting global human and environmental health in the future (Carlsson *et al.*, 2021). This chapter also presents policy and management recommendations from the scientific literature that address possible environmental drivers of emerging disease. For example, the Intergovernmental Platform of Biodiversity and Ecosystem Services (IPBES) endorses a 'One Health' approach, linking human health, animal health and environmental sectors.

> **"The majority (70%) of emerging diseases (e.g. Ebola, Zika, Nipah encephalitis), and almost all known pandemics (e.g. influenza, HIV/AIDS*, COVID-19), are zoonoses – i.e. are caused by microbes of animal origin. These microbes 'spill over' due to contact among wildlife, livestock, and people."**
>
> (IPBES, 2020)

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*considered a global epidemic by WHO

2.1 Land-use change

> **"Losses of intact ecosystems have occurred primarily in the tropics, home to the highest levels of biodiversity on the planet. For example, 100 million hectares of tropical forest were lost from 1980 to 2000, resulting mainly from cattle ranching in Latin America (about 42 million hectares) and plantations in South-East Asia (about 7.5 million hectares, of which 80% is for palm oil…"**
>
> (IPBES, 2019)

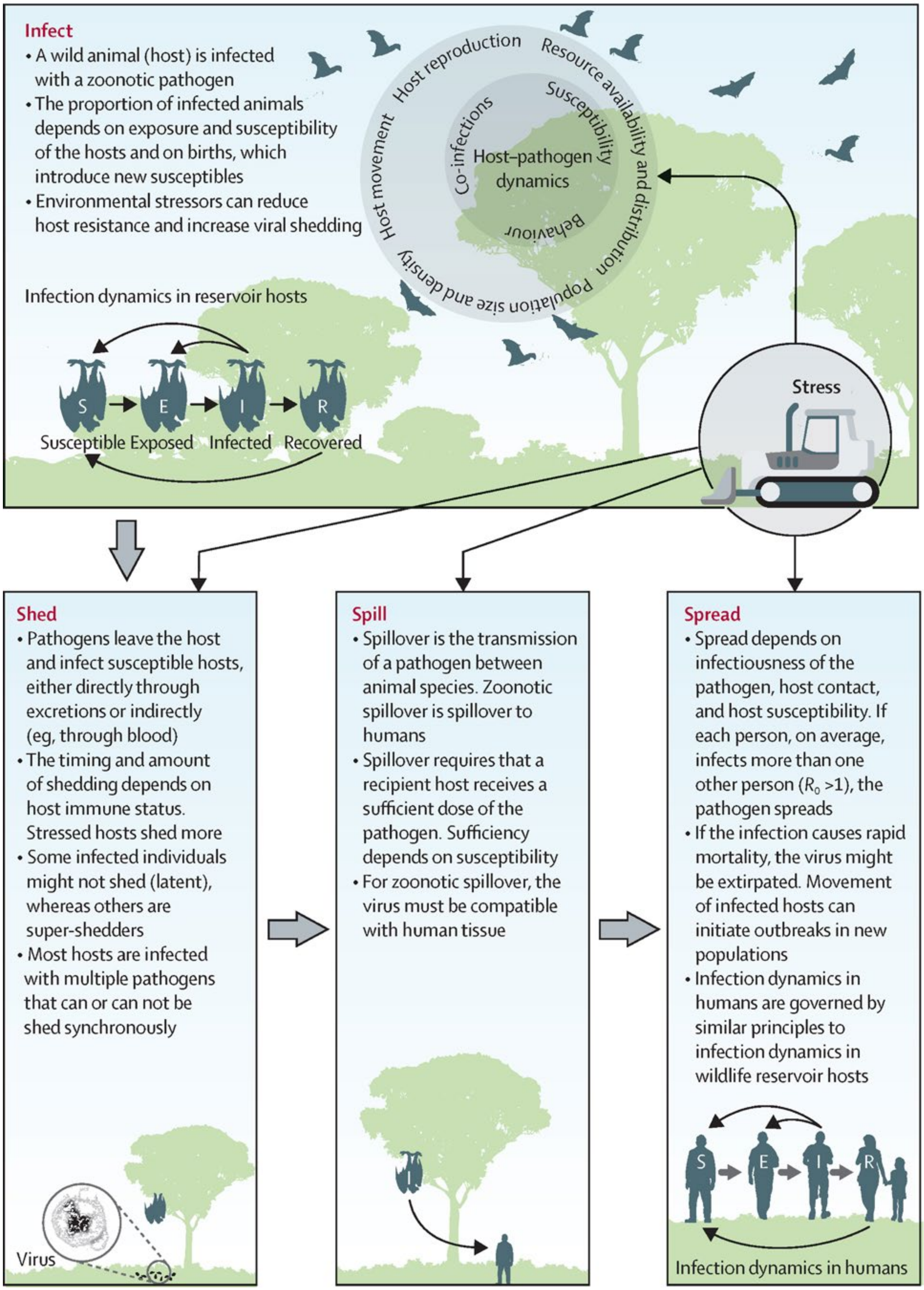
Habitat destruction due to mining, roads, increasing urbanisation and agriculture brings wildlife – and its pathogens– into greater contact with humans. This leads to a greater possibility of disease transmission from bites, handling of bushmeat, vectors (such as ticks and mosquitoes), and directly from consumption of meat (Gombeer *et al*., 2021; IPBES, 2020; Rulli *et al*., 2020; Wilkinson *et al*., 2018; Franklinos *et al*., 2019). The rapid process of land-use change globally is considered by many to be the primary driver of pathogen transmission from wildlife to humans, in a process known as 'zoonotic spillover' (Figure 3 (Plowright *et al*., 2021).

Figure 2: Illegal logging on indigenous Pirititi Amazonian lands. Source: IPBES 2020, credit quapan/CC BY2.0.

Land-use changes, or anthropogenically induced ecosystem changes, are taking place at both local and regional scales, and may induce environmental stressors, such as resource and land constraints, affecting wildlife numbers and distribution. Such environmental stressors shape the exposure and susceptibility of species to pathogen infection (Lafferty and Holt, 2003; Plowright *et al*., 2021). This human-driven alteration in wildlife dynamics can drive pathogen 'shedding' – creating opportunities for the pathogen to spread between species ('spillover'), which may result in people living in the area becoming infected, instigating infection spread between humans (see Figure 3; *ibid*).

Figure 3. Land-use-induced spillover schematic, explaining the infect-shed-spill-spread cascade.

Source: Plowright *et al.*, 2021.



Infect

- A wild animal (host) is infected with a zoonotic pathogen
- The proportion of infected animals depends on exposure and susceptibility of the hosts and on births, which introduce new susceptibles
- Environmental stressors can reduce host resistance and increase viral shedding

Shed

- Pathogens leave the host and infect susceptible hosts, either directly through excretions or indirectly (eg, through blood)
- The timing and amount of shedding depends on host immune status. Stressed hosts shed more
- Some infected individuals might not shed (latent), whereas others are super-shedders
- Most hosts are infected with multiple pathogens that can or can not be shed synchronously

Spill

- Spillover is the transmission of a pathogen between animal species. Zoonotic spillover is spillover to humans
- Spillover requires that a recipient host receives a sufficient dose of the pathogen. Sufficiency depends on susceptibility
- For zoonotic spillover, the virus must be compatible with human tissue

Spread

- Spread depends on infectiousness of the pathogen, host contact, and host susceptibility. If each person, on average, infects more than one other person (R_0 >1), the pathogen spreads
- If the infection causes rapid mortality, the virus might be extirpated. Movement of infected hosts can initiate outbreaks in new populations
- Infection dynamics in humans are governed by similar principles to infection dynamics in wildlife reservoir hosts

This infect-shed-spill-spread cascade, when caused by land-use change, has been termed 'land-use-induced spillover'. At present, understanding of the links between land use and wildlife disease dynamics is in its infancy, and mostly conceptual, based on correlations; with few landscape-scale investigations into the scientific mechanisms behind them (Plowright *et al*., 2021; Wilkinson *et al*., 2018).

One ecosystem factor may be the 'dilution effect'. Hosts are key in determining infection transmission cycles and, therefore, human health risks, and it has been suggested that healthy ecosystems with high diversity of pathogen host species may 'dilute' prevalence of infection, reducing risk of spillover (Civitello *et al*., 2015). For example, there is strong evidence of the role of different species on tick-borne *Borrelia* transmission, as seen in the southern USA, where preferential feeding by ticks from lizards, rather than mammals, seems to explain geographic differences in human infection and subsequent Lyme disease prevalence (Ginsberg *et al*., 2021). Conversely, there is stronger evidence for a positive link between biodiversity levels and tick-borne Lyme disease at broad spatial scales, but equivocal evidence for a negative link at varying levels of biodiversity within forests, suggesting complex, scale dependent biodiversity–disease relationships (Wood and Lafferty, 2013). There is also evidence that high diversity can amplify transmission between wild species, and therefore it is important to consider the net effects of dilution and amplification in specific contexts (Luis, Kuenzi and Mills, 2018; Randolph and Dobson, 2012).

Much research has focused on whether some taxa are more likely to host and transmit zoonotic diseases, with research showing that species that are more resilient to human impacts, including land-use change, are more likely to transmit zoonotic pathogens, though species that have suffered population reductions due to human impacts may also share viruses with humans (Johnson *et al*., 2020). Spillover risk is correlated with human-wildlife contact and behavioural changes in pathogen hosts due to land-use change, but how land-use change such as deforestation affects virulence, pathogen diversity and transmission has been understudied (Gibb *et al*., 2020; Faust *et al*., 2018).

Wilkinson *et al*. (2018), for example, investigated some of these factors at the landscape scale, modelling human exposure to microbes for different types of habitat fragmentation – applying this to African tropical forests and Ebola Virus Disease case study data. The results of this study, and others that link land-use change and incidence of zoonotic disease, such as forest fragmentation and recent loss and Ebola Virus Disease outbreaks, highlight that it is possible to identify high risk areas for the mitigation and surveillance of novel disease emergence, and that mitigation measures may reduce this risk while conserving biodiversity (e.g. Rulli *et al*., 2017; Olivero *et al*., 2017). Indeed, looking at high resolution datasets on forest cover, agricultural and developed land, Rulli *et al*. (2021) suggest that locating where changes affect Asian horseshoe bats – the species that most commonly carries SARS-related coronaviruses – can highlight areas at risk of spillover through increased human-bat contact. Faust *et al*. (2018), meanwhile, suggested that intermediate levels of land-use change pose the highest risk of spillover. For example, their work shows that humans and livestock are more likely to come into contact with wildlife when more than 25% of original forest cover is lost.

Mapping areas at risk of rising human cases of existing zoonoses, due to land-use change, is also important. For instance, in the São Paulo area of Brazil, Scinachi *et al.*, (2017) sampled dogs for antibodies to the bacterium *Rickettsia rickesttsii*, which causes Brazilian spotted fever in humans, finding a heightened risk associated with areas of rainforest fragmentation. Similarly, Sato *et al.* (2019) showed that deforestation in Malaysian Borneo is linked to rising cases of a type of malaria spread from macaque monkeys.

As countries become more affluent, meat consumption amongst the population increases (Rulli *et al.*, 2021; IPBES, 2020). The increase in demand for cheap meat in wealthy countries, among other factors, leads farmers to clear forests and other habitats, often to make way for pasture land for cows and sheep to graze on, or for growing food crops for livestock. Deforestation and forest fragmentation can change the dynamics of wildlife communities, possibly allowing some wildlife species (with individuals hosting pathogens) to become relatively more abundant in managed landscapes (for example, agro-ecosystems and urban areas) – particularly in the case of some generalist bat and other mammal species (Rulli *et al.*, 2021; Gibb *et al.*, 2020).

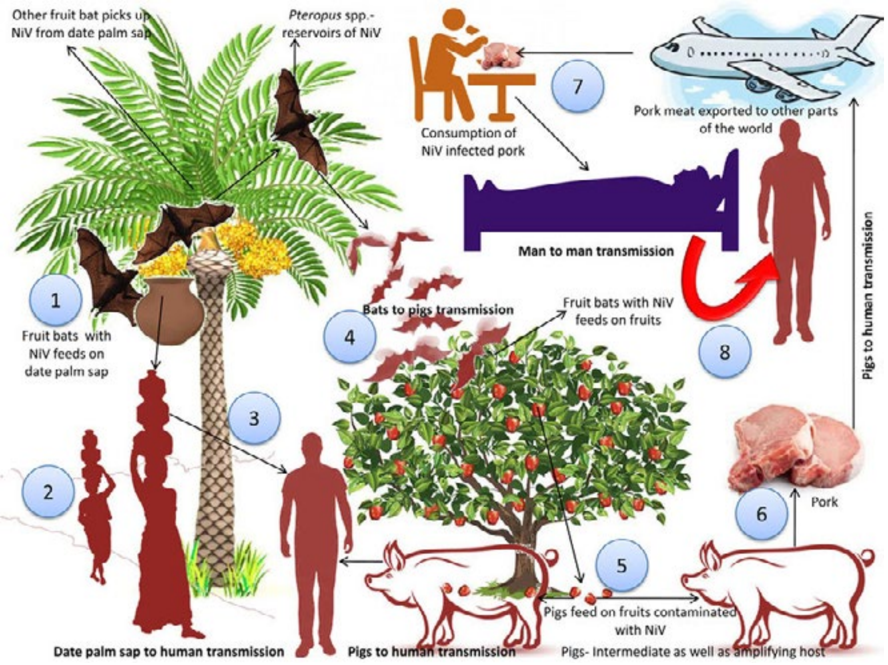
Figure 4: Aerial view of palm tree field in Borneo, Indonesia (©Getty images/Naya Nurindra, public domain)

In China, most of the meat supply is produced locally (94%), which explains the high density of agricultural stock in rural areas, including the forest margins (Rulli *et al.*, 2021). There has also been a concurrent increase in demand for so-called wild animal food delicacies. This increase in meat consumption leads to increasing wildlife-human interactions in multiple ways, including forest disturbance in remote locations in China, and in other countries via transnational trade links (*ibid.*). China's urban growth, combined with increasing agricultural demands, has led to a huge loss of forest cover over the last 30 years. Efforts have been made to replant forests, however they amount to only a fraction of the forest lost, and fragmentation continues; planting must create more continuous forest tracts to benefit wildlife (*ibid.*).

China appears to have the largest number of hotspots for the concurrence of high forest fragmentation, livestock density and human presence within areas where potentially zoonotic coronavirus bat hosts exist (*ibid.*). The researchers do not suggest a cause and effect between these land-use attributes and virus transmission to humans – but instead, highlight the existence of a co-dependence pattern among different risk factors in China, in areas where SARS-related coronavirus hosting horseshoe bats occur.

The patterns identified by this study – hotspots, and those areas at risk of becoming hotspots – can be used to investigate the nexus between coronavirus emergence and land-use change. Areas at risk of becoming hotspots due to forest fragmentation, human settlements, or agricultural stock density, could be monitored, and steps taken locally to prevent this from occurring. Similar efforts are being undertaken to identify hotspots of bat presence and human contact.

Box 1: Ebola and Nipah virus disease outbreaks, bats, and environmental change



Transmission of the Nipah virus (©2019 Informa UK Limited, trading as Taylor & Francis Group, available via license CC BY 4.0)

Over the last 30 years, outbreaks of viruses such as the Ebola virus, influenza A (pandemic H1N1, H7N9) virus, Middle East respiratory syndrome coronavirus, Hendra virus, and Nipah virus – causing major socioeconomic consequences – have indicated the interdependence of human, animal and ecosystem health, as research links spillover to land-use change (Plowright *et al.*, 2021).

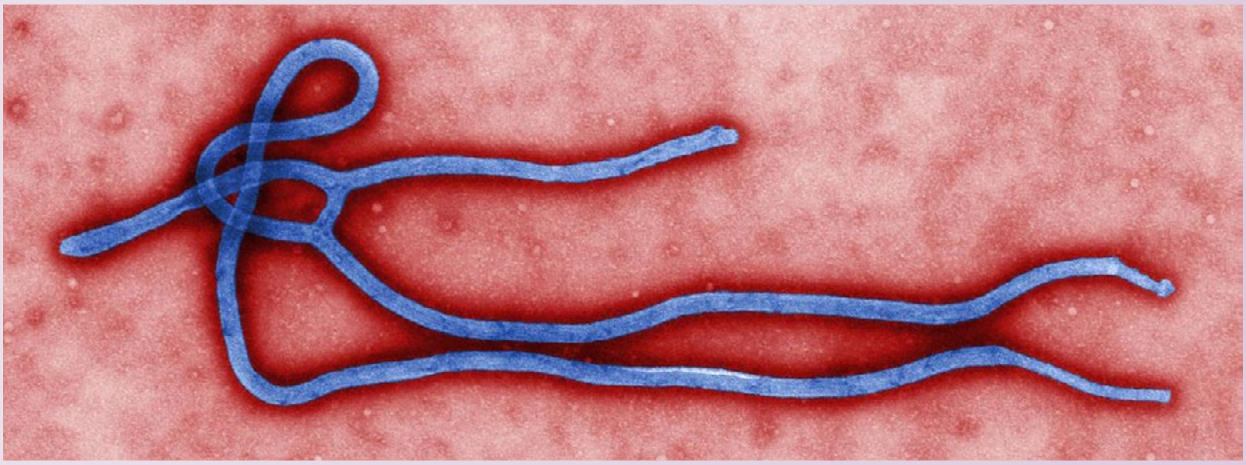
Numerous animal species can serve as zoonotic pathogen reservoirs, including primates, rodents, ungulates (cloven-hooved animals), carnivores and birds (Mollentze and Streicker, 2020). Bats in particular have been identified as the reservoir species for spillover of several zoonotic pathogens to humans, including coronaviruses, Ebola virus, rabies virus, Nipah virus and Hendra virus (Olival *et al.*, 2017).

Bat distribution, abundance and density are dependent on availability of food, mates and roosting sites. In many countries, the destruction and fragmentation of bat habitats over the last few centuries has reduced key resources, and forced bats to adopt different behaviours, for example moving from native forest to feeding in human-dominated landscapes and roosting in urban parks and man-made structures (McKee *et al.*, 2021; Plowright *et al.*, 2021). This behaviour change brings people and bats carrying zoonotic disease into closer contact – increasing the chance of spillover of a novel pathogen to the human population.

Ebola virus disease outbreaks in people, post-2002, have been linked with recent forest clearance and habitat fragmentation in Central and West Africa (Olivero, 2017; Rulli *et al.*, 2017). While low access to health systems and sanitation have exacerbated their spread, and the underlying mechanisms of this spillover remain unclear, factors such as increased human-animal contact or even stress within bat populations (the putative hosts) may be implicated. When bats become nutritionally or physiologically stressed, for example, due to clearance of their preferred habitat, these factors may increase crowding for food resources and more animals are likely to be infected, presenting a larger spillover risk (Plowright *et al.*, 2021; Rulli *et al.*, 2017).

Some wildlife species which are known to have been infected with ebolaviruses – bats, gorillas, chimpanzees and duiker – are able to survive in, or even prefer, disturbed forest habitats. It could be that humans are exposed to these wildlife species and their pathogens through bushmeat consumption, bites or scratches. Chimpanzees and gorillas are unlikely to be hosts of Ebola for long, though, and are likely to be just as impacted as people by the disease (Hayman, Sam John and Rohani, 2022).

Figure 5. Ebola virus virion, scanning electron micrograph image.
(Source: CDC/Cynthia Goldsmith, Public domain, via Wikimedia Commons)



Similarly to Ebola virus spillover from bats in Africa is Nipah virus spillover to humans in Bangladesh – occurring, in part, as a result of centuries of forest cover loss, leading to a behaviour change in the *Pteropus medius* bat population. Nipah virus is a virus (a paramyxovirus) which causes annual outbreaks of fatal encephalitis in Bangladesh, and lower average winter temperatures seem to affect the likelihood of Nipah being transmitted to humans.

The increased incidence of spillovers of Nipah in cooler winters may be due to bat behaviour and metabolic changes in cooler temperatures. Fruit bats lacking forest habitats depend more on abundant cultivated fruits in human-inhabited areas (McKee *et al*., 2021). In cooler winters they may become more nutritionally distressed and shed more virus, meanwhile taking advantage of the bigger date palm harvest in winter (when there are fewer other fruits growing) – so increasing the probability of them contaminating the sap. The shift to bats residing in areas of high human density, and opportunistically feeding on cultivated fruits, with the shared use of date palm sap by bats and humans is suggested as the main route for Nipah virus spillover during winter months (*ibid*.).

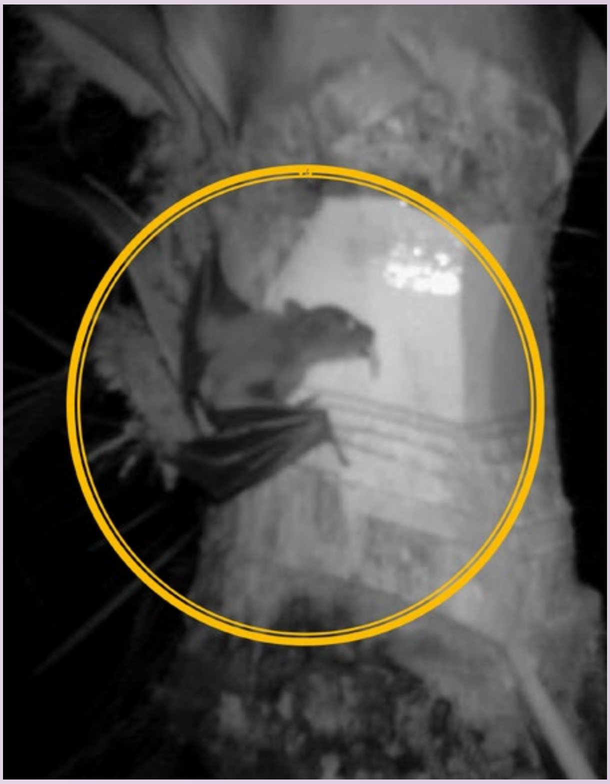
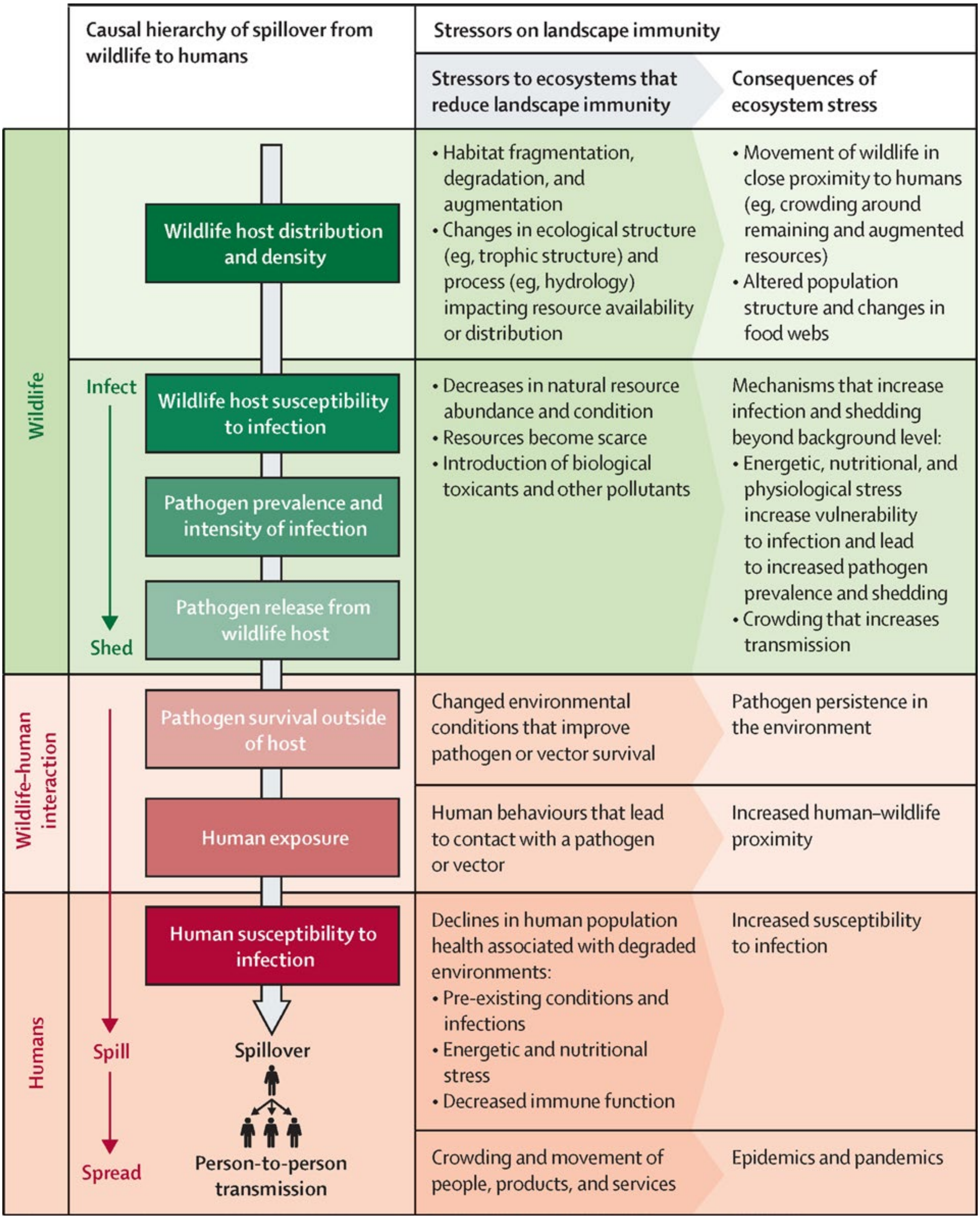


Figure 6. A fruit bat licking sap from the shaved surface of a date palm tree in Bangladesh, in the winter of 2010; one of the potential modes of zoonotic transfer of Nipah virus to humans.
Source: Khan *et al*., 2012.

A range of environmental processes affect infectious disease circulation. However, land-use change is important, as it is an action able change that communities can influence, unlike some other factors (Plowright *et al.*, 2021). Disease ecologists and land-use scientists working in collaboration can identify features of land systems in the local context that allow preventative steps to be taken to limit spillover of disease to humans, taking into consideration trade-offs and the local community's needs (*ibid*).

Figure 7. Illustration of the infectious disease spillover cascade: loss of landscape 'immunity' as a pandemic trigger.
(Source: Plowright *et al.*, 2021)



	Causal hierarchy of spillover from wildlife to humans	Stressors on landscape immunity	
		Stressors to ecosystems that reduce landscape immunity	Consequences of ecosystem stress
Wildlife	Wildlife host distribution and density	• Habitat fragmentation, degradation, and augmentation • Changes in ecological structure (eg, trophic structure) and process (eg, hydrology) impacting resource availability or distribution	• Movement of wildlife in close proximity to humans (eg, crowding around remaining and augmented resources) • Altered population structure and changes in food webs
	Infect Wildlife host susceptibility to infection Pathogen prevalence and intensity of infection Pathogen release from wildlife host Shed	• Decreases in natural resource abundance and condition • Resources become scarce • Introduction of biological toxicants and other pollutants	Mechanisms that increase infection and shedding beyond background level: • Energetic, nutritional, and physiological stress increase vulnerability to infection and lead to increased pathogen prevalence and shedding • Crowding that increases transmission
Wildlife–human interaction	Pathogen survival outside of host	Changed environmental conditions that improve pathogen or vector survival	Pathogen persistence in the environment
	Human exposure	Human behaviours that lead to contact with a pathogen or vector	Increased human–wildlife proximity
Humans	Human susceptibility to infection Spill Spillover	Declines in human population health associated with degraded environments: • Pre-existing conditions and infections • Energetic and nutritional stress • Decreased immune function	Increased susceptibility to infection
	Spread Person-to-person transmission	Crowding and movement of people, products, and services	Epidemics and pandemics

2.1.1 What is needed to address land-use-associated disease risk?

If land-use change threatens health through disease spillover, then understanding how to prevent such spillover is key. Bernstein *et al*. (2022) argue that that the costs of reducing deforestation, along with better surveillance of pathogen spillover, global data sharing, and management of wildlife trade, amount to 1/20th of the value of lives lost each year to emerging viral zoonoses.

An interdisciplinary, applied research effort drawing on landscape ecology, wildlife immunology and disease ecology is required to advance knowledge of land-use consequences for wildlife and human health (Plowright *et al*., 2021; White & Razgour, 2020) – recognised in the One Health approach endorsed by WHO, FAO and the World Organisation for Animal Health (OIE). Understanding the mechanisms of the shed-spill-spread cascade of zoonotic pathogens will enable better protection of 'landscape immunity', i.e. the ecological conditions that reduce the risk of pathogens spilling over from reservoir hosts to local human populations (Rulli *et al*., 2021).

The IPBES 2020 report suggests policies addressing land-use change as a cause of pandemic emergence should include:

- Using pandemic, and emerging disease risk, health impact assessments – in development and land-use projects.
- Reforming financial aid for land-use to target risks to biodiversity and health (IPBES, 2020).

Box 2: Definition of One Health approach

In December 2021, **The Food and Agriculture Organization of the United Nations** (FAO), the **World Organisation for Animal Health** (OIE), the **United Nations Environment Programme** (UNEP) and the **World Health Organization** (WHO) welcomed the newly formed operational definition of One Health from their advisory panel, the One Health High Level Expert Panel (OHHLEP):

One Health *is an integrated, unifying approach that aims to sustainably balance and optimize the health of people, animals and ecosystems.*

It recognizes the health of humans, domestic and wild animals, plants, and the wider environment (including ecosystems) are closely linked and inter-dependent.

The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for clean water, energy and air, safe and nutritious food, taking action on climate change, and contributing to sustainable development.

The four organizations are working together to mainstream One Health so that they are better prepared to prevent, predict, detect, and respond to global health threats and promote sustainable development.

2.2 Agriculture

A farmer veterinary walks inside a poultry farm (©Getty Images/roibu, public domain)

Global population growth, urbanisation and increasing affluence in many countries has led to a shift in diet – including an increased demand for animal products, instigating agricultural expansion to meet these needs. Changes in animal husbandry, as a result of this increased demand, are often occurring at the cost of natural ecosystems (Rulli *et al.*, 2021). Land use change entailing encroachment on wildlife habitats, through the establishment of pastures, plantations or intensive livestock farms close to forest margins, may increase the pathogen flow from wildlife to humans directly, or via other species, such as livestock that people are in close contact with, and livestock farming has been linked with emerging infectious disease in some areas (Khamassi Khbou *et al.*, 2021).

Industrial farming is a particular risk for livestock being susceptible to wildlife pathogens that are transmitted to them; after decades of breeding, parts of animals' genomes can become highly homogenous, meaning entire herds can be adversely affected (because host genetic diversity offers protection against pathogens as some individuals may have natural resistance) (*ibid.*; Zhang *et al.*, 2015). Intensive livestock production often means a large number of immunosuppressed animals are kept in close proximity to each other, increasing vulnerability to emergence, and spread of epidemics. Industrial farming practices, alongside transportation of animals for slaughter – sometimes long distances – can lead to the spread of wildlife-originated pathogens quite quickly, across large spatial scales (e.g. Yang *et al.*, 2020).

The role of domestic animals in transmitting coronaviruses to humans remains unclear. However, during the 2002-2003 SARS-CoV outbreak, the virus is thought to have been transmitted from bats via intermediate hosts to humans. Although this intermediate host has not been identified, livestock were found to have been infected, too, and may pass the disease to humans during handling on farms and during meat processing. Humans may also pass SARS-CoV to animals including pigs (Chen *et al.*, 2005). Similarly, in the 2017 outbreak of fatal swine acute diarrhoea syndrome (SADS-CoV, caused by a novel coronavirus – HKU2 – which killed 24 693 piglets in China in the same area as the SARS outbreak), the causative agent showed remarkable similarity to coronavirus variants found in swabs of bats in this region. This suggests that bats are transmitting coronaviruses to pigs, which could then potentially infect humans that interact

Figure 8: Intensive farming for animal products entails large numbers of animals being kept in close proximity. Pigs may be an intermediate host for the emergence of novel CoVs. Source: www.animalequality.org.uk

with them (Zhou *et al*., 2018). This study highlights the importance of identifying coronavirus diversity and distribution in bats to mitigate future outbreaks that could threaten livestock, public health and economic growth.

A characteristic of coronaviruses is that, although lower compared to many RNA viruses, they have a relatively high mutation and recombination rate, meaning host-jumping and cross-species transmission and subsequent host adaptation is possible (Pachetti *et al*., 2020). As discussed, horseshoe bats can act as a reservoir for most SARSr-CoVs (the coronavirus types that led to SARS and COVID-19 in humans). Other wildlife species, such as pangolins, might act as reservoirs and amplify the coronavirus strains in a different manner – but these are less well-studied (Lam *et al*., 2020).

Rulli *et al*. (2021) looked at horseshoe bats as the reservoir host for SARSr-CoVs, with livestock distribution included in the analysis. The researchers included pigs, but not poultry, as the coronavirus responsible for swine acute diarrhoea syndrome has infected pigs but there is no evidence so far of these types of coronaviruses infecting birds. SADS emerged in China (Guangdong Province) in 2017, and was found to be genetically close to bat CoV HKU2 (Zhou *et al*., 2018). The high density of pig farms and slaughterhouses in the Guangdong region, alongside the wide distribution of bat species, explained the cross-species transmission. As pork is a widely eaten food in non-Muslim countries, pigs may be an intermediate host for the emergence of novel CoVs of high public health concern in the future. Close contact between humans and pigs also led to the jump of swine influenza viruses (H1N1 and H1N2) and the Nipah virus.

The range of animals consumed by humans for meat that were infected with one of the many types of coronavirus in previous disease outbreaks, is quite extensive – including cattle, buffaloes, camels, horses, rabbits, pigs, chickens, dolphins, whales and harbour seals, as shown in Table 3 (Khamassi Khbou *et al*., 2021). European livestock has not escaped coronavirus infections, with buffaloes in Bulgaria and Italy found to have bubaline coronavirus in an outbreak in 1985, and porcine epidemic diarrhoea virus in pigs in Belgium and the UK, in 1983 and 1971, respectively (*ibid*). Raised for fur rather than meat, mink farms in Denmark, the Netherlands and Spain were hit by COVID-19.

Table 3. List of the main coronaviruses infecting animals eaten for meat. Source: Khamassi Khbou *et al*., 2021.

Animal species	Coronavirus (abbreviation)	Genus	Year of first description (country)	Disease severity	Main symptoms	Vaccine
Cattle	Bovine coronavirus (BCoV)	Beta	1973 (USA)	Mild to severe	Neonatal diarrhoea Winter dysentery Respiratory signs	Inactivated or MLV
Buffaloes	Bubaline coronavirus (BuCoV)	Beta	1985 (Bulgaria)	Mild	Diarrhoea	
Dromedaries	Middle East respiratory syndrome coronavirus (MERS-CoV)	Beta	2012 (KSA)	Mild	Rhinitis, nasal discharge Tracheitis	
Horse	quine coronavirus (ECoV)	Beta	1999 (USA)	Mild	Diarrhoea	
Rabbits	Rabbit coronavirus (RbCoV)	Beta	2012 (China)	Subclinical		
Pigs	Porcine hemagglutinating encephalomyelitis virus (PHEV)	Beta	1957 (Canada)	Severe	Diarrhoea, neurological signs	
	Transmissible gastroenteritis virus (TGEV)[a]	Alpha	1946 (USA)	Severe	Diarrhoea	Inactivated or MLV
	Porcine respiratory coronavirus (PRCV)	Alpha	1983 (Belgium)	Subclinical-Mild	Nasal discharge, pneumonia	
	Swine acute diarrhoea syndrome coronavirus (SADS-CoV)	Alpha	2016 (China)	Severe	Diarrhoea	
	Porcine epidemic diarrhea virus (PEDV)	Alpha	1971 (UK)	Severe	Diarrhoea	Inactivated or MLV or VBV
	Porcine delatcoronavirus (PDCoV)	Delta	2009 (China)	Mild to severe	Diarrhoea, vomiting	
Chickens	Infectious bronchitis virus (IBV)[a]	Gamma	1930 (USA)	Mild (adults) to severe (young)	Nasal discharge, snicking, watery eyes and lethargy	Inactivated or MLV or VBV
Dolphine	Bottlenoise whale (BdCoV)	Gamma	2014 (China)	Subclinical		
Whale	Beluga whale (BWCoV)	Gamma	2008 (USA)	Severe	Pulmonary disease and acute liver failure	
Harbor seals	Not assigned yet	Alpha	1987 (USA)	Mild to severe	Acute enteritis	

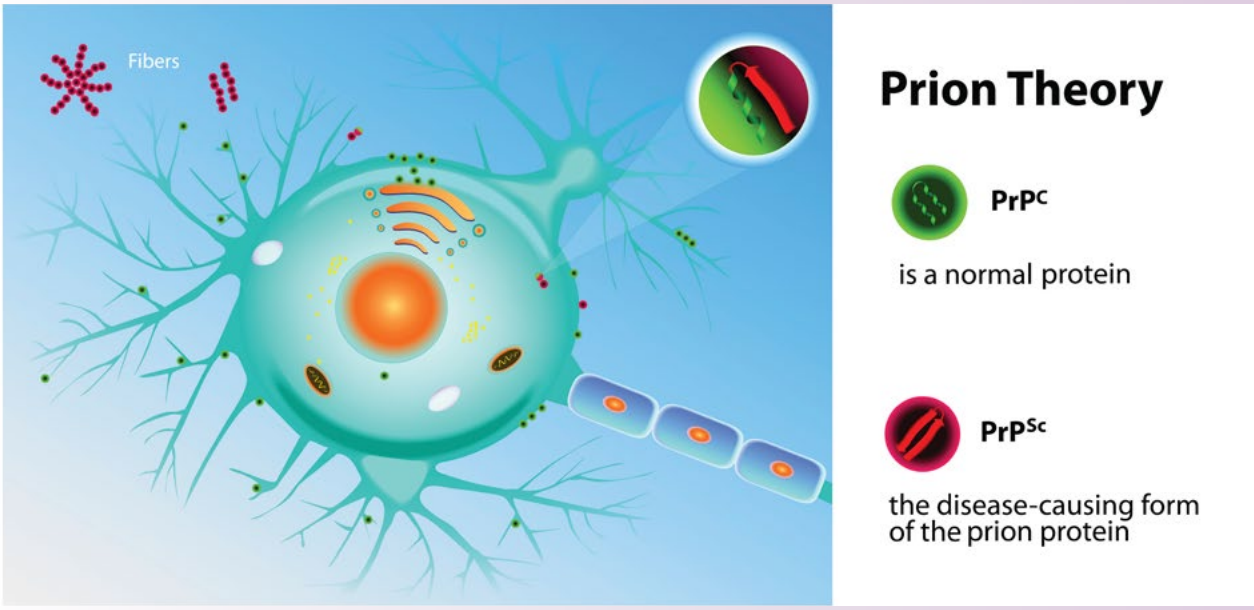
Abbreviations: Alpha, Alphacoronarivus; Beta, Betacoronavirus; Delta, Deltacoronavirus; Gamma, Gammacoronavirus; KSA, Kingdom of Saudi Arabia; MLV, modified live vaccine; UK, United Kingdom, USA, United States of America; VBV, vector based vaccine.

[a.] Notifiable disease to the World Organisation of Animal Health (OIE)

Box 3:
Mad cow disease, a non-communicable disease risk from industrial farming practices

Industrial farming practices increase the risk of communicable diseases, such as COVID-19, but can also lead to non-communicable disease risk to humans from consumption of infected meat – as occurred with bovine spongiform encephalopathy (BSE) or 'mad cow disease' (IPBES, 2020; Keetch, 1997). In the 1990s in the UK, an intensive farming practice of feeding processed bonemeal products from sheep to cattle – which are naturally herbivores – led to cows developing 'mad cow disease', with some people that consumed infected meat developing the human form of the disease, called 'variant Creutzfeld-Jakob Disease' (Collinge, 1999). The disease is spread not by a virus or bacteria, but by non-viral proteins called 'prions' that are present in infected nervous system tissue.

This practice of feeding bonemeal – introduced to increase livestock production – was banned and the disease outbreak was brought under control (Center for Food Safety, 2021). This outbreak of disease had significant costs, and led to increased human disease risk: many countries still today will not accept blood donations from British people resident in the UK during that time.



Prion Theory. Mad Cow Disease (©Getty images/ttsz, public domain)

As a result of the infection, an 'over 30 months scheme' was introduced, to compensate farmers for the slaughter of cattle and to avoid cattle entering the human food chain: 1 772 000 cattle were slaughtered under the scheme (Keetch, 1997). The scheme was abolished in 2005, and instead it became illegal for cattle born before 1996 to be sent to an abattoir for human consumption. Although a different mechanism of increased disease risk in humans and animals, this example highlights the huge financial costs that can arise from diseases caused by unsafe industrial farming practices, which arise in the drive to increase meat production and profit.

Spillover of infectious disease such as SARS, COVID-19 and SADS from wildlife to humans is likely to require the coexistence of a wildlife reservoir species and humans in the same environment – alongside intermediate hosts, especially farmed wildlife and livestock, because they are in closer contact with humans. It is also likely to require hosts having high densities in the regions where these spillover risks are likely to happen – as is the case in parts of China. It is possible that, as the human population grows, and meat consumption continues to increase, further spillover of novel viruses will occur in the future, if steps aren't taken to lower risks in hotspot areas.

Although there is no clear link between the spread of COVID-19 and agricultural practices, the IPBES suggests transformative change is required to reduce the types of production and trade that may contribute to virus spillover and transmission via intermediate hosts (e.g. non-sustainable palm oil, exotic wood harvesting, products requiring mine extraction, meat and other products of globalised livestock production) (IPBES, 2020). Taxes could be used, or levies on meat consumption, livestock production or other forms of consumption associated with spillover risk.

2.3 Climate change and increased disease risk in Europe

Climate change has become implicated in disease emergence, and is likely to cause substantial future pandemic risk, by movement of pathogens – alongside people, wildlife, reservoirs and vectors – in ways that lead to new species contacts, increased contacts and disruption of natural host-pathogen dynamics (IPBES, 2020).

The early part of the 21st century has seen an unprecedented rise in vector-borne disease in Europe (Medlock and Leach, 2015). Climate change is causing expansion of the ranges of disease vectors, and allowing vectors to survive and breed after being transported beyond their natural range, for example leading to outbreaks of dengue fever in Croatia, chikungunya in France, and tick-borne encephalitis in Scandinavia (Austin, 2021; IPBES, 2020; Gould *et al.*, 2010). Malaria has re-emerged in Greece, and West Nile virus has emerged across parts of Eastern Europe (*ibid.*).

Meanwhile, the rise in tourists from Europe travelling to countries which have endemic diseases not normally found in European countries – such as dengue fever, Zika virus and chikungunya – has led to several examples of infected tourists returning, having been bitten by tiger mosquitoes, causing local outbreaks in the area they live (Gould *et al.*, 2010). For example, in 2019, there was an outbreak of dengue fever amongst people who had not travelled overseas, in the region of Auvergne-Rhône-Alpes. In response to these outbreaks, swift action is taken by authorities to spray areas and reduce the mosquito population – thus limiting the spread of the disease (Connexionfrance, 2019).

The spread of the invasive tiger mosquito, *Aedes albopictus*, across Europe is particularly concerning, as they are more competent vectors for more dangerous pathogens than the native European species of mosquito (Gould *et al.*, 2010). The Centre for Ecological Research in Hungary manages a citizen science project mapping the distribution of the invasive mosquitoes across the country called 'The Mosquito Project' (see Figure 9). More than 400 reported sightings of tiger mosquitoes in the country were verified by scientists in 2021.

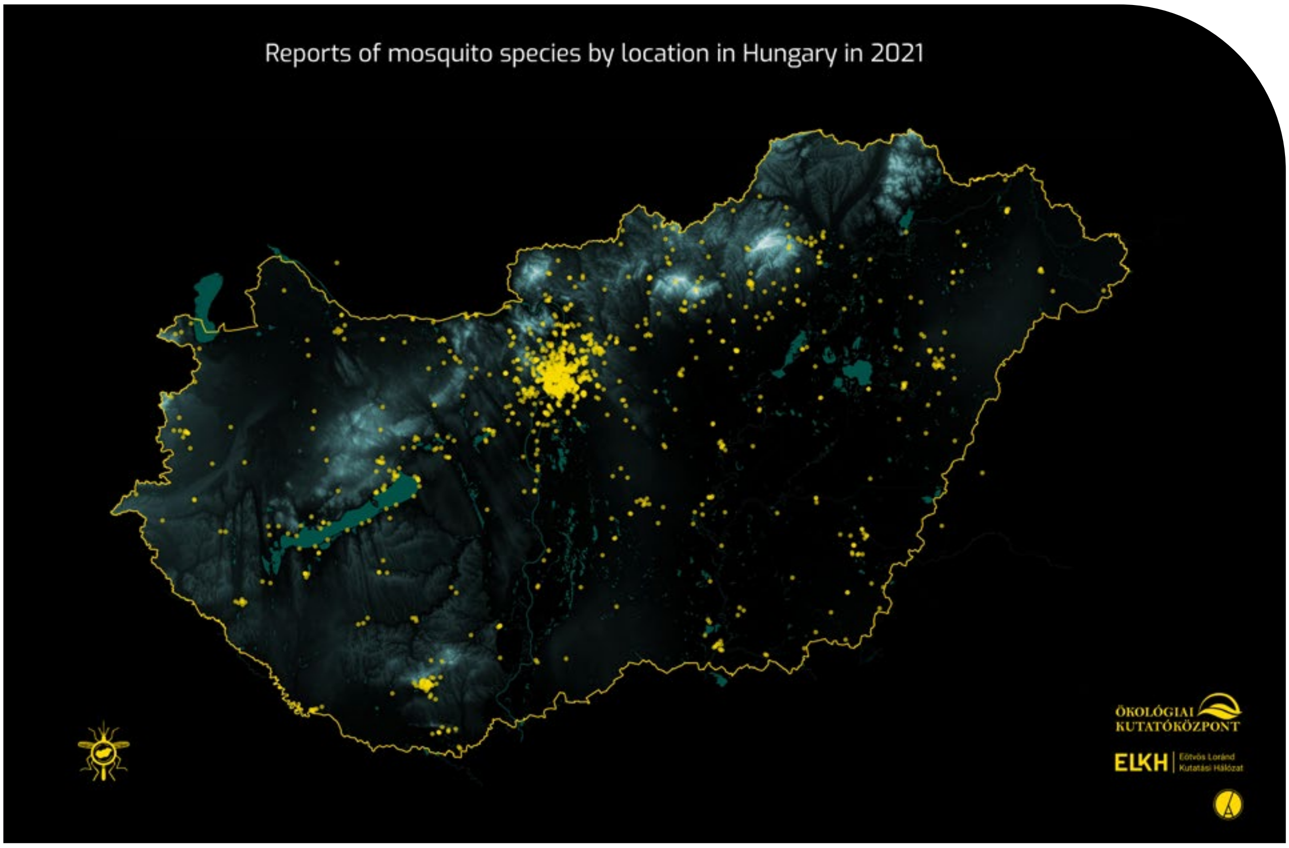


Figure 9. Over 400 reports of tiger mosquitoes in Hungary were mapped and verified in 2021.
(Source: Centre for Ecological Research, Hungary, MOSQUITO MONITOR available at: https://szunyogmonitor.hu)

Climate change has a significant impact on mosquito-borne disease, where very small increases in temperature may allow the survival of mosquitoes transported to new areas where people lack immunity to the diseases they carry. Similarly, tick-transmitted diseases, such as Lyme disease (caused by *Borrelia burgdorferi s.l.*), tick-borne relapsing fever (caused by a number of Borrelia species, predominantly *Borrelia miyamotoi* in Europe), tick-borne encephalitis and Crimean-Congo haemorrhagic fever viruses, are continuing to increase in frequency and range (Hansford *et al*., 2015; Medlock and Leach, 2015; Mannelli *et al*., 2012). This is in part due to climate change creating longer mild seasons when the ticks are active, and the broadening of their geographic ranges northwards – into previously colder regions, and up to higher altitudes. *Borrelia miyamotoi* has now been observed in numerous European countries including the Czech Republic, Denmark, Estonia, France, Germany, Netherlands, Norway, Poland, Romania, Sweden, UK and Switzerland (Cutler *et al*., 2019).

Figure 10: The deer tick, Ixodes ricinus, is one vector of diseases affecting animals and humans; the tiger mosquito, Aedes albopictus, is increasing its range; the blood parasite Borrelia. Sources:
https://lymediseaseuk.com/2020/09/24/efforts-to-engage-local-councillors-in-lyme-awareness/ixodes-ricinus-4858026_1920
https://phil.cdc.gov/Details.aspx?pid=1969
https://phil.cdc.gov/; https://phil.cdc.gov/Details.aspx?pid=14495

In addition, certain hosts of ticks and tick-borne diseases are becoming relatively more abundant and increasing their range – such as the white-footed mouse in America. This rodent is highly competent at transmitting Borrelia bacteria (that causes Lyme disease in people) to ticks that feed on them (Ostfeld and Keesing, 2000). In a species-rich environment, with a greater range of wildlife that is less competent at transmitting such bacteria, the likelihood of ticks transmitting the bacteria to humans diminishes; this is known as 'dilution'. However, with environmental degradation due to climate change, land-use change and urbanisation, species richness is lowered, increasing the risk of transmission of tick-borne disease to humans (*ibid*.). For these reasons tick-borne diseases in humans are on the rise worldwide, including in Europe due to encroachment on habitat, as well as a widening geographic spread and active season for ticks due to climate change.

Amplification of tick-borne disease risk in degraded environments increases the chances of tick-transmitted diseases spilling over into expanding human populations. In Eastern Europe in the 1990s a number of factors collided, which led to a surge in tick-borne encephalitis virus (TBEV) infection in the population. These factors included land-use change, climate change and huge socio-economic changes, causing a rise in disease outbreaks (Randolph, 2008).

Global climate change is intensifying, with 2019 being the second hottest year on record, so environmental degradation and wildlife range changes are likely to become magnified over time, with the potential to initiate more deadly pandemics in the future (Austin, 2021). Infectious diseases that had become less of a problem in some parts of the world may have a resurgence, such as malaria and dengue fever (*ibid*; JRC, 2018); indeed, dengue fever has already seen a rise in cases over the last 20 years, globally (Zeng *et al*., 2021: although data from Europe were lacking). Climate-related extreme weather events, such as flooding and drought, will also contribute to disease emergence risks, and anticipating the impacts of climate change on disease spillover risk is an important aspect of 'One Health' frameworks (IPBES, 2020).

Box 4: Reverse zoonoses – diseases transmitted from humans to wildlife

Of concern to wildlife conservationists, in terms of biodiversity preservation, are novel diseases that are transmitted from humans, livestock and domesticated animals to wildlife species, sometimes known as reverse zoonoses when from people.

Hypermucoviscous (HMV) *Klebsiella pneumoniae* is a common, mucosal bacteria, usually harmless for animals and humans (though in hospitalised humans this strain of the bacteria can also cause more serious infection). Although it is not a novel pathogen in marine mammals, research suggests that it is passed from humans to seals via sewage discharged into the sea. Notably, antibiotic resistant forms of *Klebsiella pneumoniae* have been detected in wild seals (Duff *et al.*, 2020).

New Zealand sea lions, *Phocarctos hookeri*, are an endemic endangered species whose numbers have been depleted over the last couple of decades, and remain low in large part due to mortality from the HMV strain of *Klebsiella* (Michael *et al.*, 2019). Sepsis caused by this hypervirulent bacteria has been linked to 60% of seal pup deaths at sub-Antarctic Enderby Island. The same bacteria has also been found to cause serious health problems and mortality in California sea lions (*Zalophus californianus*) (Jang *et al.*, 2010).

It has been suggested that non-human primates including vervet monkeys (*Chlorocebus aethiops*) may acquire HMV *Klebsiella pneumoniae* from humans, too (Whitehouse *et al.*, 2010). Reverse zoonoses are also a threat to (non-human) great ape species – all of which are endangered, or critically endangered. Chimpanzees (*Pan troglodytes*) and mountain gorillas (*Gorilla beringei beringei*) for instance, have been found to be particularly affected by disease transmission from humans, and biosecurity measures have been suggested to protect them from exposure to tourists, researchers and villagers potentially carrying human pathogens (Dunay *et al.*, 2018). Yellow fever virus, introduced from Africa to the Americas during the slave trade, now persists in South American jungles, affecting both primates and humans.

COVID-19 also threatens apes: captive gorillas at North American zoos have contracted COVID-19, and researchers have warned that tourists visiting wild ape habitats should practice social distancing to avoid passing on the disease (Molyneaux *et al.*, 2021). It has been suggested that care should be taken with visitors, to wear surgical masks, observe good hygiene procedures, and to adhere to a limit on the daily number of tourists that visit a great ape group. In addition, it could be prudent to vaccinate the wild living great apes against diseases such as Ebola virus disease, which have previously decimated populations (Leroy *et al.*, 2004).

Box 5: Ticks and fly vectors of disease are likely to increase in Europe due to climate change

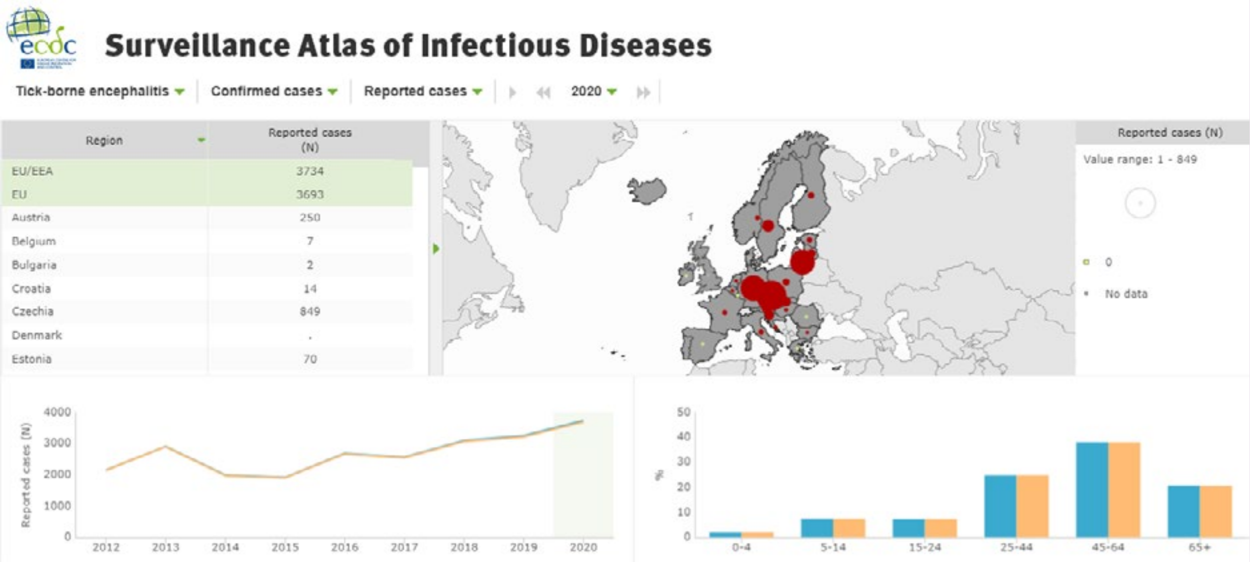
Climate change is likely to increase the impact of vector-borne diseases on human and animal health worldwide, as it affects the biology of the ticks and flies and the transmission cycles of the pathogens, as well as causing human populations to be more vulnerable to the diseases (JRC, 2018; Ogden and Lindsay, 2016; Ostfeld and Keesing, 2000).

Vectors of disease respond differently to increases in temperature, rainfall and humidity associated with climate change. Tick-borne diseases will be likely characterised by long term changes – increasing over time as can be seen in Europe (Figure 11). Fly-borne diseases (carried by mosquitoes and midges for example), in contrast, respond quickly to short-term changes in weather, leading to possible epidemics, meaning there may be surges in infectious disease in the short-term and overall longer-term disease risk increases (Ogden and Lindsay, 2016).

Ticks in Europe carry bacterial, parasitic and viral pathogens to humans and animals. At least 27 tick-borne viruses ('tiboviruses') have been detected in Europe, including some that cause very serious human disease (tick-borne encephalitis virus, Crimean-Congo haemorrhagic fever) and animal disease (louping ill, African swine fever virus). Other tiboviruses causing less serious diseases are infrequently reported.

Some tick-borne pathogens appear to be widening their distribution. For example, babesiosis is a disease of humans and animals caused by various species of the blood parasite genus *Babesia*, spread by different ticks. In Britain, several cases caused by *Babesia* species not previously found in the country have been recorded in recent years. In 2015-2016, a number of dogs infected by *Babesia* canis – previously confined to the USA and parts of continental Europe – were reported in the east of England. The parasite may have come from ticks usually found in western Europe, possibly imported on pets. Meanwhile, *Babesia venatorum* – a species found in China and continental Europe – was detected in sheep in Scotland in 2019, with potential to infect humans. Another species, *B. odocoilei*, was shortly afterwards detected for the first time in the UK, in deer. In 2020, the first case of locally acquired babesiosis in humans was diagnosed in Britain, due to *B. divergens* – one of two species prevalent in ticks in some parts of the UK, known to infect livestock.

Figure 11: Monitoring in Europe shows that cases of tick-borne encephalitis are increasing in frequency.
Source: ECDC Surveillance Atlas of Infectious Diseases, https://atlas.ecdc.europa.eu/public/index.aspx



Surveillance Atlas of Infectious Diseases

Region	Reported cases (N)
EU/EEA	3734
EU	3693
Austria	250
Belgium	7
Bulgaria	2
Croatia	14
Czechia	849
Denmark	.
Estonia	70

Surveillance of vector-borne disease

Within Europe, and worldwide, surveillance of vector-borne disease in wildlife reservoirs is one method of understanding the potential pathogen risks present in the ecosystem, which could infect humans and domestic animals locally. The EU Joint Research Centre, in collaboration with the ICBEG Institute, is currently mapping the distribution of pathogen-carrying mosquitoes and has highlighted the impact that climate change will have on patterns of vector-borne disease (JRC, 2018). The European Centre for Disease Control and the European Food Safety Authority are also collecting data on vectors and pathogens in the VectorNet project.

Trapping of invasive species and collecting roadkill for analysis are passive methods of surveillance. In one European city a study examined roadkill (hedgehogs, weasels, moles and pine martens) and detected a number of pathogens from tissue samples and ticks collected from carcasses, including human zoonotic pathogens – *Anaplasma phagocytophilum* ecotype I, *Borrelia afzelii*, *B. spielmanii*, *Borrelia miyamotoi*, *Rickettsia helvetica* and *Bartonella* species (Szekeres *et al.*, 2019). This type of surveillance could be used as part of a more comprehensive monitoring protocol, for risk assessment of potential human infection in an area.

Borrelia miyamotoi

Borrelia miyamotoi is a spirochetal bacterium that cause a relapsing fever, flu symptoms and neurological symptoms in some people. It was discovered in France in 2013, having been previously found in Germany, Sweden and Estonia (Vayssier-Taussat *et al.*, 2013). In 2014 it was found in ticks in the UK (Hansford *et al.*, 2015). Climate warming and other environmental changes have contributed to the expansion of several tick species into higher latitudes, with a longer tick season, increasing ranges of tick host species, and the consequent increase in exposure of humans to tick-transmitted infections, including *Borrelia miyamotoi* (Bouchard *et al.*, 2019).

Infection with *B. miyamotoi* does not result in the classic bullseye rash, which can occur with Lyme disease infection. In contrast to the related bacteria which cause Lyme disease (*Borrelia burgdorferi*), ticks can act as both carrier and reservoir for the disease as the pathogen can be transmitted from mother ticks to larvae ('transovarial') (Cutler *et al.*, 2019). It is of emerging concern in Europe, as it can co-occur with other tick-transmitted infections such as Lyme disease, *Babesia microti* (a blood parasite) and others, causing unusual symptoms. The transmission efficiency of the pathogen to humans is higher than for Lyme disease, so if a person is bitten by an infected tick they are more likely to get the disease (*ibid.*). In addition, it is not routinely tested for, and in some European countries, such as the UK, there is presently no antibody test available within the national health system.

A German long-term monitoring study found increasing prevalence of *B miyamotoi* over time, and suggested further monitoring of the impact of climate change on transmission of tick-borne diseases, alongside greater awareness amongst clinicians of this emerging tick-transmitted infection (Blazejak *et al.*, 2018). In the Netherlands studies suggest that some 36 000 humans are bitten each year by *B. miyamotoi* (European strain)-infected ticks (Cutler *et al.*, 2019). However, few human cases are reported; this is believed to be due to gross under-reporting and lack of serological testing, making the assessment of the impact of this infection challenging. Understanding how this pathogen affects Europeans it infects and improving diagnostic testing for it in humans is important, alongside monitoring of levels in the ecosystem. *B miyamotoi* has now been detected in a range of vertebrates including mice, voles, squirrels, chipmunks, European hedgehogs, raccoons, blackbirds, great tits, chiff chaff, song thrush, European robin and European greenfinch (*ibid*). Within the UK, a 2014 study found that *B. miyamotoi* was present over several years in 3 distinct geographical areas – Salisbury, Dartmoor and the New Forest – showing some evidence for endemicity in the environment (Hansford *et al.*, 2015).

2.4 Wildlife trade and infectious disease risk

> **“Initial findings from samples collected at several international airports identified parts originating from nonhuman primate (NHP) and rodent species, including baboon, chimpanzee, mangabey, guenon, green monkey, cane rat and rat. Pathogen screening identified retroviruses (simian foamy virus) and/or herpesviruses (cytomegalovirus and lymphocryptovirus) in the NHP samples. These results are the first demonstration that illegal bushmeat importation into the United States could act as a conduit for pathogen spread.”**
>
> (Smith *et al.*, 2012)

The consumption of wild animals has occurred throughout history, and in many countries is an important source of nutrition for local and indigenous communities. There are serious risks to biodiversity associated with high levels of hunting, poaching and legal and illegal animal trafficking, however, including extinction of targeted species and potential ecosystem collapse. In addition, the spread of zoonoses has been linked to wildlife trade (illegal, legal, domestic and international) prompting increasing concern about how best to regulate and minimise the disease risk it poses (IPBES 2020; Smith *et al.*, 2012).

Wildlife trade is associated with a range of activities, including wildlife farming (rearing of non-domesticated species) for food, pets, medicine, fur and leather, and buying and selling of live animals at wildlife markets for consumption in homes and restaurants. A wildlife market in Wuhan is suspected by some as the possible source of the initial outbreak of COVID-19 (IPBES, 2020; Xiao *et al.*, 2021; WHO, 2021a). The slaughter and sale of wild animal meat locally and internationally can also introduce novel pathogens to nearby, or more distant, populations (Smith *et al.*, 2012; Peros *et al.*, 2021).

Huanan Seafood Wholesale Market (©Wikipedia Commons CC-BY-4.0)

Box 6: Human-wildlife-livestock interactions: identifying potential hotspots for bat-originated coronavirus outbreaks in future

Asian horseshoe bats are the genus (*Rhinolophus*) and family of bats (*Rhinolophidae*) that most commonly carry the severe acute respiratory syndrome (SARS)-related coronaviruses. In a recent study, Rulli *et al.* (2021) sought hotspots for potential zoonotic transmission of coronaviruses from Asian bat species to humans in a region greater than 28.5 million km, which is home to *Rhinolophus* bats. The analysis (which included forest cover, cropland distribution, livestock density, human population, human settlements, bat species distribution and land-use changes across this population range) found that areas in China populated by this bat family exhibited higher forest fragmentation and concentrations of livestock and humans, than in other countries. The authors suggest this distribution pattern of human-livestock-wildlife interactions in China, as well as in a few other global locations, could indicate hotspots for potential zoonotic transmission of SARS-related coronaviruses from animals to humans.

Genomic sequencing of SARS-CoV-2 found that the virus is closely related to a strain present in horseshoe bats, but it is still unclear whether the spillover of SARS-CoV-2 would have occurred directly from bats to humans, or through an intermediate species (Rulli *et al.*, 2021; WHO, 2021a). For example, a strain of coronavirus very similar to SARS-CoV-2 was detected in the Malayan pangolin (*Manis javanica*) (Lam *et al.*, 2020; Rulli *et al.*, 2021). Pangolins have thus been proposed as a possible intermediary, however this has not been confirmed. This endangered species – one of the most trafficked species in the world, due to its use in traditional medicine and for food – is frequently sold into Chinese wildlife markets illegally, after being smuggled into the country from other areas of South East Asia. There are also other hypotheses on the origin of the virus, yet regardless of the specific pathway of the pathogen flow for SARS-CoV-2, researchers are certain that emerging zoonotic diseases are often related to human interactions with wildlife.

Figure 12: Analysis has identified hotspots for potential zoonotic transfer of coronaviruses from Asian horseshoe bats. Photo shows Rhinolophus affinis. Source: Shutterstock/ Binturong-tonoscarpe

Figure 13. A pangolin, rescued from an online wildlife trader, during an undercover investigation by the Pangolin Reports team – a network of journalists documenting the smuggling of pangolins. The pangolin was later released by the Department of Wildlife and National Parks Peninsular Malaysia
(Credit: The Pangolin Reports: Trafficked to Extinction. Creative commons license: CC BY-NC-ND 4.0 https://globalstory.pangolinreports.com/#china-coda)

After the COVID-19 outbreak in Wuhan, the Chinese authorities closed a wildlife market identified as a potential source of spillover – and many others across the country – with orders to destroy the animal stock. When surveyed after the start of the COVID-19 outbreak, 94% of Chinese residents were in favour of more stringent legislation on wildlife trade, and most respondents intended to stop eating wildlife for food (IPBES, 2020).A similar level of concern was expressed after previous infectious outbreaks such as with SARS in 2002 in China. Yet there is no evidence that the initial intention to change habits as a response to past zoonotic transfers from wildlife led to longer-term behaviour changes, or a lessening of the trade in wildlife in live markets (Zhang and Yin, 2014; IPBES, 2020). However, this time China has taken unprecedented action – amending its wildlife protection law to ban the consumption of almost all wild animals. China is also revising its list of protected animals to raise the protection level of threatened species often consumed for food or medicine, such as the pangolin and yellow-breasted bunting (Koh, Li and Lee, 2021).

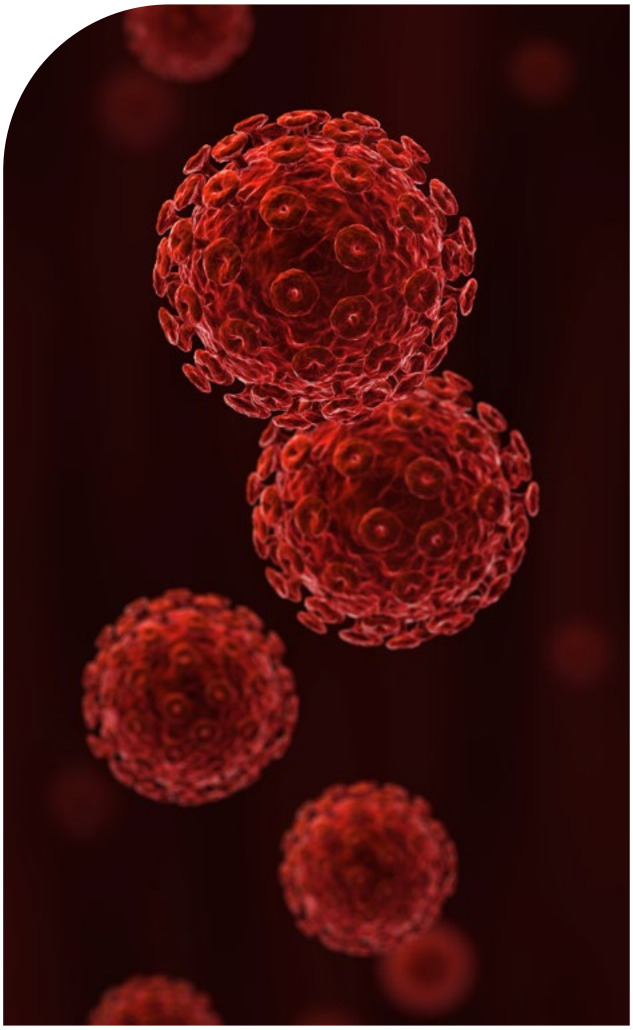
The COVID-19 pandemic has mainstreamed the conversation on wildlife conservation for human wellbeing, and informed a policy framework for enforceable wildlife management in China – all actions which can help minimise the risk of zoonotic transmission and pandemics in the future. However, to help ensure the successful implementation of these pandemic-prevention legislative changes in the longer term, the Chinese government has been encouraged to provide support to those who depend on wildlife protein for an income or for food. Also, it has been suggested to minimise human contact with novel vectors, an additional action to minimise degradation of natural habitats would help – for example via the establishment of a national park system (*ibid.*).

In 2019, EU Member States reported 6 441 seizures of CITES-listed (the Convention on International Trade in Endangered Species of Wild Fauna and Flora) species; and some illegal shipments will have certainly gone undetected (TRAFFIC, 2021). For example, authorities in Belgium have repeatedly detected illegal transport of wildlife trade commodities, such as plant-derived medicinal products, ivory, seahorse bodies and reptiles coming from West and Central Africa, *en* route to China – via air and postal systems (Musing *et al.*, 2018).

Bushmeat (or wild meat) is meat derived from wildlife and includes all wild, terrestrial or semi-terrestrial species. Primates, pangolins, antelopes, rodents and reptiles, among many other taxa, are commonly involved in the bushmeat trade and, as such, CITES-listed and non-CITES listed species are involved. Based on sampling carried out at Charles de Gaulle airport, Paris, in June 2008, one study estimated that over 270 tonnes of bushmeat could might be imported over the course of a year, via this airport alone – some 7% of searched passengers were carrying bushmeat (Chaber *et al.*, 2010). However, only 2.5% of luggage is searched for animal products, so it is likely that a lot more is coming through (Noordhuizen *et al.*, 2013). Other studies indicate large amounts of bushmeat reaching other European countries, for example Wood *et al.* (2014) suggest 500-1 500 kg may arrive yearly in Switzerland, from West Africa, while 80kg was estimated to have reached Zantavem airport, Brussels, in 2017-2018 (Chaber *et al.*, 2019). The African bushmeat market in Brussels has a domestic clientele of West and Central African expatriates, who indicate that the consumption of bushmeat is out of a desire to remain connected to their home countries. DNA-analysis of 15 bushmeat pieces bought in Brussels showed mammal species, including CITES-listed species, were being sold (Gombeer *et al.*, 2021).

Few studies have investigated the role of bushmeat trade and consumption as a potential source of human infections. However, some Ebola virus disease outbreaks have been linked to contact with bushmeat (gorilla, chimpanzee, duiker or fruit bat) infected with the viral pathogen (Mann *et al.*, 2015), and at least 13 pathogens (viruses, bacteria and parasites) of public health concern have been discovered in wildlife traded illegally across international borders, including simian foamy virus on primates intended for consumption (Bezerra-Santos *et al.*, 2021).

Alongside carefully considered curbs on bushmeat trade, raising awareness and promoting practices such as wearing gloves to handle wildlife, cleaning equipment used, and thorough cooking, are important for reducing risk of disease transmission (Kümpel *et al.*, 2015). However, conservationists have warned that bans on hunting or trade of protected species hunted for bushmeat could have perverse effects in terms of conservation – risking alienation of stakeholders from conservation efforts, or even motivating people to try and eradicate host populations (Pooley, Fa and Nasi, 2015).



HIV spreading (©Getty images/fpm, public domain)

The early 1980s outbreaks of HIV/AIDS caused by HIV-1 virus that is still spreading today have been traced back to apes and might have been initiated from hunting and butchering a chimpanzee or gorilla infected with the virus in Central or West Africa (Sharp and Hahn, 2010). It is likely these transmissions had occurred earlier in history too; however, it was the connectedness of African communities in the 20th century that allowed the rapid spread of the virus within the region. Then airlines and shipping facilitated the spread globally of the HIV-1 virus (Cohen *et al.*, 2008; IPBES, 2020). HIV-2, which likely originated from wild sooty mangabeys in West Africa, has largely not been transmitted outside Africa.

A monkeypox outbreak in the US in 2003 – the first known occurrence in the Western Hemisphere – is believed to have originated from a shipment of Gambian pouched rats for sale as pets (Smith *et al.*, 2012; CDC, 2003). No human-to-human transmission occurred in the US outbreak, although this is known to occur in Africa. Indeed, legal trade in live animals is also recognised as a transmission pathway for zoonotic diseases. The World Organisation for Animal Health (OIE) offers information on an official list of 116 diseases of domestic and wild animals to help safeguard animal health in the context of this trade. In 2014, it launched a public web application listing diseases of wild animals, the WAHIS-Wild Interface, including diseases not on the primary list. One analysis showed that this list includes 82 zoonotic pathogens, which caused more than 3 100 reported cases of human disease in 54 countries between 2008 and 2016 (Can, D'Cruze and Macdonald, 2019). Pathogens passed from birds were of most concern for human health, featuring in half these reports. The researchers note that trade bans on wild animals alone can stimulate illegal trade, so measures that reduce economic dependency on such trade, plus raising awareness among consumers of the health threats posed by exotic pets, are important.

Pathogen surveillance focused on wildlife trade is paramount. The risks posed to human health have been highlighted in the link between wildlife markets and early cases of SARS in 2002 and COVID-19 in 2019. The SARS virus outbreak in 2002 originated in Guangdong Province in China, with the first cases clustered amongst chefs and restaurant owners who had purchased wildlife from large animal markets (Smith *et al.*, 2012). The masked palm civet, sold at these markets, tested positive for the virus, and was believed to be the wildlife source of the disease outbreak (Guan *et al.*, 2003). The earliest-known case of COVID-19 originated in Hubei Province, China in November 2019. A majority of early cases visited a market in Wuhan (Huanan Seafood Market), and although some studies suggest transmission was via another person or people at the market, it is also possible they were infected by wildlife there (WHO 2021a).

> **“Despite few studies of the mechanisms that drive risk, recent data demonstrate that the percentage of bamboo rats infected by coronaviruses increases through the wildlife trade value chain in Vietnam, from 6% in rat farms, to 21% in large live animal markets, to 56% at the point of slaughter in restaurant”**

Source: IPBES, 2020 (citing Huong *et al.*, 2020)

Table 4. Main commodity types seized by Belgium between 2007 and 2016 contravening CITES or the EU Wildlife Trade Regulations. Source: Musing *et al.*, 2018, data from EU-TWIX database.

COMMODITY GROUPS	NO. OF SEIZURE RECORDS
Reptile bodies, parts and derivatives	218
Ivory	216
Medicinals	204
Live plants	199
Mammals (live, bodies, parts and derivatives)	144
Live birds	69
Live reptiles	66
Seahorse bodies	65
Other	83
Total	**1264**

In the context of wildlife destined for human consumption, studies have highlighted that infection with coronaviruses amplifies along the supply chain (e.g. Huong *et al.*, 2020; Lee *et al.*, 2020). That is, much transmission between wildlife likely takes place during transit and other trade operations. The increasing complexity of wildlife trade networks – with high density of animals, bulk transport over long distances, and international trade with livestock and wildlife mixed together – is considered a high-profile contributing factor to the threat of zoonotic transmission of novel pathogens to people (IPBES, 2020). This industrialised trade provides substantial opportunity for cross-species microbial transmission, with currently a poor regulatory framework and law enforcement in place to protect wildlife. The trade may have enabled SARS-related viruses to recombine among species, shown by infections in pangolins with viruses that have genes closely related to SARS-CoV-2 (*ibid.*). With some aspects of the wildlife trade increasing the risk of emerging diseases in animals farmed for food, this could impact on food security as well as public health.

It has been suggested that to detect spillover events and so prevent further epidemics similar to COVID-19, research should focus on surveillance of wildlife to identify high-risk pathogens; surveillance among people who have contact with wildlife to identify early spillover events; and improvement of market biosecurity regarding the wildlife trade (Daszak, Olival and Li, 2020).

2.5 Tourism

One of the main reasons for the increasing pandemic threat in the 21st century is a rapidly growing, and mobile, human population – with tourism becoming more popular and affordable, including wildlife tourism (Gössling, Scott and Hall, 2020). There is some direct evidence of tourism causing individual cases of important infectious diseases affecting humans (including Marburg virus from bats, and malaria from a Macaque monkey), as well as evidence of diseases affecting wildlife – so disease transfer is possible (CDC, 2009; Hartmeyer *et al.*, 2019). Tourism has been impacted greatly by the COVID-19 pandemic, as restrictions in movement were put in place globally to prevent the spread between countries. Tourism jobs in many developing countries were affected and, in reflecting on the impacts of this pandemic, there may be an opportunity to accelerate the transformation of sustainable tourism.

In East Africa, researchers have expressed concern regarding tourists passing COVID-19 to endangered wild chimpanzees and gorillas. During chimp-tracking trips at Kibale National Park in Uganda, tourist behaviour of touching trees, sneezing, coughing, touching their faces and urinating could all result in transmission of the virus to the chimpanzee populations they are visiting (Glasser *et al.*, 2021). Loss of income from wildlife tourism, meanwhile, has been linked to an increase in poaching in Uganda's Bwindi Impenetrable National Park, and the accidental killing of an endangered silverback gorilla in 2020 (Kalema-Zikusoka *et al.*, 2021). By September 2020, the benefits of re-opening tourism in the park, with emphasis on mask-wearing and distancing, were considered to outweigh the risks to primates from COVID-19, and of increased poaching due to lack of revenue to support enforcement.

Even Antarctica is no longer a COVID-19-free continent, and as such concern has been expressed that humans could transfer COVID-19 to the wildlife on that continent, through research or tourism-related activities (Barbosa *et al.*, 2021). The close proximity of people in research stations and cruise ships enable greater human transmission, while movement could promote spread across the continent. Among Antarctic wildlife, initial analyses suggest cetaceans (whales and dolphins) are at a greater risk of infection than seals and birds. Researchers suggest measures be taken by researchers handling wildlife, and the precautionary principle be applied.

Box 7: White-nose syndrome in bats – an example of a tourist transmitting the virus to bats?

Since its discovery in Albany, New York, in winter 2006, white-nose syndrome (WNS) has decimated bat colonies across the US and Canada. Infected colonies' numbers were reduced by 80-97%, and since that time the fungal infection has spread 2 000 miles, to colonies of hibernating bats across the continent (Cryan *et al*., 2013). Several species have been particularly hard hit, including little brown bats (*Myotis lucifugus*), northern long-eared bats (*M. septentrionalis*), and federally listed (endangered) Indiana bats (*M. sodalis*). The causative fungus, *Pseudogymnoascus destructans*, has long been noted in European colonies, but without causing large-scale fatality, as is the case for North American bat species who had previously not been exposed to the pathogen. The first cave the fungus was documented in was a tourism cave, visited by tens of thousands of tourists each year, and the disease has since spread outward from that site.

As North American bats are isolated from other bat species – European bats for example – they were extremely vulnerable to the WNS pathogen when it was spread to them from another continent. The translocation of the pathogen from Europe into a native bat colony in America in a single event is the current theory as to how this epidemic started (Olival *et al*., 2020). The susceptibility of North American bats to WNS is not only devastating numbers of certain species, but also potentially leaving infected bats more prone to contracting viruses, and shedding more of these viruses (*ibid*.).

Figure 14. Bat suffering with white-nose syndrome.

(Source: Marvin Moriarty/USFWS, CC BY 2.0 <https://creativecommons.org/licenses/by/2.0>, via Wikimedia Commons)

Since the emergence of white nose syndrome in bats (see Box 7), and the spillover of SARS from bats leading to an epidemic in humans, more attention has been focussed on infectious disease in bats and the potential for spillover from humans to bats and vice versa (Olival *et al.*, 2020). Bats can host particularly pathogenic viruses and pass these to humans: in part this is because they have quite unique physiological make-up, meaning they can repair their own DNA, suppress some of their immune system and have a very large metabolic range (*ibid*). In addition, the life history of some bats means they exist in peri-urban areas, often crossing human and wildlife interfaces, which could lead to spillover to humans of novel pathogens.

Concern has been raised that spillover of SARS-CoV-2 from infected humans in North America to bats they handle, or come into close contact with, could lead to the virus becoming either more or less pathogenic to bats, or other wildlife, domesticated animals, or humans – through genetic mixing in one or more novel hosts (*ibid*). The public health consequences of a more virulent SARS-CoV-2 virus could be severe. As with the researchers on Antarctica and wildlife tourists visiting chimpanzees in East Africa, guidelines to minimise disease transmission could be utilised for bat handlers and tourists in North America (Glasser *et al.*, 2021; Barbosa *et al.*, 2021).

2.6 Air Quality

COVID-19 had a greater impact on the human population in some urban centres, compared with others, worldwide (Lolli *et al.*, 2020). Some studies suggest that levels of ambient air pollution at the time of the COVID-19 outbreak in a city or region – or in the period of time preceding the outbreak – may have influenced the rate of transmission of the virus amongst the population, leading to more infections, deaths and a quicker spread (Zhu *et al.*, 2020; Dobricic *et al.*, 2020). However, these studies use large-scale statistical data (across long time periods and over large areas) on levels of air pollutants, such as particulate matter (PM2.5, PM10), nitrogen oxide gases (NOx) and sulphur dioxide –and struggle to account for some confounding factors that may contribute more greatly to the spread of the virus. These other variables, such as high population density in industrialised cities with high levels of air pollution, meaning that person-to-person transmission is more likely to occur – make it difficult to separate out the impact of air pollution (*ibid*).

Other studies suggest that these tentative correlations of increased COVID cases, and increased numbers dying from COVID, alongside higher levels of air pollution, instead indicate that higher levels of air pollution predispose the population to being more susceptible to contracting and becoming very ill with COVID-19 (Magazzino, Mele and Schneider, 2020). For example, nitrogen dioxide (NO2), which is released by the activity of vehicles, power plants and other industrial facilities, can have detrimental effects on respiratory function.

Particulate matter air pollution is known to pose significant health risks for cardiovascular and respiratory disease, ischaemic heart disease, stroke, chronic obstructive pulmonary disease (COPD), lower respiratory infections, lung cancer and type-2 diabetes (Burnett *et al.*, 2018). This is set against similar significant risk factors for COVID-19 patients, identified as hypertension, COPD, cardiovascular disease and cerebrovascular disease (Dobricic *et al.*, 2020). The links between SARS and air pollution were suggested some time ago; however, the link between long- and short-term exposure to air pollution, and the severity of SARS-CoV-2 infections has still to be verified (*ibid.*).

Italy was one of the first European countries to be significantly affected by the COVID-19 pandemic, especially in the industrialised cities of the north. It was suggested that air pollution in these cities may have contributed to the large number of people infected, and the high number of deaths. For example, Lolli *et al.* (2020) examined meteorological conditions and air pollution in several affected cities in northern Italy, finding that PM2.5 was correlated with transmission of SARS-CoV-2 – along with cooler, drier environments. For this reason, it has been suggested that unfiltered, air-conditioned indoor environments might aid the spread of the virus (*ibid.*). However, as discussed, other factors such as population density, age and the approach and knowledge of healthcare practitioners, would also have been key factors involved in the fast spread and impact of COVID-19 in Italy. For instance, 23% of the population in Italy is over 65 – the highest share in the EU – and the country also has the highest average age, of 46.7 years (Goumenou *et al.*, 2020). At present, research into the contribution of air quality to transmission, and into susceptibility of the resident population to the effects of the virus, is still ongoing. However, air pollution cannot yet be ruled out from affecting the transmission and severity of COVID-19, on human populations in polluted areas – further research is needed to clarify this (Dobricic *et al.*, 2020).

3. Impacts on the environment

As environmental issues might have contributed to the onset and spread of the COVID-19 pandemic, so too the pandemic has influenced environmental issues. Although some of the early discourse around the pandemic suggested it may be beneficial for the natural world, with lockdowns leading to sightings of animals in areas where humans usually dominate (Kretchmer, 2020) and dramatic reductions in car and air traffic (Eurocontrol, n.d.; Le Quéré *et al.*, 2020), in reality the environmental impacts of COVID-19 are more complex.

Air quality improved in many areas due to enforced reductions in travel, but in some cases ozone levels increased and there is a risk that pollution levels could return to, and even surpass pre-pandemic levels in a 'return to normal' (Le Quéré *et al.*, 2020; Venter *et al.*, 2020). The widespread use of personal protective equipment (PPE) saved lives, but also led to a huge increase in plastic waste (Silva *et al.*, 2021a). In the animal world, some species expanded their range as a result of a reduced human footprint, but others suffered without their usual food sources (Reid, 2020).

Clearly, the effects of the pandemic on the environment have not been universally beneficial and any environmental gains could be lost without government and social action. In this chapter we discuss each of these impacts, and what the changes brought about by COVID-19 might mean for the future of the natural environment.

3.1 Plastic waste

3.1.1 Personal protective equipment (PPE)

The pandemic created a rapid and urgent need for personal protective equipment (PPE) for healthcare professionals, including face masks, shields, gowns and gloves. The demand was so great that shortages were observed across the world (Burki, 2020), leading the World Health Organization to call for a 40% increase in manufacturing (WHO, 2020a).

Outside of healthcare settings, individuals have also been encouraged – and in some circumstances required – to wear a personal face covering, resulting in a significant increase in the use of disposable, single-use face masks. These masks, which include surgical masks and N95 respirators, are produced from polymers (plastics) and represent the majority of masks available for sale.

> **"PPE needs for the global population, as lockdowns are lifted, have been estimated at 129 billion face masks and 65 billion gloves per month."**
>
> (Prata *et al.*, 2020)

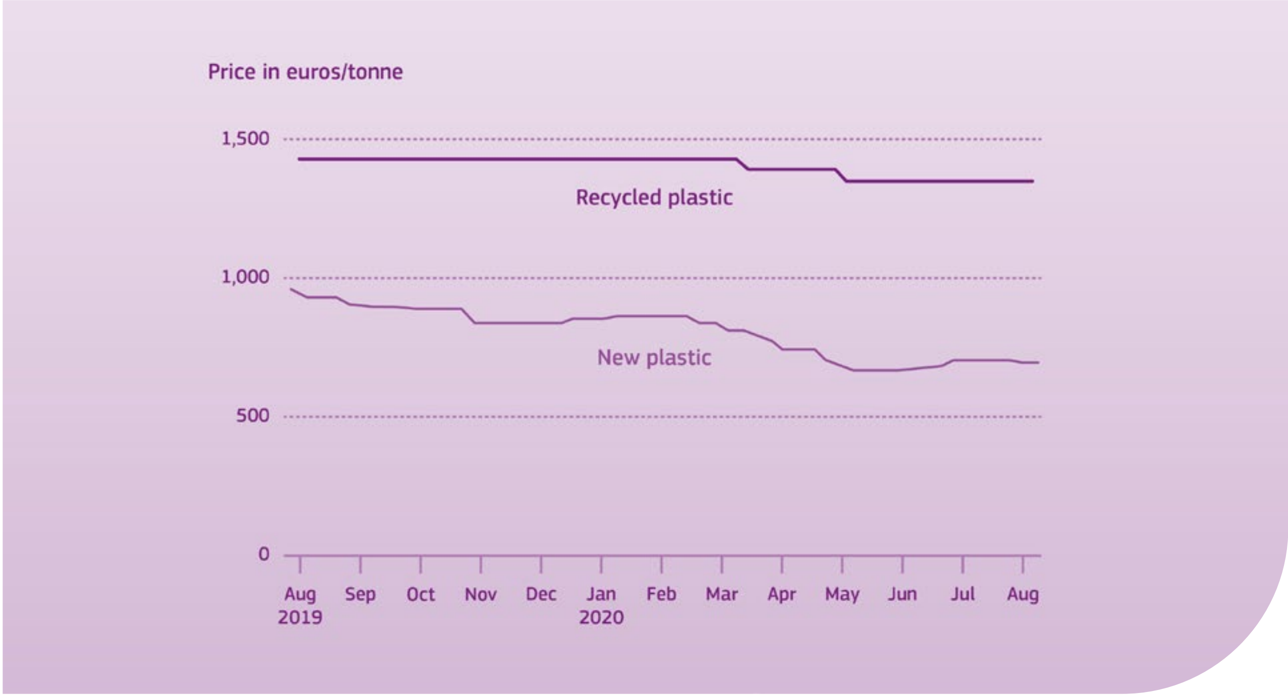
The widespread use of single-use face masks could generate a huge amount of additional plastic waste. Imports of face masks to the EU rose from about 25 000 tonnes per month, pre-pandemic, to between 45 000 and 70 000 tonnes monthly in April - September 2020 (EEA, 2021). Estimates suggest some 445 million single-use face coverings might have been discarded daily in Europe in 2020 (Benson *et al.*, 2021). Most EU countries advise disposing of masks and gloves in mixed municipal solid waste, however littering of these items has also occurred. Analysis of litter-picking records in the citizen science app Litterati found that in some months of 2020, the proportion of masks reached as much as 3% of all items collected in some EU countries (Roberts *et al.*, 2021a). In the UK alone, if every person used one single-use mask each day for a year, it would create 66,000 tonnes of plastic waste, with a contribution to climate change 10 times greater than that of using re-usable masks (Allison *et al.*, 2020).

3.1.2 Other forms of plastic waste generation and declines in recycling

The pandemic also saw an increase in demand for plastic for other purposes, such as containers for takeaway food and packaging for online purchases (Brock, 2020; EEA, 2021), and related waste generation. The onset of the pandemic also influenced recycling rates, for example through impacts on domestic disposal habits, waste sorting and recycling operations, and economic competitiveness of plastic raw material. Impacts on waste management in general – and more specifically also waste shipments – led governments and international institutions to adopt specific guidance on waste management (e.g. EC 2020a; EC 2020b).

Lockdowns, and consequent reductions in travel, reduced demand for petroleum and the resultant drop in oil prices made it cheaper to manufacture plastics from fossil fuels (Adyel, 2020). Although new or virgin plastic is generally cheaper to buy than recycled plastic, the gap widened during the pandemic. Since the onset of the pandemic, drinks bottles made of recycled plastic have become up to 93% more expensive than those made of virgin plastic (Brock, 2020). The vulnerability of the recycling sector to such macroeconomic drivers has been highlighted prior to the pandemic, for example when oil prices plunged in 2014, emphasising its dependence on supportive policies.

Figure 15: The gap between virgin and recycled plastic widens.
Source: Redrawn from *Independent Commodity Intelligence Services*



These issues have been compounded by increased demand for plastic packaging through the boom in online shopping, food takeaway, and reluctance to purchase loose, ‘unprotected’ items, as a result of perception that wrapped items were safer (Klemeš *et al.*, 2020, Prata *et al.*, 2020). In North America, a number of U.S. states and the Canadian city of Vancouver delayed single-use plastic bans, reintroduced single-use plastics and even prohibited the use of re-usable shopping bags due to concerns about the spread of the virus (Silva *et al.*, 2021a). Several states also stopped recycling programmes due to fears of COVID-19 spreading in facilities (Zambrano-Monserrate, Ruano and Sanchez-Alcalde, 2020). Waste management has also been disrupted in European countries, however there has been no delay to the planned Single-Use Plastics Directive (EU) 2019/904 of July 2021. While not all Member States have yet notified their implementation to the Commission, this obligation has not been waived.

Of concern is that although the marked increase in medical single-use plastic may drop off as the pandemic wanes, the accelerated shift towards e-commerce may lead to a permanent plateau in the amount of single-use plastics in the economy (Ebner and Iacovidou, 2021).

3.1.3 Disposal

The scale of plastic use necessitated by the pandemic exceeded the capacity of regular waste management strategies. In a clinical setting, PPE has generally been classified as potentially infectious, requiring incineration followed by landfilling of the residue. This is a concern as uncontrolled incineration of medical waste (which is largely plastic), as has occurred in some parts of the world, releases greenhouse gases as well as other dangerous compounds, such as heavy metals and dioxins (Silva *et al.*, 2021a).

> **If only 1% of masks were disposed of incorrectly, it would result in 10 million masks per month entering the environment**
>
> (WWF, 2020)

A related concern is the inappropriate disposal of PPE by the public. Members of the public have been found to litter face masks, gloves, and other types of PPE. A survey of French citizens for example revealed that 5% – over 2 million people – admitted disposing of face masks on public roads (EEA, 2021).

From littering, masks and other forms of PPE can enter the oceans. The French non-profit *Opération* Mer Propre reported finding gloves, masks and bottles of hand sanitiser in the Mediterranean Sea (Kassam, 2020). Similarly, Oceans Asia (2020) has identified significant mask debris in the water around Hong Kong and estimates that 1.56 billion face masks may have entered the oceans during 2020.

This poses immediate problems for marine life. Disposable masks have a lifespan of 450 years (Davidson, 2020) and fish and birds can ingest and become entangled in them. What’s more, as discarded face masks break down due to weathering, ultraviolet (UV) light and abrasion, they generate plastic particles less than 5 mm, also known as microplastics. Microplastics are a threat to marine life, can enter the food chain, and may propagate microbes and invasive pathogens (Fadare and Okoffo, 2020). They can also have human health effects, through exposure to microplastics in seafood for example (Smith, 2018). As a result, the EU Technical Group on Litter under the Marine Strategy Framework Directive has recently included face masks in their marine litter monitoring lists (Fleet, Vlachogianni and Hanke, 2021). Future research needs include better knowledge of mask fragmentation and the contaminants they may release, including ecotoxicological effects. Researchers have pointed to the need for polymer materials that do not degrade into microplastics (Silva *et al.*, 2021b).

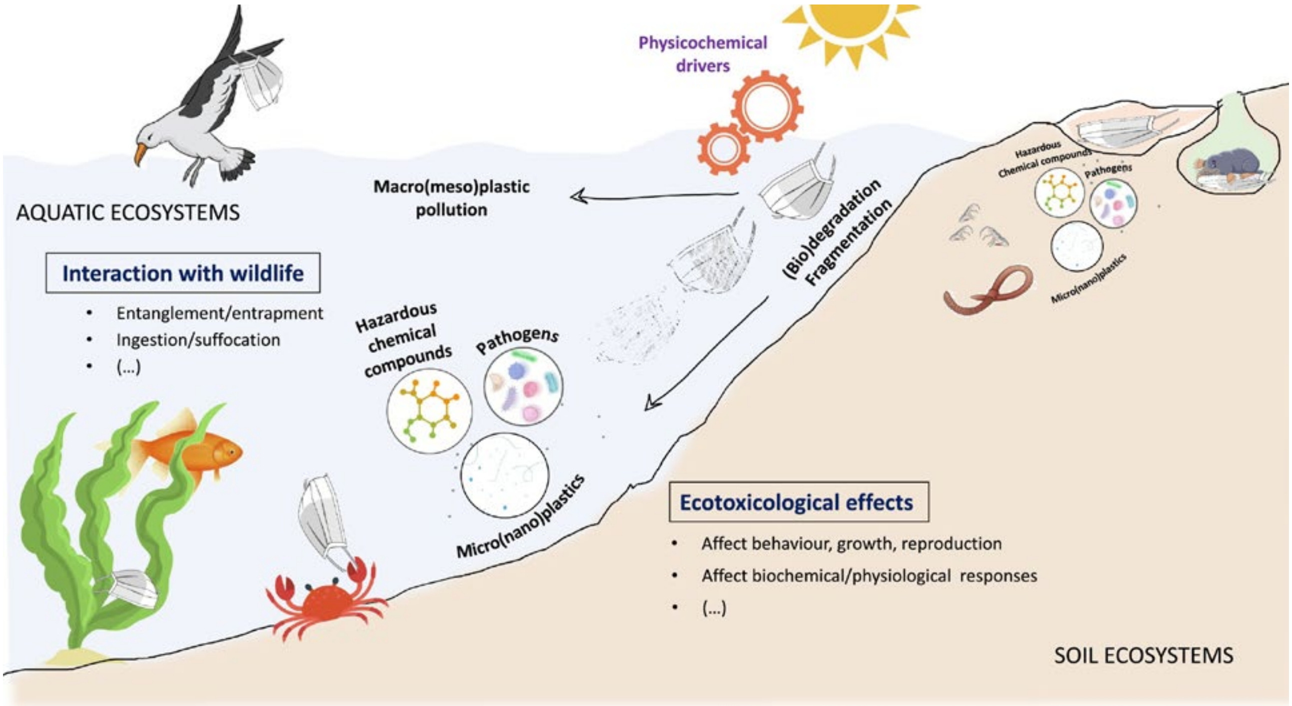


Figure 16: Polymer-based PPE entering the environment may pose a threat to aquatic organisms and ecosystems.

Source: Silva *et al.*, 2021b

3.1.4 Sustainable management of plastic waste

Better waste management systems are needed for the unprecedented amount of contaminated plastic waste. In clinical settings, the safe disposal of contaminated waste is paramount and for large volumes of such waste incineration remains the best approach (Silva *et al.*, 2021a; Basel Convention, 2020). For municipal waste however, a circular economy approach might be appropriate. Feedstock recycling of mixed plastic waste for example generates half the CO2 emissions of incineration and could be used to complement mechanical recycling approaches (Vanapalli *et al.*, 2021).

Other solutions include the promotion of sustainable alternatives to plastic and single-use PPE. Unfortunately, PPE made from bioplastics and natural plant fibres are not necessarily advantageous in terms of lifecycle emissions and land use, however development of products made from agricultural by-products or recycled materials may prove useful. Among the public, re-usable, cloth face masks with several layers for effective filtration, can drastically reduce waste, though their efficacy depends on proper use and has been disputed by some (MacIntyre *et al.*, 2015; Clase *et al.*, 2020). Government action, such as public health campaigns on how to wear, remove and wash reusable masks, could encourage proper use (Allison *et al.*, 2020).

Where single-use, plastic face masks are used, it may be possible to safely increase the number of uses they can offer. The dry heat of electric cookers, for example, which are found in many homes, can effectively sanitise N95 face masks for re-use (Oh *et al.*, 2020). Other recommended methods for mask decontamination include UV irradiation, hydrogen peroxide vapour and steam sterilisation, which could be used in clinical settings (Peters *et al.*, 2021).

Governments can incentivise circular-economy approaches, using policies that prevent and penalise plastic pollution and support recycling, and the full implementation, monitoring and further development of limits on the use of single-use plastic.

3.2 Water Quality

3.2.1 SARS-CoV-2 in wastewater

Although primarily an airborne virus, genetic material from SARS-CoV-2 has been identified in stool samples from infected patients (Chen *et al.*, 2020) and the presence of viral SARS-CoV-2 RNA in wastewater has been repeatedly reported (Shah *et al.*, 2022; Ahmed *et al.*, 2020). Although at much lower levels than in nasopharyngeal fluids, SARS-CoV-2 can be detected in both urine and faeces, including in asymptomatic and pre-symptomatic individuals. After excretion, SARS-CoV-2 is diluted in toilet water and then in other municipal wastewater constituents including greywater, such as from showers and washing machines (Larsen and Wigginton, 2020). This has led to concerns about 'potential' spread of the virus in wastewater (Jones *et al.*, 2020; Bogler *et al.*, 2020) – but there have been no studies to date confirming that such an infection pathway exists.

Figure 17: Wastewater testing can be employed in a sentinel system to highlight new outbreaks of COVID-19.
Source: Felipe Caparros / Shutterstock

Viral genetic material is stable at the temperatures and time frames involved in travel through the sewerage system (i.e. from toilets to the waste water treatment plant) (Larsen and Wigginton, 2020) and while SARS-CoV-2 can largely be removed from wastewater by conventional wastewater treatment, it is not eliminated (Jones *et al.*, 2020). The risk of transmission via wastewater and sewage – including aerosols generated at sewage treatment plants and in washrooms – has therefore received attention. For example, a recent systematic review assessed the risk of viral/bacterial infections (including COVID-19) in public washrooms, finding no evidence of airborne transmission of enteric or respiratory pathogens (Vardoulakis, Espinosa and Donner, 2022).

As SARS-CoV-2 has been found in sewage sludge (Peccia *et al.*, 2020), it could be present in soils and nearby surface and groundwater, which could be contaminated by run-off or leaching (Conde-Cid *et al.*, 2020), and urban flooding events could potentially also pose transmission risk through exposure to untreated sewage (Han and He, 2020). However, analysis to date suggests that the likelihood of infection due to contact with contaminated wastewater – or any waters contaminated with faeces, such as swimming pools – is extremely low (WHO, 2020b). The possibility of transmission via sewage sludge also seems remote, and exposure to wastewater has not yet been demonstrated as the cause of transmission in any case of COVID-19 (Jones *et al.*, 2020; Sobsey 2022).

This could be because virus particles are 'enveloped' with a double lipid membrane sensitive to detergent, which may inactivate the virus in wastewater; sewage commonly contains detergent chemicals. Enveloped viruses are considered some of the least resistant microbes to environmental stressors. In addition, enzymes present in the digestive tract may destroy infectiousness of viral particles (Robinson *et al.*, 2022; Sobsey, 2022). To determine risk from wastewater, distinguishing viral RNA and complete virions that carry risk of infections, is vital, and the subject of ongoing research.

> **"The World Health Organization, Water Environment Federation, US Centers for Disease Control and Prevention and others do not consider environmental fecal wastes and waters as sources of exposure to infectious SARS-CoV-2 causing COVID-19 infection and illness."**
>
> (Sobsey, 2022)

Figure 18: The Werdhölzli sewage treatment plant in Zurich. Analysis of wastewater can indicate levels of COVID-19 in the population. (Photo: City of Zurich)

3.2.2 Monitoring SARS-CoV-2 in wastewater

Monitoring SARS-CoV-2 traces in wastewater offers a useful early warning system for predicting outbreaks, and a tool to complement epidemiological data. It may offer information on infection dynamics in a population, through correlation between the amount of SARS-CoV-2 genetic material found in wastewater and the number of infected people in the area. The European Commission has recognised the value of wastewater surveillance to identify the presence of SARS-CoV-2 in the community and also to indicate areas where the virus is absent (EC, n.d.; Gawlik *et al.*, 2021). However, various factors mean that this association is not simple – for example shedding of viral particles may continue for months after a person recovers, and particles may come from visitors as well as local residents. Wastewater surveillance can also be used to detect and monitor different variants in a population (La Rosa *et al.*, 2021b).

Early reports of SARS-CoV-2 in wastewater came from an analyses in Italy (La Rosa, 2021a) and the Netherlands (Lodder and de Roda Husman, 2020), using a molecular assay which detects SARS-CoV-2 genetic material. A similar method was also applied in Australia early in the pandemic (Ahmed *et al.*, 2020) and could be employed more widely to provide early warning of a COVID-19 surge, by detecting the virus in asymptomatic as well as symptomatic individuals and revealing infection dynamics earlier than diagnostic testing (Larsen and Wigginton, 2020). A faster type of assay has recently been developed, which looks for three target genes and could prove more cost effective (Navarro *et al.*, 2021).

Monitoring of sewage sludge in New Haven, U.S., was shown to identify SARS-CoV-2 up to four days ahead of hospital admissions (Peccia *et al.*, 2020). Similarly, a study at a major wastewater treatment plant in Massachusetts in the U.S. could provide up to 10 days advanced notice ahead of confirmed case data (Wu *et al.*, 2022). A systematic review from 2021 shows wastewater signals preceded confirmed cases by up to 63 days, with 13 studies (of 92) reporting sample positivity before the first cases were detected in the community (Shah *et al.*, 2022). A European Sewage Sentinel System for SARS-CoV-2 has been outlined, to complement other surveillance systems (Gawlik *et al.*, 2021).

At least 50 studies have reported an association of wastewater viral load with community cases. However, there are a range of factors that can affect results; for example, certain characteristics of wastewater, such as ammonia and pH, show significant associations with viral RNA concentrations (Ahmed *et al.*, 2022; Amoah *et al.*, 2022). Researchers have pointed to the need for analyses to adhere to best practice guidelines for reliable results, and the need for a common framework to integrate data from different Member States (Bivins *et al.*, 2021; Gawlik *et al.*, 2021).

Box 8: Wastewater surveillance of COVID-19:

Is cost effective

Surveillance of a treatment plant costs an estimated €25 000 per year. National programmes could cost €1 to €3 million depending on the number of plants included

Is multi-purpose

Wastewater surveillance can be used to provide early warning of an outbreak, as a management tool, and to help identify infection sources

Can be used where epidemiological data is lacking

Wastewater surveillance should be used in combination with epidemiological data where possible. Unlike clinical testing, it is not dependent on access to healthcare

Avoids some biases

Wastewater surveillance does not have the same biases of traditional indicators, such as number of diagnosed cases, which depends on access to diagnostics and may not include asymptomatic cases (it is independent of healthcare-seeking behaviour). However, it does have other biases, such as assuming people are connected to central wastewater systems (in 12 Member States, at least 20 % of the population is not)

Can provide near real-time information on infection dynamics

Detecting SARS-CoV-2 in wastewater provides a rapid indicator of infection – tracking community outbreaks within days – unlike data on hospitalisations and deaths, which lags behind infections by weeks

Sources: EC, n.d.; Larsen and Wigginton, 2020; Gawlik *et al.*, 2021; Galani *et al.*, 2022

Acknowledging limitations and the necessity of adhering to ethical guidelines for public health surveillance, measuring the presence of SARS-CoV-2 in wastewater has been recommended by the European Commission as a reliable and cost-effective means of tracking spread (EC, n.d.), as well as governments in the United Kingdom (Ott, 2020), United States (CDC, 2021), and other developed nations. Data should, however, be supplementary to conventional surveillance. Wastewater surveillance may be particularly useful in developing countries as it is relatively cheap and may provide information on spread of diseases where access to healthcare, and therefore epidemiological data, is lacking (EC, n.d.; Gawlik *et al.*, 2021).

3.2.3 Risk to marine mammals

There is previous evidence of marine mammals becoming infected with pathogens from humans and other land-based mammals, such as influenza (Fereidouni *et al.*, 2014). An estimated 15 species of marine mammals may be susceptible to SARS-CoV-2, including whales, dolphins, seals and otters – based on their expression of the angiotensin converting enzyme 2 (ACE2) receptor that enables the virus to access cells (Mathavarajah *et al.*, 2020). Some researchers have recommended minimising infection risk among marine mammals through wastewater treatment, monitoring and testing marine mammal populations, restricting contact with captive marine mammals that are at risk, and considering vaccination of marine mammals where feasible (*ibid*). However, there is so far no evidence of transmission among marine mammals and since the risk from wastewater is very low, resources might be best directed elsewhere (Maal-Bared *et al.*, 2021).

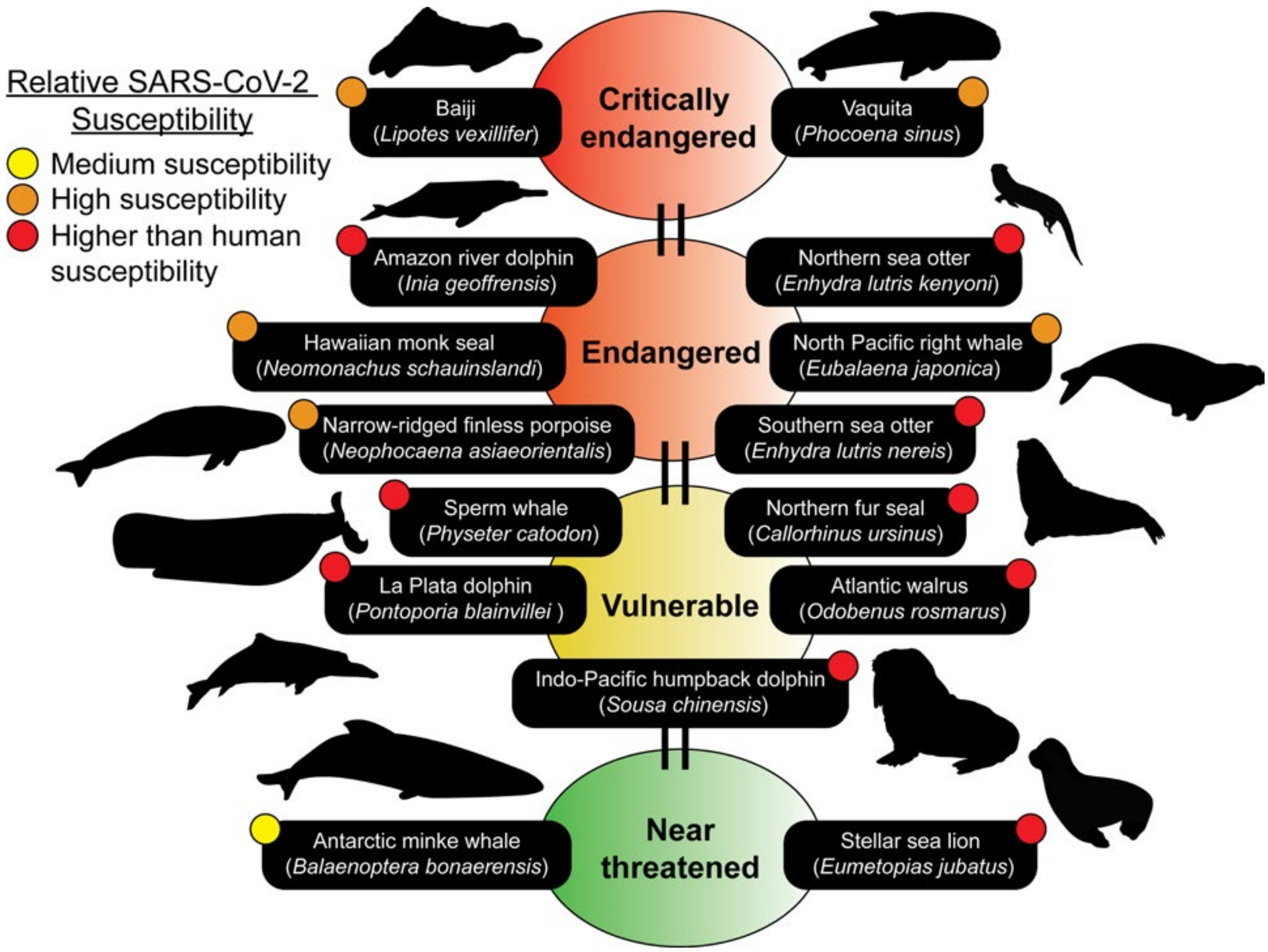


Figure 19: Relative SARS-CoV-2 susceptibility among marine mammals.
Original source: Mathavarajaha *et al.*, 2021, Sci Total Environ. 760:143346.

3.2.4 Water demand and sanitation

Since frequent washing has been identified as a key factor in limiting COVID-19 spread, access to safe water and sanitation plays a significant role. Although increased household water consumption (e.g. from more frequent hand washing) has been reported in Europe during the pandemic, this has been offset in some countries by a reduction in water footprints of electricity generation during lockdowns (Cahill *et al.*, 2022; Roidt *et al.*, 2020). Whether new patterns persist is a pertinent question for water utilities.

Meanwhile, as many as one in five people around the world lack access to safe water, in communities that anyway bear a disproportionate share of global health burdens (UNICEF and WHO, 2019). Problems of sufficient, safe supplies of water also extend to higher-income countries; an estimated 57 million people in Europe and North America lack piped water at home (WWAP, 2019). Addressing access to handwashing is imperative to helping these communities slow the spread of infections, while forecasting models should incorporate disparities in sanitation (Brauer *et al.*, 2020). At household level, boiling, filtration, solar and UV irradiation, or appropriate chlorine products can all be effective in minimising risk from contamination. Meanwhile, water systems in buildings which have not been used for prolonged periods of time, due to lockdowns, for example, should be flushed through to replace stagnant water.

3.3 Air quality

One of the most immediately noticeable environmental impacts of the pandemic was reduction in travel, and therefore changes to air quality. The issue of air quality is particularly pertinent in the context of the pandemic, as air pollution and its associated health impacts have been correlated with COVID-19 outcomes.

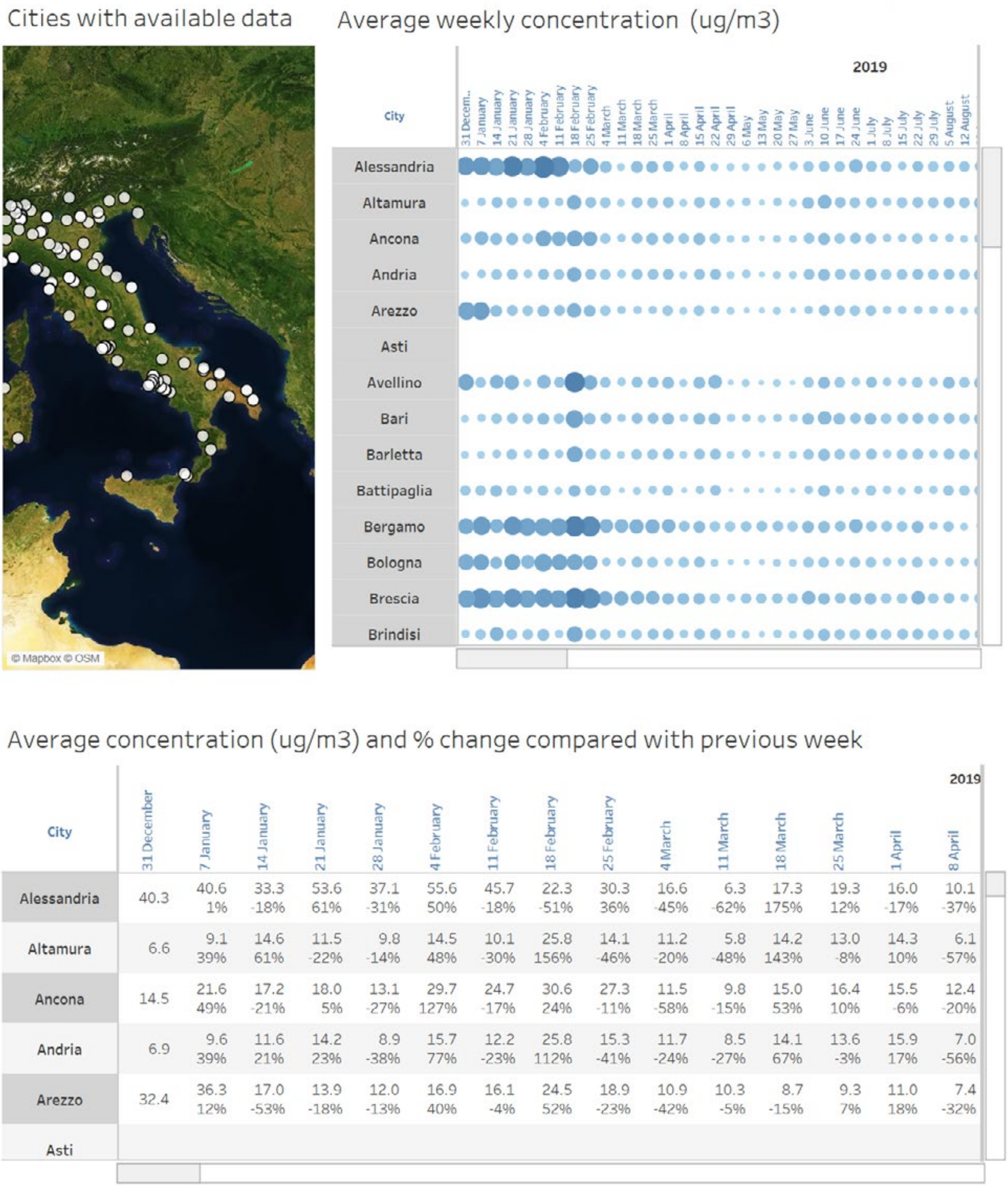
As described in Chapter 2, air pollution may contribute to deaths from COVID-19. A study in Northern Italy (Conticini, Frediani, and Caro, 2020) identified a correlation between COVID-19 deaths and high levels of atmospheric pollution, while a study in the United States (Wu *et al.*, 2020) found that exposure to fine particulate matter (PM2.5) was also associated with higher COVID-19 mortality rates – an increase of just 1μg/m^3 in PM2.5 being associated with a 15% increase in COVID-19 mortality rate. However, it is important to be aware that these are estimates and other factors may have influenced these findings, such as transmission dynamics and risk factors such as age. Efforts to explain the link include hypotheses that chronic exposure to PM2.5 impairs lung defences by disrupting epithelial (barrier) cells, causing respiratory inflammation and exacerbating COVID-19 (Frontera *et al.*, 2020; Fiorito *et al.*, 2022).

3.3.1 Lockdowns and their effect on air pollution and CO2 emissions

COVID-19 lockdowns led to drastic changes in work and travel, which were associated with significant changes in air pollution. During the early stages of the pandemic (April 2020), global daily CO^2 emissions decreased by an estimated 17% compared to mean 2019 levels and, at their peak, CO^2 emissions in individual countries decreased by an average of 26% (Le Quéré *et al.*, 2020). In Europe, power generation from coal dropped by almost 40% and oil consumption by around a third because of lockdowns. Average NO^2 levels in European air were halved (ESA, 2020; Myllyvirta and Thieriot, 2020; Venter *et al.*, 2020) and particulate matter up to a third in some countries (*ibid.*)

Table 5: Changes in work and travel saw drastic changes in air pollution levels during the pandemic.

Country / Area	COVID-19 and air pollution across the world
Brazil 	During the partial lockdown in Rio de Janeiro, **NO_2** median values were up to **33%** lower and **CO** median values up to **44%** lower compared to the same period in 2019 (Dantas *et al.,* 2020).
China 	In China, the number of operating vents of key polluting industries decreased by some **25%** due to the pandemic. Emissions of nitrogen oxides (NOx) decreased by as much as **34%** in some areas (He *et al.,* 2020).
Ecuador 	In Ecuador, there was initially a **13%** reduction in **NO_2** concentrations after the COVID-19 lockdown (March 16-31, 2020). In the most populated cities, reductions were even higher, at around **23%** (Pachecho *et al.,* 2020).
Egypt 	Greenhouse gas emissions in Egypt reduced by **4%** during the pandemic (compared to 2015–2019 levels). In Cairo, **NO_2** levels decreased by **15%** and **carbon monoxide (CO)** levels decreased by around **5%** (Mostafa *et al.,* 2021).
Europe 	Multiple sources confirm **NO_2** levels dropped by **40–50%** during lockdowns in Europe (ESA, 2020; Myllyvirta and Thieriot, 2020; Sicard *et al.,* 2020).
India 	India saw a **40–60%** reduction in **particulate matter** pollution and a **30–70%** drop in **NO_2** levels during their lockdown (25 March–3 May 2020) (Singh *et al.,* 2020).
Iraq 	In Iraq, **NO_2** emissions reduced by up to **40%** with lockdowns and the overall **air quality index** (AQI) in Baghdad improved by **13%** (Mohammed Hashim *et al.,* 2020).
Saudi Arabia 	In regions of Saudi Arabia, concentrations of PM10 dropped by as much as **91%** between January 2019 to May 2020, while NO_2 and SO_2 dropped by **44%** and CO by **34%** (Othman Aljahdali *et al.,* 2021).
United States 	A case study in California found a **49%** drop in levels of **CO, 38%** drop in **NO_2** and **31%** drop in particulate matter 2.5 (**PM2.5**) during the lockdown (March 19–May 7), compared to before (January 26–March 18) in 2020. (Liu *et al.,* 2020).
United Kingdom 	During the most stringent travel restrictions in the UK (30 March-3 May 2020) there was a **69% reduction in traffic** and mean reductions of **38%** in **NO_2** and **16%** in **PM2.5**, compared to averages in the same period 2017–19 (Jephcote *et al.,* 2021).



Average concentration (ug/m3) and % change compared with previous week

2019

City	31 December	7 January	14 January	21 January	28 January	4 February	11 February	18 February	25 February	4 March	11 March	18 March	25 March	1 April	8 April
Alessandria	40.3	40.6 1%	33.3 -18%	53.6 61%	37.1 -31%	55.6 50%	45.7 -18%	22.3 -51%	30.3 36%	16.6 -45%	6.3 -62%	17.3 175%	19.3 12%	16.0 -17%	10.1 -37%
Altamura	6.6	9.1 39%	14.6 61%	11.5 -22%	9.8 -14%	14.5 48%	10.1 -30%	25.8 156%	14.1 -46%	11.2 -20%	5.8 -48%	14.2 143%	13.0 -8%	14.3 10%	6.1 -57%
Ancona	14.5	21.6 49%	17.2 -21%	18.0 5%	13.1 -27%	29.7 127%	24.7 -17%	30.6 24%	27.3 -11%	11.5 -58%	9.8 -15%	15.0 53%	16.4 10%	15.5 -6%	12.4 -20%
Andria	6.9	9.6 39%	11.6 21%	14.2 23%	8.9 -38%	15.7 77%	12.2 -23%	25.8 112%	15.3 -41%	11.7 -24%	8.5 -27%	14.1 67%	13.6 -3%	15.9 17%	7.0 -56%
Arezzo	32.4	36.3 12%	17.0 -53%	13.9 -18%	12.0 -13%	16.9 40%	16.1 -4%	24.5 52%	18.9 -23%	10.9 -42%	10.3 -5%	8.7 -15%	9.3 7%	11.0 18%	7.4 -32%
Asti															

Figure 20: This European Environment Agency data viewer shows the effect of lockdowns on air quality in European cities. In this sample screenshot, levels of PM 2.5 in Italian cities in 2020 are visualised.
Source: https://www.eea.europa.eu/themes/air/air-quality-and-covid19

Although several emissions drastically reduced in many parts of the world, effects on ozone (O_3) were mixed and, in some cases, levels of O_3 increased. This is possibly a side effect of reduced NO_x emissions, as NO can quench ozone, and highlights the difficulty of balancing the reduction of both primary and secondary pollutants (Sicard *et al.*, 2020; Venter *et al.*, 2020). Furthermore, although global reductions in CO2 levels were significant, they still only correspond to 2006 emissions levels (Le Quéré *et al.*, 2020).

Most changes are also likely to be temporary, as they have not been accompanied by major structural changes in economic systems. In Chongqing, China, for example, NO_2 levels dropped by almost 50% between February 2019 and February 2020. However, by February 2021, they had returned to almost double pre-COVID levels (ESA, 2021). NO_2 levels also returned to 'near-normal' levels in many parts of Europe by July and August 2020 (ESA, 2020).

Box 9: Avoided health impacts due to reductions in air pollution

Epidemiological studies and risk modelling link air pollution exposure to health effects and premature death (Lelieveld *et al.*, 2015). As trends in air pollution were interrupted by lockdowns, some researchers have estimated the avoided health impacts.

One source estimates that measures against COVID-19 in Europe will lead to:

- **1.3 million** fewer days of work absence
- **6,000** fewer new cases of asthma in children
- **1,900** avoided emergency room visits due to asthma
- **600** fewer pre-term births
- **11,000** fewer air pollution-related deaths

Other research has indicated that **13 600 - 29 500** premature fatalities may have been avoided in Europe due to reduced PM2.5 concentrations in 2020, depending on resumption of economic recovery.

Sources: Myllyvirta and Thieriot, 2020; Giani *et al.*, 2020

3.3.2 Air quality post-pandemic

As the data indicates, improvements in air quality as a result of COVID-19 control measures are likely to be temporary in the absence of further government action. There are however opportunities to implement economic incentives aligned with low-carbon pathways in order to capitalise on air quality improvements, which could influence emissions for decades to come. Inaction means gains could be lost, as demonstrated by the 2008/09 financial crisis: global CO_2 emissions declined in 2009, immediately to increase far above the long-term average in 2010 (Le Quéré *et al.*, 2020).

The risk that the post-pandemic future could have an even higher emissions trajectory than pre-pandemic is a real one. In Europe, some have called for delays to Green Deal programmes in favour of economic growth (Euractiv, 2020), while the automotive industry has also called for delays to vehicle emissions standards to allow the industry to recover (Eriksen, 2020).

However, some changes initiated by the pandemic are likely here to stay. Many cities have already taken steps towards a more sustainable and pedestrian-friendly design. This is important for air quality, as around half of the reduction in global CO_2 emissions seen during the pandemic can be attributed to changes in surface transport (Le Quéré *et al.*, 2020). Milan, for example, has implemented a pedestrianisation scheme, re-allocating space from cars to cycling and walking. The scheme includes 35 km of streets and measures including temporary cycle lanes, widened pavements, 30 kmph speed limits and priority areas for pedestrians and cyclists (Comune di Milano, 2020; Stavrinou, 2020). Bogotá, London, New York and Paris have also rededicated street space for pedestrians and cyclists, in schemes which may become long-term (Le Quéré *et al.*, 2020).

Although public transport became less popular in 2020 and 2021 – partly due to less travel overall – some European research suggests that car use for commuting did not necessarily increase when people returned to workplaces (Eisenmann *et al.*, 2021; Jenelius & Cabecauer, 2020; van der Drift, Wismans and Olde Kalter, 2021). Despite a decline in overall car sales during the pandemic, meanwhile, electric car sales in Europe have continued to grow. Electric car sales more than doubled their 2019 levels in 2020 in Europe (Gorner and Paoli, 2021) and in the largest markets sales in the first four months of 2020 were around 90% higher than in the same period of 2019 (Gül *et al.*, 2020).

The European Green Deal includes targets to provide fresh air, cleaner energy and improved public transport (see Box 11). The Green Deal demonstrates the central role of policy in shaping a sustainable future post-pandemic and shows that it is possible to decouple economic development from air pollution (Acuto *et al.*, 2020; EC, 2019).

Box 10: The European Green Deal: Europe's pathway to a sustainable future

The European Green Deal aims to make Europe climate neutral by 2050 in order to improve the well-being of people and the planet. Its aim to make transport more sustainable could support a greener transport sector post-pandemic.

The Green Deal sets out to:

Reduce emissions from cars by **55%** by 2030

Reduce emissions from vans by **50%** by 2030

Have **zero emissions** from new cars by 2035

The European Commission is also launching policies and initiatives to promote the market for electric and hybrid vehicles, including investment in a charging network. From 2026, road transport in the EU will be covered by **emissions trading**, which will incentivise cleaner fuel use and enable further investment in clean technologies.

These policies work together with the **Zero Pollution Action Plan** which, by 2030, aims to:

Reduce the number of premature deaths caused by air pollution by **55%**

Reduce the share of EU ecosystems where air pollution threatens biodiversity by **25%**

Reduce the share of people chronically disturbed by transport noise by **30%**

Sources: EC, 2021a; EC, 2021b.

3.4 Animal and ecosystem impacts

As the human presence retreated under lockdown, there were reports of animal sightings in new locations, including goats in the streets of Llandudno, Wales, wild boars in the centre of Barcelona, Spain and pumas on the streets of Santiago, Chile (McDonnell and Poblete, 2020; Reid, 2020).

Less traffic may also have benefited wildlife in other ways, particularly species that rely heavily on vocal communication. Birds in urban areas for example may have been able to reduce the volume and pitch of their songs, enabling them to invest greater resources and energy in growth. Reduction of road maintenance activities, such as road verge cutting, may also have allowed wildflowers to flourish, providing more food for pollinators such as bees and butterflies (Reid, 2020). In China, improvements to air quality benefited vegetation to the extent that spring arrived 8.4 days earlier in 2020 and vegetation was 17% greener as compared to 2015-2019 (Su *et al.*, 2021).

While less human disturbance benefited some wild species, for others it was devastating. Scavenger species such as gulls, feral pigeons and peri-urban rats suffered from reduced opportunities to forage on human food sources. Increased competition for natural food sources could cause starvation, lower breeding success and even population declines (Reid, 2020), as demonstrated by the monkey population of Bangkok, Thailand fighting over food scraps following a loss of tourism in the area (Ratcliffe, 2020).

Box 11: Animals infected by COVID-19

There have been numerous reports of both wild and domestic animals being infected with COVID-19 due to contact with infected humans or animals, including:

- **Cats:** domestic cats have tested positive for SARS-CoV-2 in 21 countries. Cats have also been shown to pass on the virus to other felines without showing any symptoms.
- **Dogs:** dogs have tested positive for SARS-CoV-2 in 16 countries.
- **Deer:** The United States Department of Agriculture (USDA) confirmed SARS-CoV-2 in wild white-tailed deer (Odocoileus virginianus) in Ohio. The same species has tested positive in Canada. Notably, tests suggest that transmission is sustained, occurring between individuals. If deer comprise a new reservoir of SARS-CoV-2 viruses, this opens new pathways for evolution and novel variants.
- **Ferrets:** one domestic ferret tested positive for SARS-CoV-2 in Slovenia.
- **Gorillas:** two gorillas at the San Diego Zoo Safari Park, U.S. tested positive for SARS-CoV-2. This is a concern as human respiratory viruses are already a leading cause of death for several primates.
- **Hamsters:** tests on imported pet hamsters in Hong Kong showed they were carrying variants of SARS-CoV-2 not previously circulating in the locale. Multiple cases of the hamsters transmitting the virus to humans were recorded.
- **Lions and tigers:** Lions and tigers have tested positive for SARS-CoV-2 at zoos in Europe, Asia, North and South America. Other big cats in zoos have also become infected following contact with an infected human including pumas, cougars and snow leopards.
- **Mink:** in 12 countries, mink on farms have tested positive for the virus, and also wild mink in the USA.

Research suggests that many other mammals, including some species of cattle, monkey, pig, poultry, rabbit, vole and shrew can also become infected and some can spread the infection to other animals.

Although a vaccine is not currently available in Europe for pets and other animals that can be infected by SARS-CoV-2, they are under development.

Sources: CDC, 2020; Fox, 2020; Gibbons, 2021; Hale *et al.*, 2022 : OIE, 2022; Rozenbaum, 2021; USDA, 2021; Wang *et al.*, 2020 ; Yen *et al.*, 2022.

Another side effect of the pandemic, and an increased amount of time spent at home, was an increase in the number of people seeking a pet, especially dogs. Pets have an environmental impact, from displacing and predating native species to the carbon emissions associated with their food and maintenance (Marra, 2019). There are also concerns about the levels of care received by new pets, with many owners not being prepared for the commitment (RSPCA, 2020). As a result, an increasing number of pets have been abandoned (e.g. Battersea Dogs and Cats Home, 2020). If abandoned and released into wild habitats, some species can become invasive, and imported exotic pets can also introduce diseases (Lockwood *et al.*, 2019).

3.4.1 Animals in agriculture

COVID-19 also had impacts on animal welfare in agricultural settings. Infections among workers in meat processing plants for example had a major impact on human, animal and environmental welfare. In the U.S., a number of plants were shut down due to COVID-19 outbreaks among workers. This put particular pressure on the pig and poultry sectors, which are especially intensive and have very limited flexibility in their production systems.

In the U.S., there was a 45% reduction in processing capacity in the pig industry at one stage of the pandemic. This led to around 250,000 extra pigs per day not being slaughtered, resulting in significant overcrowding of animals. In the poultry sector, the number of birds able to be stunned and killed was increased in order to recapture some of the reduced capacity. This may have increased the number of birds exposed to incomplete stunning – a major animal welfare concern. In some cases, animals were transferred to other processing plants to be slaughtered, exposing animals to increased transport stress. Some producers also had to cull their animals under an ‘emergency killing’ scenario, in ways that likely included suffering (Marchant-Forde and Boyle, 2020).

3.4.2 Mink and the fur trade

One of the animals most affected by the coronavirus pandemic is the mink, which is farmed for its fur in many countries. SARS-CoV-2 infections have swept through a number of mink farms, leading to mass cullings (CDC, 2020).

As discussed in Chapter 2, outbreaks among mink are an example of a reverse zoonosis – animals being infected by a human pathogen – and mink were also able to re-infect humans. Over a million mink on fur farms in Denmark, Spain and the Netherlands were infected with SARS-CoV-2 (Fox, 2020). An investigation of transmission on mink farms in the Netherlands found that 68% of residents, employees, and individuals with whom they had been in contact showed evidence of SARS-CoV-2 infection. Of these, for whom analysis was possible, several showed evidence of mink-to-human transmission (Munnink *et al.*, 2021). Mink to human spread has also been implicated in cases in Denmark, Poland and the U.S. (CDC, 2020).

> **“Viral samples from the Danish population identified 300 people with variants containing mutations thought to have first emerged in mink”**
>
> (Mallapaty, 2020b)

The spread of SARS-CoV-2 amongst mink was particularly concerning due to the identification of mutations in this population. In Denmark, this prompted the Prime Minister to announce plans to end mink farming in the country, which would involve culling around 17 million mink. The initial mutations were later shown to be relatively neutral – i.e. not associated with faster spread or more significant risk of illness or death (Mallapaty, 2020b). However, uncontrolled spread of SARS-CoV-2 in mink farms could allow the virus to evolve more dangerous mutations, potentially evading vaccine efficacy, and millions of minks were culled to protect human health (*ibid.*). This tragic case raises the issue of the effect of the fur trade, and the global wildlife trade more generally, on animal and human welfare. This is especially pertinent under the pandemic, given that the novel coronavirus may have first originated at a market selling wild animals.

For a zoonosis to occur, a pathogen must cross the species barrier, which is rare and can only occur when humans come into close contact with wild animals – something promoted by the wildlife trade. Live animal markets, such as the one implicated in the COVID-19 pandemic, provide fertile ground for a pathogen to cross the species barrier. Such markets, illegal poaching and animal trafficking thus all increase the likelihood of a zoonosis occurring, as do other environmental changes caused by humans, such as destruction of habitats and eco-tourism (Reid, 2020).

3.5 Antimicrobial Resistance

Antimicrobial resistance is among most urgent health threats of the 21st century. Unfortunately, one of the impacts of the pandemic could be increased antimicrobial resistance, through overuse of antibiotics, biocides and disinfectants.

Co-infections in patients with COVID-19 may call for antimicrobial treatment, yet WHO guidance warns against antibiotic prophylaxis. A global review of over 500 studies nevertheless found 70% of patients with COVID-19 in the first half of 2020 received antibiotics – a rate far higher than the incidence of secondary infection calling for treatment (Langford *et al.*, 2021). Meanwhile, increased use of biocide-based products, indoors and outdoors, will lead to increased loads in wastewater and the environment – a driver of survival of bacterial strains carrying resistant genes (Hora *et al.*, 2020). Accumulation in surface waters also threatens aquatic life (Dewey *et al.*, 2022).

Increased hand hygiene, social distancing and decreased international travel may act to reduce resistant pathogen selection, however the risk from disproportionate use of antimicrobials in healthcare and environmental cleansing outweighs this short-term gain (Knight *et al.*, 2021).

The dynamics of antibiotic resistance during the pandemic are still being investigated, however it seems that progress in antibiotic stewardship – the appropriate management of antimicrobials to mitigate resistance – has suffered a setback. Research is needed to assess the effects of the pandemic on antimicrobial resistance, together with continued vigilance and increased awareness of the severity of the threat. There is also an opportunity to assess the efficacy of existing and new techniques for removing disinfectants and antibiotics from wastewater.

4. Learning lessons from COVID-19 links with the environment

Since the beginning of the COVID-19 pandemic, there has been a growing recognition globally that the emergence of this virus is not an isolated incident. Rather, it fits as part of a pattern of epidemics, coinciding with habitat destruction through resource exploitation, urbanisation and climate changes (Whiting, 2020). Ecosystems and their services have a pivotal role in regulating the emergence and risk of zoonotic diseases, and recognising that the COVID-19 crisis is also an environmental crisis is paramount (Everard *et al.*, 2020). Human dependence on global ecosystems for all aspects of existence is already incontrovertible and fully supported in the science. Literature on the specific links between biodiversity crises and zoonotic disease risks is increasing, and there are urgent calls to advance interdisciplinary knowledge in this area (*ibid.*; Plowright *et al.*, 2021; IPBES, 2020).

It remains to ask: what changes must be made to create healthier, sustainable economies and societies, which in turn will help to decrease the occurrence and effects of future epidemics and pandemics? How will we address the “triple crisis” of interdependent climate change, biodiversity loss and pandemics? How will we manage transformative change in the short time available?

Some approaches which could increase the resilience of ecosystems and human health together have been discussed earlier in this brief. For example, effective habitat conservation and restoration measures, including protected areas and habitat and ecosystem restoration programmes as well as sustainable land-use change and resource extraction, could reduce pressures on, and increase buffers for, ecosystems and people, reducing pandemic risks. Two other aspects, discussed in more detail below, are changing habits and behaviours to decrease pandemic risk and vulnerability; and developing better monitoring and prediction capabilities for environmental factors that could contribute to pandemic emergence or impacts.

4.1 COVID-19 and behaviour change

The response from governments to COVID-19 led to dramatic changes in travel and work behaviours. The significant drop in oil consumption and power generation from coal in Europe as a result of the lockdowns, and the observed reduction in NO_2 concentrations were unprecedented.

The lockdown-associated drops in CO2 levels have fast returned to their rapidly increasing, business-as-usual levels, though. However, these temporary reductions did highlight the scale and possibility of the major infrastructural and economic changes needed to curb current human-activated climate changes. As shown in the latest IPCC report, we are dangerously close to exceeding the 1.5°C threshold for global temperature rise: our societal norms need to shift rapidly and drastically to limit any further damage to the planet’s climate and ecosystems (IPCC, 2021).

The pandemic impacts and response have also caused setbacks to environmental progress, for example, creating an uptick in the use of single-use plastics, which was already a critical environmental issue. Such aspects could be better executed in future, if circular economy approaches and sustainable alternatives are planned for, incentivised and promoted.

The pedestrianisation of urban areas and the rise of remote working are habit shifts that could herald lasting changes in the way cities and economies are structured. Other aspects, such as reduced and more responsible consumption of meat, and the avoidance of products that represent high pandemic-risk land-use change or agriculture (especially products derived from unsustainable wildlife trade or wildlife farming) could be encouraged by governments. Some practical, general ways to approach this are (IPBES, 2020):

- measures to increase food security in areas where consumption of wildlife is common
- taxes or levies on meat consumption, production, livestock production or other forms of consumption
- sustainability incentives for companies to avoid high pandemic-risk land-use change, agriculture, and use of wildlife-derived products identified as a particular zoonotic disease risk
- mainstreaming the economic cost of pandemics into consumption, production, and government policies and budgets

It is crucial that Europe does not view pandemic emergence as a problem external to this continent, but recognises how climate change, economic patterns and behaviour within this region are linked to health risks. With climate change, the ranges of certain animal vectors are increasing, and signals are already apparent that this has led to increased disease risk in Europe. As another example, with regard to wildlife trade, Belgium's status as a major intermediary in the illegal transport of CITES-listed commodities has prompted TRAFFIC and WWF to recommend that the CITES Management Authority increase its investigations of export and re-export permits from third countries (Musing *et al.*, 2018). They also recommend regular training of customs officers, targeted controls and national cooperation between enforcement and prosecution staff (*ibid.*). Enhanced law enforcement collaboration on all aspects of the illegal wildlife trade is also needed. At a ground level, educating communities in infectious disease hotspots regarding health risks is also recommended (IPBES, 2020).

4.2 Predicting and preventing pandemics

Critical knowledge gaps need to be closed to improve our understanding of the links between the risk of disease emergence and ecosystem degradation, restoration and land use. Scientific research will play a key role in predicting geographic origins of future pandemics and in identifying key reservoir hosts and pathogens most likely to emerge.

Monitoring wildlife health is an essential component of global disease prevention; Plowright *et al.* (2021) highlight the need for transdisciplinary approaches to investigate transmission between animals and humans. Research is also needed to investigate how environmental and socioeconomic changes correlate with disease emergence. IPBES (2020) recommend using large-scale data to target viral discovery, surveillance and outbreak investigation.

Researchers have begun to look at the possibilities of ecosystem modelling incorporating-epidemiology for studying disease dynamics in ecosystems (Hassell *et al.*, 2021). At a landscape scale, this approach could highlight how disturbance to ecosystems puts people and animals at risk from emerging pathogens, and indicate 'tipping points' in an animal populations that signal high risk of zoonotic infection. This approach is not without challenges, though; spillover events may occur in unusual, unpredictable circumstances where humans interact with wild animals, or indeed via domestic animals (Roberts *et al.*, 2021).

Acknowledging the interdependence of human and ecosystem health, Europe's Joint Research Centre is investigating aspects of virus transmission related to environment and economy in the project "Coronaviruses and environment: One health approach". Work will screen and map coronaviruses in animals, and detect mutations that allow transmission to humans. Links between environmental conditions, transmission and persistence of coronaviruses will also be considered, as well as the role of economics in virus risk.

Waste water surveillance has been recognised as an early warning method for detecting the emergence and re-emergence of SARS-CoV-2 communities, the identification of hot spots, tracking back of first occurrences of the virus by investigating conserved wastewater samples for SARS-CoV-2 RNA, and ascertaining the appearance of mutations and variants (WHO, 2021b). It provides a rapid indicator of infection, unlike data on deaths or hospitalisation, which lag behind actual infections and only give a snapshot of what has already happened. (EC, n.d.; Larsen and Wigginton, 2020).

At present, individual countries have different approaches to pandemic preparedness. After the 2009 H1N1 influenza ('swine flu') pandemic, European states were strongly encouraged by the WHO to revise their national pandemic plans to prepare for future pandemics, and to publish their pandemic plans. However, only 11 of the EU28 countries subsequently made their pandemic preparedness plans publicly available[1]. The European Health Emergency preparedness and Response Authority (HERA) has now been introduced to join up health security in the EU and rapidly respond to cross-border health emergencies. HERA will bring together dedicated horizon scanning, national expertise and monitoring data such as from wastewater surveillance, sharing insights in the European Health Data Space and European Open Science Cloud.

Progressing and harmonising international governmental agreement on pandemic prevention would bring clear benefits for humans, animals and ecosystems (an international treaty was proposed by the Spanish and French governments in 2021). A holistic view of human, ecosystem and planetary health (such as with 'One Health' approaches) may support the generation of strategies to prevent future pandemics (IPBES, 2020). For the global community, a new intergovernmental health and trade partnership could help to reduce zoonotic disease risks in the international wildlife trade (*ibid.*). Indeed, enhanced coordination has already begun, with 26 experts appointed in May 2021 to serve as members on the One Health High Level Expert Panel (OHHLEP). Commissioned by the Food and Agriculture Organization (FAO), the World Organisation for Animal Health (OIE), the United Nations Environment Programme (UNEP) and the World Health Organization (WHO), these experts will provide policy-relevant scientific assessment on the emergence of health crises arising from the human-animal-ecosystem interface (as well as advising on research gaps); and guidance on a long-term strategic approach to reducing the risk of zoonotic pandemics, with an associated monitoring and early-warning framework.

> **"One Health, linking humans, animals and the environment, can help to address the full spectrum of disease control – from disease prevention to detection, preparedness, response, and management – and to improve and promote health and sustainability."**
>
> FAO, OIE, WHO and UNEP, 2021

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[1] https://www.euro.who.int/en/health-topics/communicable-diseases/influenza/pandemic-influenza/pandemic-preparedness/national-preparedness-plans/publicly-available-plans-prepared-after-2009-pandemic

Table 6: OHHLEP Working Groups

OHHLEP's four working groups will address initial focus areas:

Working Group	Examples of tasks
One Health Implementation	• identify case studies demonstrating good practice • develop a theory of change to take One Health from a theoretical concept to the daily practice of collaborative work
Inventory of current knowledge in preventing emerging zoonoses	• Systematic review of useful documents, tools, networks • Identify successful strategies
Surveillance, early detection and rapid data sharing in the prevention of emerging zoonoses	• Define One Health surveillance • Identify existing systems facilitating sharing of surveillance data • Develop a practically implementable surveillance framework and good practice guidelines
Factors causing spillover and subsequent spread of diseases	• List all potential factors and systematically analyse evidence for risk of zoonotic spillover • Consider tools for risk assessment

Source: One Health High Level Expert Panel (OHHLEP) (who.int)
https://www.who.int/groups/one-health-high-level-expert-panel/meetings-and-working-groups

4.3 An opportunity in crisis

This brief has looked at environmental factors that potentially contribute to the emergence of disease and the effects of COVID-19, and environmental impacts that have arisen from COVID-19. COVID-19 has shown that science and scientists are vital in securing planetary health and resilience and it has also demonstrated the importance of a One Health approach. Invaluable scientific disciplines such as public health, epidemiology, microbiology, virology, engineering and geo-environmental and land-systems research are all needed to work collaboratively in the current global response to COVID-19 and to avoid and give early warning of future pandemics.

Tackling COVID-19 has already produced new scientific capacities and networks; for example, the GEO Community Response to COVID-19, which lists earth observation projects' support, recovery and response actions related to the pandemic.[2] Win-win-win solutions, for human health, biodiversity and the climate are potentially possible – but funding to support research capacity and projects in crucial areas will be needed.

International collaboration among scientists will be key to address the risks and support policy decisions regarding future pandemics. In particular, further research focus on the zoonotic pathogen spreading pathways should be a conservation and biosecurity priority (Plowright *et al.*, 2021). Such results could feed into an integrated, holistic set of science-based policy and management measures that effectively and cost-efficiently minimise zoonotic disease risk.

This is a pivotal moment, in which essential environmental progress and research priorities could easily be sacrificed to an exclusive focus on recovering economic growth (e.g. in the form of delays to Green Deal programmes or to vehicle emissions standards). We see this is unfortunately already happening. Far too few of the monumental financial recovery packages are currently invested in a resilient green recovery which accelerates the desperately needed fast and deep transformative change.

It will be vital to learn the lessons of previous economic crises – for example, using the momentum of disruption to instigate low-carbon pathways and air quality improvements, rather than returning to unprecedentedly high emission levels, as happened after the 2008/9 financial crisis. In the balance hangs the success of efforts to limit disastrous temperature rise, irreversible biodiversity losses and future pandemic mortality risks. If political and financial capital can be mobilised and wisely invested in measures to protect the health of ecosystems, human health will be the return on investment (Bernstein *et al.*, 2022; Dobson *et al.*, 2020).

The opportunity currently presenting itself is extraordinary. Innovation – for example in medical testing, treatment and vaccination – has helped the world mitigate the spread and effects of the virus, but the task is now recognising how to reduce the risk of pandemics, and knock-on effects such as increased plastic pollution. During the recovery from COVID-19, research points to the need for extensive, substantial shifts in our societies, activities and understanding. It has never been more crucial to fully align human health, societal betterment and economic growth with the health and resilience of the environment and its wildlife inhabitants, which will be the best way to avoid, or reduce the impacts of, future pandemics. The choice is ours, but it will have an impact on all generations to come.

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[2] https://earthobservations.org/covid19.php

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