

Zoonoses

a ticking time bomb

Emerging diseases originating in animals
and their impact on humanity

By Dr Justine Butler, Viva!

Viva!



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Summary

Zoonotic diseases are diseases that spread from animals to humans. They include familiar ones, such as the common cold, influenza (flu), polio, AIDS and measles and other lesser known ones such as SARS, MERS, Nipah virus and Ebola. Most recently, Covid-19 has joined this growing list, having jumped from bats or other wild animals, to humans, leading to a pandemic.

There are over 200 zoonotic diseases and 56 of them affect two-and-a-half billion people and cause nearly three million deaths every year. Zoonotic diseases are emerging with increasing frequency and three out of every four new ones come from animals.

Covid-19 has caused a huge number of deaths across the globe and resulted in a third of the planet on lockdown. It is probable that Covid-19 was caught from wild animals in a Chinese wet market. It has focussed the world's attention on how our mistreatment of wild and farmed animals, has resulted in dire consequences for our health.

Of course, we've been here before! In 2003, the severe acute respiratory disease, SARS, jumped from bats to humans via civet cats that had been captured in the wild and brought to market. In 2012, Middle East respiratory syndrome (MERS), was again spread from bats but this time via the increasing number of farmed camels, some bred for racing.

Bird flu (avian influenza virus) captured the headlines in the late 1990s when it jumped from wild water birds to domestic poultry and then to humans, causing a number of deaths. Millions of birds were slaughtered but it was too late as the virus had already mutated and its many forms were travelling around the world in migratory birds, infecting domestic poultry, pigs and all manner of other animals, including humans. Hundreds have subsequently died.

All flu pandemics (Spanish, Asian, Hong Kong and swine flu) have come from birds or pigs and we are now faced with a host of mutating viruses, circulating amongst both wild and domestic birds as well as pigs. They are poised to emerge in humans and when they do, there is the potential for a pandemic of devastating proportions. The virus H5N1, for example, kills 60 per cent of those it infects compared to seasonal flu that kills 0.1 per cent!

Ebola and the HIV virus that causes AIDS, are both zoonotic diseases that came about through people eating bushmeat, such as bats, monkeys and chimpanzees. The Nipah virus emerged in Malaysia when it jumped from fruit bats to pigs and then to humans. Despite a million pigs being slaughtered, this lethal disease that kills between 40 and 70 per cent of those it infects, could re-emerge at any point.

Measles passed to humans from cows infected with the rinderpest virus that caused 'cattle plague'. Despite Rinderpest having been eradicated, measles in humans persists and is thought to have killed some 200 million people, mostly children.

In addition to an increasing number of zoonotic diseases, we also face the looming catastrophe of antibiotic resistance – superbugs that fail to respond to normal medical treatment. The majority of antibiotics globally is used in animal agriculture and it is a storm of our own making.

The majority of both zoonoses and antibiotic-resistant diseases are the result of human activity, with factory farming and wild animal markets lying at the heart of the problem. The solution could not be easier – go vegan now!

Zoonotic diseases

Animals can sometimes carry harmful germs that can spread to people and cause illness – these are known as zoonotic diseases or zoonoses. Such diseases may be caused by viruses, bacteria, parasites or fungi. They may be mild or serious, and in some cases may cause death. Animals can sometimes appear healthy even when they are carrying a virus, for example, that can make people very ill.

How many people are affected?

Taken together, 56 zoonoses are responsible for an estimated 2.5 billion cases of human illness and 2.7 million deaths a year. The top 13 diseases caught from animals, cause 2.4 billion cases of illness and 2.2 million deaths (Grace *et al.*, 2012).

Scientists estimate that more than six out of every 10 known infectious diseases in people can be spread from animals, and three out of every four new or emerging infectious diseases in people come from animals (CDC, 2014).

The World Health Organisation (WHO) agrees: *“During the past decades, many previously unknown human infectious diseases have emerged from animal reservoirs, from agents such as human immunodeficiency virus (HIV), Ebola virus, West Nile virus, Nipah virus and Hanta virus. In fact, more than three quarters of the human diseases that are new, emerging or re-emerging at the beginning of the 21st century are caused by pathogens originating from animals or from products of animal origin”* (WHO, 2004).



Diseases and the animals they are linked to

COVID-19

Coronaviruses are a large group of RNA viruses that cause diseases in mammals and birds. They are so-called because the virus looks like it is covered with pointed structures surrounding it like a crown.

An RNA virus is a virus that has ribonucleic acid (RNA) as its genetic material as opposed to deoxyribonucleic acid (DNA). Notable human diseases caused by RNA viruses include the common cold, influenza, SARS, Ebola, polio, measles and Covid-19.

Mammalian coronaviruses, including those that infect humans, are evolved from bat coronaviruses. Bats are a natural host often harbouring multiple viruses for long periods with no apparent symptoms (Chan and Chan, 2013).

Coronaviruses evolve by mixing and matching their genes with other viruses. This process, known as 'recombination', makes for a moving target, constantly changing and evolving. Recombination can occur when a cell is infected by more than one virus strain, the recombinant virus carries genes from both 'parents' in the same way children may exhibit unique characteristics coming from both their parents.

Coronavirus infection symptoms vary depending on the species affected, in chickens it can cause an upper respiratory tract disease, while in cows and pigs it can cause diarrhoea. In humans, it causes respiratory tract infections that can be mild, such the common cold, or lethal, such as SARS, MERS and Covid-19, the name of the disease caused by the coronavirus discovered in China in 2019. The virus was initially called 2019-nCov but is now commonly referred to as SARS-CoV-2.

It's likely that SARS-CoV-2 came from a live 'wet' market in Wuhan in China, where poultry, civets, snakes, pangolins, bats, beavers, foxes, dogs and many other animals were sold. Wet markets are called 'wet' because animals are often slaughtered in front of customers. They are filled with caged animals many captured illegally in the wild. Animals are skinned sending a cocktail of microorganisms into the air. The dreadful, cramped conditions and mix of wild and domestic creatures, alongside the throngs of people is a pandemic in the making.

However, the problem is not just confined to wet markets. As industrialised farming has expanded in China, small-scale farmers have moved over to the wildlife market and have been geographically pushed too into



remote areas inhabited by bats. So factory farming is as much to blame.

Covid-19 can be spread through inhaling tiny respiratory droplets of virus in the air or from picking up the virus on your hands from surfaces then touching your mouth, nose or eyes. It may be carried in the saliva, blood, urine, mucous, faeces or other body fluids of an infected animal or person. Imagine a market, with cages of different animals stacked on top of each other with people packed in too. Animals being slaughtered, skinned, chopped up and handled – you could hardly make a more perfect breeding ground for an emerging virus!

Several independent research groups have confirmed that SARS-CoV-2 is very similar to bat coronavirus, indicating bats as the natural host (Guo *et al.*, 2020). However, although SARS-CoV-2 is 96 per cent identical to bat coronavirus (Zhou *et al.*, 2020), it is thought to be a recombinant virus, with elements from bats and another unknown species (Ji *et al.*, 2020). So scientists think that SARS-CoV-2 originated in bats but may have passed to humans via an intermediary host (Salata *et al.*, 2019).



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Initially, snakes or bamboo rats were favoured candidates, however research suggests that it was more likely to be pangolins (Zhang *et al.*, 2020). Pangolins are an endangered wild animal, eaten as a delicacy in many parts of the world, they are the most trafficked animals on the planet. Coronavirus collected from caged pangolins obtained from an unspecified research organisation apparently showed over 99 per cent genome sequence identity to SARS-CoV-2 (Sun *et al.*, 2020).

However, it later transpired that the 99 per cent did not refer to the entire genome but to a specific site known as the receptor-binding domain (RBD). The whole-genome comparison found that the pangolin and human viruses only share 90.3 per cent of their DNA, although 90 per cent sounds like a lot, it casts doubt on the role of pangolins as an intermediary host, or at least the pangolins they tested. The SARS virus shared 99.8 per cent of its genome with a civet coronavirus, which is why civets were considered the source (Cyranoski, 2020).

Another view is that humans could have been infected directly by bats. Often called China's 'bat woman' because of her virus-hunting expeditions into bat caves, virologist Zheng-Li Shi and colleagues at the Wuhan Institute of Virology have spent years isolating coronaviruses from bats from caves in China's Yunnan province. Shi's research shows that viruses can pass directly from bats to people living near caves. Again, trading in bats at wet markets brought them into close contact with many people. We didn't need pangolins to catch Covid-19.

In 2013, in a remote cave in Yunnan province, these virologists identified a single population of horseshoe bats harbouring virus strains very similar to SARS-CoV-2.



Back in the laboratory they found these viruses were able to infect human cells (Ge *et al.*, 2013). In 2016, a team of researchers from Switzerland and the US found that this virus could replicate in human airway cells. They described it as being 'poised for human emergence' (Menachery *et al.*, 2016). A failure to act on these warnings means an opportunity to protect human health was missed.

Human activity, such as the expansion of animal agriculture, has changed three-quarters of the planet's surface, squeezing wildlife into ever-smaller corners. Head of the UN Environment Programme (UNEP), Inger Anderson says "As we continue to encroach on fragile ecological ecosystems, we bring humans into ever-greater contact with wildlife. Further, illegal wildlife trade and illegal wet markets are not infrequent causes of such diseases. Around 75 per cent of new and infectious diseases are zoonotic and, in fact, about 1 billion cases of illness and millions of deaths occur every year from these diseases" (UN News, 2020).

We need to stop deforestation and tackle the illegal wildlife trade, the fourth most common crime committed worldwide. Nature is critical to our survival: it provides us with oxygen, regulates weather patterns, pollinates crops and produces food. Anderson says that "keeping nature rich, diverse and flourishing is part and parcel of our life's support system" (UN News, 2020).

Our relationship with animals can no longer be just focussed on exploitation, the way meat is produced is now considered to be a global threat. It's not just a case of banning wet markets, although that can't come soon enough. We need to stop factory farming too.



SARS

The severe acute respiratory syndrome or SARS outbreak in 2002-2003 was the first global pandemic of the 21st century. It began in late 2002, when cases of a mystery pneumonia-like illness began occurring in Guangdong province in China.

The outbreak was brought under control in July 2003 with 8,098 reported cases and 774 deaths. Infection killed about one in 10 affected. China, Hong Kong and Taiwan were the worst affected countries, although the virus also spread to Canada, where there were 251 cases. In the UK, four cases were recorded with no deaths.

It wasn't until 2017 that scientists hunting for the source of the virus finally found their smoking gun in a remote cave in Yunnan province. They identified a single population of horseshoe bats harbouring a number of viruses genetically similar to the one that infected humans in Guangdong in 2002 (Hu *et al.*, 2017). Like Covid-19, the virus causing SARS was a coronavirus, they called it SARS-CoV.

Initially civet cats were considered to be the natural host for SARS-CoV, but were later found to be an intermediary host after bats were identified as the natural hosts. It's now believed that the virus was transmitted to civets from Yunnan horseshoe bats and civets carrying the virus were transported to markets and restaurants in Guangdong, which ultimately led to the SARS outbreak in humans (Chan and Chan, 2013).

Other animals in markets that tested positive for SARS-CoV included domestic cats, red foxes, lesser rice field rats, geese, Chinese ferret-badgers and wild boar. However, the samples were collected at times when the markets were heavily contaminated so it is impossible to say whether these animals were actively shedding or passively carrying the virus (Chan and Chan, 2013).

When viruses in wildlife infect humans, often their natural host's habitat has been disturbed. They may accumulate a number of mutations that enable them to jump species. Due to human activities, SARS-CoV expanded its host of infection, first to civets and then humans (Sun *et al.*, 2020).

The fact that SARS-CoV emerged from bats is not surprising. Before SARS, every few years or so for a number of decades, viruses linked to bats have been emerging, including Marburg virus causing haemorrhagic fever in 1967, Ebola virus causing haemorrhagic fever in 1976, Hendra virus causing severe pneumonia in 1994 and Nipah virus causing neurological and respiratory diseases in 1998 (Chan and Chan, 2013). All passed to people via intermediary hosts – wildlife or farmed animals exploited and killed by humans.

Prevention of future outbreaks could be achieved by adopting a multidimensional approach that considers

both natural and social aspects of the SARS epidemiology. This means monitoring what viruses are present in nature but more importantly, governments need to issue laws and policies to protect wildlife and prohibit consumption of wild animals (Sun *et al.*, 2020).

In one study, Professor Diana Bell and colleagues from the University of East Anglia's School of Biological Sciences warned: *"A major lesson from SARS is that the underlying roots of newly emergent zoonotic diseases may lie in the parallel biodiversity crisis of massive species loss as a result of overexploitation of wild animal populations and the destruction of their natural habitats by increasing human populations"* (Bell *et al.*, 2014).

We are decimating wild landscapes, killing wild animals or caging them and sending them to market. Invading and disrupting ecosystems will inevitably shake viruses loose from their natural hosts. It's time to go vegan!

"Finally, but not lastly, in developing human society including building massive constructions for residence and transportation, potential ecological impact on wildlife and possible consequences of breaking natural balance of the ecosystems should be carefully evaluated" (Sun *et al.*, 2020).

Scientists warn that a deadly outbreak could emerge again. The cave where the SARS-CoV viruses were found is just one kilometre from the nearest village and recombination among the viral strains is fast. In 2017, scientists warned that: *"The risk of spillover into people and emergence of a disease similar to SARS is possible"* (Hu *et al.*, 2017). We should have listened!



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MERS

Middle East respiratory syndrome or MERS is also caused by a coronavirus (MERS-CoV) also thought to have originally spilled over from bats, this time into camels, in which it is now endemic. It was first detected in a patient living in Jeddah in Saudi Arabia, in June 2012. However, it's thought that MERS-CoV, or related viruses have been circulating among camels at least since 1983 (Müller *et al.*, 2014).

Like Covid-19, MERS-CoV causes respiratory infection in humans, ranging from asymptomatic to severe pneumonia. In camels, the intermediary host, the virus only causes a mild infection but it spreads efficiently between animals (Widagdo *et al.*, 2019).

Camels are now considered an important reservoir of MERS CoV and evidence suggests that there have been multiple independent incidents of MERS CoV transferring from camels to humans (Paden *et al.*, 2018). The index case (sometimes called patient zero) is the first documented case in a disease epidemic within a population. Several of the index cases for MERS outbreaks had close contact with camels from different regions of the United Arab Emirates (Paden *et al.*, 2018).

Understanding how the lives of people and animals have changed over time can reveal how zoonotic diseases such as MERS have emerged in humans. Camels are raised for milk, meat, fibre (wool and hair) as well as transport and racing. Owing to substantial governmental support, says one study, camel farming and racing competitions have expanded hugely, exacerbating the already rapidly occurring desertification that led to the banning of free grazing in

2005. Consequently, camels are frequently housed in compact barns alongside workers. High-density camel farming along with increased exposure to humans, combined with the increase of camel movement for the racing and breeding industry, have led to a convergence of factors driving the spillover of MERS-CoV from camels to humans (Frag *et al.*, 2018).

Between 2012 and 2019, around 2,500 cases of MERS and over 900 deaths were recorded. So, around a third of those who are diagnosed with the disease die from it. There is no vaccine and cases continue to appear. Between the start of December 2019 and the end of January 2020, the National IHR Focal Point of Saudi Arabia reported 19 cases of MERS-CoV infection and eight deaths. In January 2020, a hospital outbreak was reported in Aseer region of Saudi Arabia with a cluster of six cases, three were health care workers, two were patients and one was a visitor. One of these cases died on 4 February 2020 (WHO, 2020).

Like Covid-19, MERS causes more severe disease in people with underlying chronic medical conditions such as diabetes, kidney problems, chronic lung disease and compromised immune systems. The World Health Organisation say that people with underlying medical conditions should avoid contact with animals, particularly camels. General hygiene measures, such as regular hand washing before and after touching animals and avoiding contact with sick animals, are recommended. They also say food hygiene practices should be observed and that people should avoid eating meat that has not been properly cooked and not drink raw camel milk or camel urine! (WHO, 2020). We could just stop farming and racing them!



AVIAN INFLUENZA – BIRD FLU

A classic example of a zoonotic disease. Avian influenza became commonly known as bird flu in the late 1990s when there were a number of deaths in Hong Kong. In 1996 several outbreaks of a highly pathogenic H5N1 bird flu virus occurred in farmed geese in a small town 50 miles outside the capital of Guangdong with a mortality rate in birds of more than 40 per cent. By 1997 the virus had spilled over into poultry farms and live-poultry wet markets in Hong Kong with high rates of mortality. It also infected people leading to six deaths. Infections were acquired by humans directly from chickens, without the involvement of an intermediary host. To stop the outbreak the government ordered the slaughter of more than 1.5 million chickens (Chan, 2002).



The natural hosts of bird flu viruses include wild waterbirds such as ducks, geese, swans, gulls, terns and shorebirds, in which they occur without making them ill, and have done so for millions of years. Viruses are passed on in water from one bird to another but are not problematic. Birds, in fact, serve as a reservoir for a vast diversity of influenza viruses to which most major human pandemics trace their origin.

But now, these viruses are causing increasing levels of illness and death in large numbers of land-birds, especially poultry. They have also begun jumping species, infecting different animals, including pigs, whales, horses, seals, dogs and humans. Scientists are concerned that they could be the source of the next major pandemic.

SPANISH FLU

It's estimated that about 500 million people, around one-third of the world's population, became infected with the virus that caused the Spanish flu pandemic of 1918. The number of deaths is estimated to be up to 50 million worldwide making it one of the deadliest pandemics in human history (CDC, 2019).

It's difficult to say what the precise mortality rate was as the estimated number of deaths varies widely. In Europe it's estimated that just over one per cent of those infected died (Erkoreka, 2009), that is ten times the mortality rate of seasonal flu. Others suggest a figure of 2.5 per cent or higher (Taubenberger and Morens, 2006).

The name Spanish flu arose because wartime censors in Germany, France, the UK and the US minimised early reports of illness, Spain was not involved in the war and had no such censorship, so it appeared to be hit harder than other countries. It remains unclear where the pandemic actually started, some suggest Kansas, other say Northern France or even China. Regardless of



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where it started, the outbreak spread rapidly around the world affecting many soldiers who fought during the First World War. The majority of those who died were young, healthy adults between the ages of 15 and 44.

Many factors contributed to its lethal impact, as soldiers from almost every country in the world came together to endure the horrors of war – stress, fear, cold weather, crowded conditions and poor hygiene. A recipe for disaster – it sounds like a factory farm!

How avian influenza viruses such as the one responsible for the Spanish flu pandemic jump from their natural hosts to humans is a key question that may help avert future global pandemics.

The specific source the 1918 pandemic influenza virus is unknown but we do know it was caused by an H1N1 virus with genes of avian origin (CDC, 2019). It's been suggested that that the virus may have spread from birds to humans via pigs as they are susceptible to infection with influenza viruses and have been referred to as 'mixing vessels' for human, swine and avian viruses (Ma *et al.*, 2008). At the same time as the Spanish flu emerged, so did an outbreak of flu-like illness in pigs in the US, raising the possibility that the 1918 virus originated in pigs. However, it's unclear in which direction the illness was spreading as human-pig transmission is also possible (Nelson and Worobey, 2018).

Another theory is that the virus infected humans directly from birds some time before the pandemic and that it adapted in humans into the one causing the 1918 outbreak (Taubenberger *et al.*, 2005). Some scientists suggests that it may have evolved via the mixing of bird and human viruses within human hosts (Worobey *et al.*, 2014). One study suggests that the

THE H AND N IN FLU VIRUS NAMES

Flu viruses are named after the two proteins they carry on their surface – H and N (H is for hemagglutinin and N for neuraminidase), they are little protein spikes on the virus's surface that help it invade cells.

virus's progenitor went from humans to birds then back to humans in a more lethal form (He *et al.*, 2019). However, it is difficult to trace where the 'mixing event' events took place because the real parents of the Spanish flu virus cannot be identified. However it evolved, one thing is clear, the 1918 virus was a uniquely deadly product of nature, viral evolution and the close mixing of people with animals.

Influenza viruses generated in pigs or other 'mixing vessels' or transmitted between birds and humans clearly pose a serious threat of causing the next human influenza pandemic (Ma *et al.*, 2008). A return of a pandemic virus as deadly as the Spanish flu of 1918 would likely kill more than 100 million people worldwide now (Taubenberger and Morens, 2006).

ASIAN FLU

The 1957 Asian flu pandemic was caused by an H2N2 virus originating in China in early 1956 and lasting until 1958. It is estimated to have killed around 1.1 million people (CDC, 2019a). The exact origin of the H2N2 virus is unknown but scientists think that this virus may have originated from an avian virus of wild duck origin combining with a human strain, again possibly in pigs acting as an intermediary host bridging the gap between birds and humans (Nelson and Worobey, 2018). While H2N2 has disappeared from humans, it persists in wild and domestic birds (chickens, guinea fowl and ducks). Re-emergence of this virus in humans is a significant threat due to the absence of immunity in individuals under the age of 50 (Jones *et al.*, 2014).

HONG KONG FLU

The 1968 Hong Kong flu pandemic resulted in an estimated one million global deaths (CDC, 2019b). It was caused by a strain of H3N2 descended from the H2N2 virus that caused the 1957 pandemic. The virus contained some genes from a low-pathogenic avian influenza virus and some from the H2N2 virus that had been circulating among people since the 1957 pandemic (Kawaoka *et al.*, 1989). Again, while H2N2 and H3N2 are undoubtedly of avian – possibly wild duck – origin, a potential role for pigs cannot be ruled out and the 'mixing vessel hypothesis' may explain how these zoonotic pandemic-causing diseases emerged (Nelson and Worobey, 2018).



SWINE FLU

In 2009, a flu pandemic caused by an H1N1 virus detected in Mexico spread quickly across the world. It was referred to as 'swine flu' as the H1N1 virus that caused the disease was very similar to influenza viruses circulating in pigs. In fact, scientists now say that the 2009 H1N1 pandemic was incontrovertibly of direct swine origin (Smith *et al.*, 2009).

Viruses known as 'classical swine H1N1', containing elements of human, pig and avian viruses, had been circulating in North American pigs since the Spanish flu pandemic of 1918. Between the 1930s and the 1990s, they underwent little change. However, by the late 1990s, multiple strains and subtypes (H1N1, H3N2, and H1N2) of 'triple-reassortant' swine flu viruses, containing genes from three different organisms – avian, human and swine – emerged and became predominant among North American pigs (Shinde *et al.*, 2009).

Subsequent mixing of these triple reassortant North American swine influenza viruses with Eurasian swine viruses are then thought to have resulted in the 2009 H1N1 virus which scientists call a 'quadruple reassortant' virus, because it contains gene segments of viruses originating from humans, birds, North American pigs and Eurasian pigs (CDC, 2009). The mixing of live pigs from Eurasia and North America through international trade could have created the circumstances necessary for the viruses from North American and Eurasian pigs to mix.

This was a novel or new virus, containing a unique combination of influenza genes not previously identified in animals or people. The pandemic primarily affected children and younger adults, as many older people turned out to be immune. The number of deaths during the first year the virus circulated is estimated to range from between 151,700 and 575,400 with a disproportionate number occurring in Southeast Asia and Africa where access to prevention and treatment resources were more limited (Dawood *et al.*, 2012).

It is now one of the seasonal flu viruses that circulate each winter. If you've had flu in the last few years, there's a chance it was caused by this virus.

Pig farming has changed dramatically in recent decades and, according to scientists, there are many reasons to expect that pigs will increase in importance as vectors of pandemic threats, as evidenced since 2011 by the many children infected with H3N2 after attending agricultural pig fairs in the US (Epperson *et al.*, 2013).

As factory farming spreads across the globe, diseases follow, spreading like wildfire through the densely populated sheds. Animals kept in horrific conditions are more susceptible to disease due to the extreme stress they experience from their cramped and inhumane surroundings. Bred for fast growth, their immunity is

low. It's a perfect storm of our own making. Scientists have been warning about the health risks posed by intensive units for years, including the opportunities they provide for viruses and bacteria to spread and mutate.

Professor Gregory Gray, an epidemiologist at Duke University in Durham, North Carolina in the US, considers pigs to be ideal mixing vessels for influenza viruses because the animals are susceptible to not only swine flu, but also avian and human influenza. On a visit to pig farms in China, the world's largest producer of pork, Gray said: *"There's a massive transition in China from small and medium-sized farms towards large industrialised farms, but we still see rather poor biosecurity"*. When he and his colleagues toured farms in China, they noticed that personal protective equipment is used only sporadically, barriers to stop rodents entering are rare, and pigs are sometimes housed near ducks, geese or chickens. *"It's a cauldron of virus mixing"* said Gray (Willyard, 2019).

It is high time we start considering the fact that our increased consumption of animal meat and dairy foods isn't just wreaking havoc on our health and the environment, it is sparking pandemics that kill thousands, potentially millions, of people. Scientists warn that some highly-pathogenic strains of viruses may be poised to cause the next pandemic in humans.



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H5N1

The H5N1 virus has been infecting poultry and other land-birds since the late 1950s and in 1997, 18 people were infected and six died in Hong Kong – the first known case of H5N1 in humans. In 2001, the number of chickens dying in retail markets throughout Hong Kong attracted attention and H5N1 viruses were again isolated and the government carried out a second territory-wide slaughter of chickens (Chan, 2002). During the 2005 outbreak, tens of millions of chickens and other poultry in south-east Asia were slaughtered in an effort to contain the disease.

Since 2003, over 800 people have been infected and over 450 have died, with fatalities in Indonesia, Egypt, Vietnam, China, Cambodia, Thailand and Canada. The World Health Organisation say the mortality rate for H5N1 is about 60 per cent (WHO, 2012). Most human cases of H5N1 infection have involved the individual having a history of poultry exposure such as handling, slaughtering or consuming infected poultry (Chowdhury *et al.*, 2019).

Globally, more than 15,000 outbreaks were reported in domestic birds from January 2005 to January 2018 and as of December 2006, more than 240 million poultry including chickens, ducks, turkeys and geese either died or were slaughtered to prevent the spread of H5N1 (Chowdhury *et al.*, 2019).

Highly-pathogenic versions of H5N1 have now spread from Asia to Europe and Africa, resulting in millions of poultry infections. This movement of highly pathogenic H5N1 viruses is probably due to migrating waterfowl. Wild birds, including shorebirds and gulls, as well as domestic ducks are considered to be the natural reservoir of the virus. These animals may carry and shed viruses without showing any signs of illness – they become silent carriers, sustaining and perpetuating H5N1 and transmitting it to other susceptible hosts (Chowdhury *et al.*, 2019).



The global spread of highly-pathogenic H5N1 in birds is considered a significant pandemic threat. Concerned that if the virus mutated to become more easily transmissible, David Nabarro, one of the most senior public health experts at the World Health Organisation, said the *“range of deaths could be anything between five and 150 million”*.

So far, it spreads mainly from poultry to people with just a very small handful of person-to-person cases. However, influenza viruses constantly undergo genetic changes, it would be an extremely serious cause for concern, if the H5N1 virus become more easily transmissible among humans.

H7N9

The H7N9 virus was first detected in poultry in China in 2013. Since then the number of human cases confirmed has reached 1,568 and 616 people have died (FAO, 2019). Most H7N9 infections in people result from contact with infected poultry, for example, by visiting wet markets and having contact with environments where infected poultry have been kept or slaughtered (WHO, 2014). A minority of cases appear to have resulted from limited person-to-person transmission.

Because H7N9 infections don't cause severe disease in poultry, this infection can spread 'silently' among poultry. H7N9 is now ubiquitous in Chinese poultry but like H5N1, at the moment, doesn't spread easily between people – the concern is that it is mutating and becoming more easily spread among the human population.

In 2017, samples from a man who died of H7N9 in China revealed a drug-resistant strain that appears to spread easily from animal to animal. Virologist Professor Yoshihiro Kawaoka of the University of Wisconsin said: *“If H7N9 viruses acquire the ability to transmit efficiently from person to person, a worldwide outbreak is almost certain...”* (Devitt, 2013).

H7N4

In February 2018, a 68-year-old woman was hospitalised in Jiangsu province in eastern China after being infected with the H7N4 virus (Tong *et al.*, 2018). The infected woman had handled live poultry before falling ill, so probably caught the virus from birds or the market she bought them in. This was the first recorded case of this virus infecting a human. It may have been possible that the Jiangsu H7 came from H7N9 mixing with another viral strain. This shows how unpredictable viral evolution in livestock farming can be.

Bird flu has gone from being a relatively rare occurrence to one that crops up frequently and the UK has not escaped. In November 2014, a low-severity H5N8 virus was confirmed at a farm in Yorkshire; then in



February 2015, a low-severity H7N7 virus was found at a farm in Hampshire. In 2015, a highly-pathogenic H5N1 strain was identified at a chicken farm in the Dordogne in France and it was subsequently found in a number of other farms in south-western France. It seems that it just won't go away and now H5N1 has infected migratory birds and is spreading around the world.

What caused bird flu to change into this sinister menace?

What caused bird flu to jump species? The short answer is factory-farming. Viruses' sole mission is to infect animals or plants and make more copies of themselves. If a random mutation occurs that makes this easier, the mutated version will thrive. Factory farms provide a perfect breeding ground for the emergence of new super-viruses.

In water-birds, the virus had found an ideal environment in which it could co-exist without harming the host. However, when these birds were taken to market, the virus could no longer spread from bird to bird in water so had to mutate or die. Mutations naturally occur but unless they offer some advantage, the original version will continue to dominate. In this new, stressful environment, mutations occurred and enabled the virus to spread via faeces, nasal secretions and secretions from the mouth or eyes of infected birds.

Commercial poultry farms, wet markets, backyard poultry farms, commercial and family poultry slaughtering facilities, pig farms, human dietary habits and the global trade in exotic animals have all been implicated in the spread of influenza viruses (Greger, 2006).

Intensive poultry production provides the perfect breeding ground for a mutating virus. Chickens are raised in closed, filthy, stressful and crowded, industrial facilities with little or no natural light. This is important as ultra-violet light (UV) harms viruses. We are literally handing the bird flu virus the perfect opportunity to mutate into a more deadly form, to do its worst! A perfect storm of our own making.

As a consequence, viruses are changing and beginning to jump species with increasing frequency. In 2003-2004 a number of captive tigers and leopards in a zoo in Thailand who were fed fresh chicken carcasses, died of H5N1 infection. Some tiger-to-tiger transmission is thought to have occurred (WHO, 2006). In 2006, H5N1 was isolated from a domestic cat found dead on the northern island of Ruegen in Germany – where more than 100 wild birds had died from H5N1 (WHO, 2006).

At the moment, bird flu viruses tend not to spread easily between people, but there have been a small number of cases of human-to-human infection among families caring for infected relatives. Imagine the devastation if a highly-pathogenic avian influenza virus becomes able to spread in the air like the common cold or Covid-19!

Zoonoses a ticking time bomb

The pattern of infection in recent years, with different animals and humans affected, represents a disturbing development. It may be entirely possible that a natural chain of mutations could lead to a bird flu virus acquiring the capability of airborne transmission between mammals. This could lead to a human pandemic that would circle the world in weeks. If and when an influenza pandemic arises from one of the currently circulating, highly-pathogenic strains, the death rate would be devastating.

Just as we are seeing now with Covid-19, it won't just be people who went to a wet market in China dying – it will be office workers in New York, commuters in London, tourists in Italy and students in Madrid. They will be joined by people in every city, town and village around the world, dying after shaking someone's hand, touching their face or simply breathing in, in the wrong place at the wrong time.

World Health Organisation spokesman for the Western Pacific region, Peter Cordingly, says: "...the bottom line is that humans have to think about how they treat their animals and how they farm them, how they market them – basically the whole relationship between the animal kingdom and the human kingdom is coming under stress" (CNM, 2004).

One way to take control of the situation would be for huge numbers of people to stop eating poultry, pigs and other animals and remove the viral reservoir of factory-farms. It's time to end factory farming before it ends us.

EBOLA

Ebola is one of the world's deadliest diseases killing 25 to 90 per cent of those infected, depending on the virus species. This viral haemorrhagic fever of humans and other primates is caused by ebolaviruses transmitted to people from wild animals and spread through human-to-human transmission.

Ebola was first identified in 1976, in two simultaneous outbreaks, one in Nzara in South Sudan, and the other in a village called Yambuku in the Democratic Republic of the Congo, a village near the Ebola River from which the disease takes its name.

There have since been a number of outbreaks. The 2014-2016 one in West Africa started in December 2013, after an 18-month-old boy from a small village in Guinea is believed to have been infected by bats. The boy may have been infected by playing in a hollow tree housing a colony of fruit bats, say scientists. His death was followed by that of his older sister and then his mother. The Ebola virus soon spread to Guinea's capital city and on March 13, 2014, the Ministry of Health in Guinea issued an alert for an unidentified illness.

Shortly after, the Pasteur Institute in France confirmed the illness as Ebola. Ten days later, with 49 confirmed cases and 29 deaths, the WHO officially declared an outbreak of Ebola virus disease. Two and a half years later, with widespread transmission to Guinea, Liberia, and Sierra Leone plus a handful of cases in Europe and the US, the outbreak ended with more than 28,600 cases and 11,325 deaths (CDC, 2019c).

The RNA virus spreads through direct contact with body fluids, such as blood, saliva, mucus, vomit, faeces, breast milk, urine and semen from infected humans or other animals. Fruit bats are believed to be the natural host, able to spread the virus without being affected by it.

The virus can infect humans by entering the body via the nose, mouth, eyes, open wounds, cuts and abrasions. Although it is not entirely clear how Ebola initially spread from animals to humans, it is believed it may have involved direct contact with an infected wild animal or fruit bat. Besides bats, other wild animals sometimes infected include several monkey species, chimpanzees, gorillas, baboons and duikers (forest antelope).

Bushmeat is the name for any wild animal that is killed for consumption including antelopes, chimpanzees, rats, porcupines, snakes and fruit bats. The use of bats as food raises particular concern, as bats host more zoonotic viruses than most other animals, including rodents (Luis *et al.* 2013). As we've seen, bats carry a whole range of viruses and studies have shown that some species of fruit bats can harbour the ebolavirus.

In Africa's Congo Basin, people eat an estimated five million tonnes of bushmeat per year, according to the Centre of International Forestry Research and Dr Olivier Restif from the University of Cambridge found that the scale of the bat bushmeat trade in Ghana was much higher than previously thought, with more than 100,000 bats killed and sold every year (Kamins *et al.*, 2015).



Exactly how virus spillover into humans occurs is not clear, there is often an intermediary species involved, such as chimpanzees, but evidence shows people can get the virus directly from bats. Hunting, butchering and eating wild animals can lead to the transmission of zoonotic pathogens through animal bites, scratches, body fluids, tissues or faeces (Wolfe *et al.*, 2005).

Because the world's population is expanding, close contact with wildlife will increase, which is often the first driver of emerging diseases. Deforestation is also a major contributor to recent outbreaks and cases of Ebola have often been close to recently deforested land.

"The Ebola outbreak is an opportunity to clamp down on a practice which both causes disease outbreaks and empties forests of wildlife. At a minimum, governments should zealously enforce bans on the hunting and consumption of bats and apes, two groups most commonly associated with Ebola" (Williams, 2014).

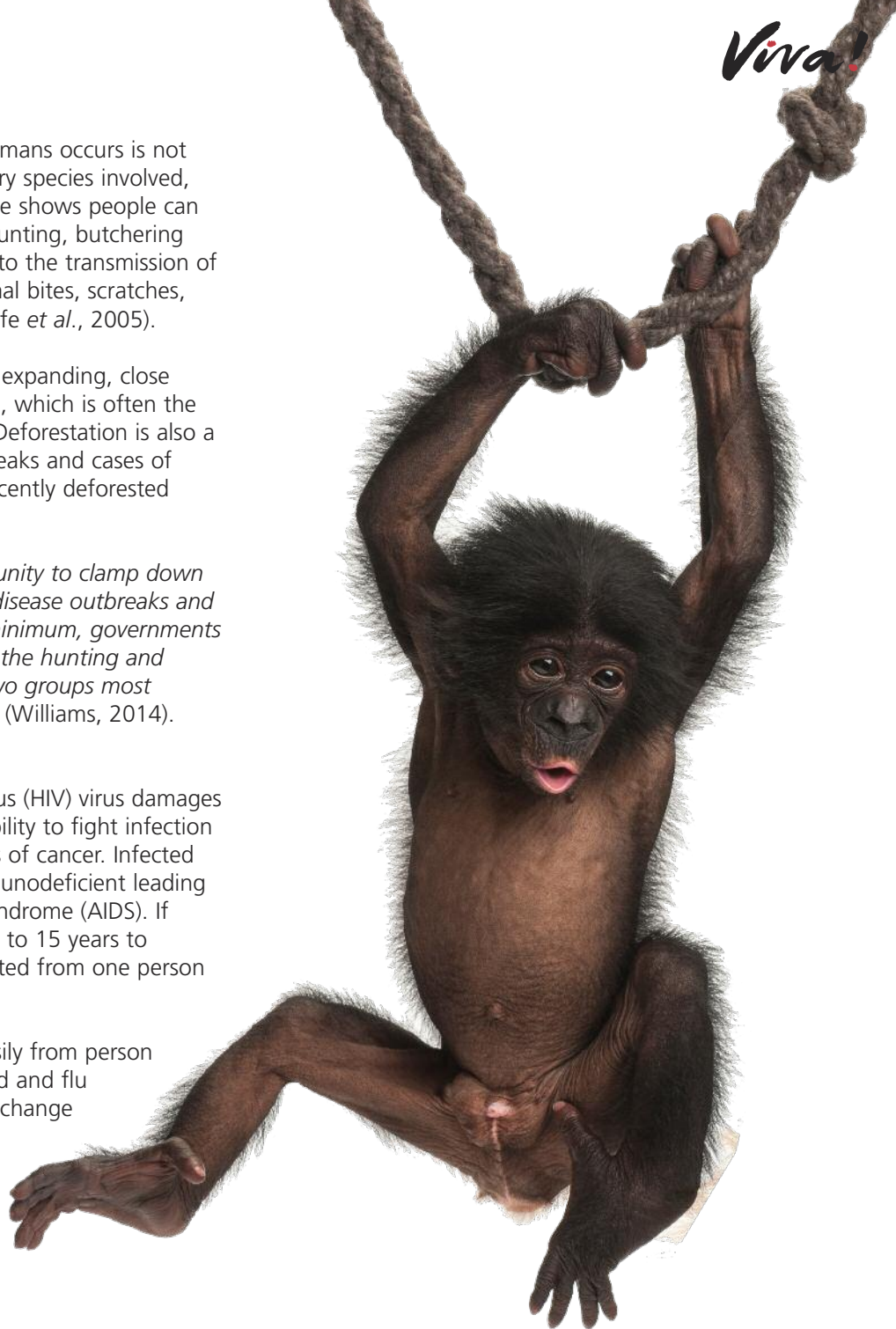
HIV/AIDS

The human immunodeficiency virus (HIV) virus damages immune cells and weakens the ability to fight infection and disease, including some types of cancer. Infected individuals gradually become immunodeficient leading to acquired immune deficiency syndrome (AIDS). If untreated, this can take from two to 15 years to develop. AIDS cannot be transmitted from one person to another, but the HIV virus can.

The HIV virus is not passed on easily from person to person through the air, like cold and flu viruses, it is transmitted via the exchange of a variety of body fluids from infected people, such as blood, breast milk, semen and vaginal secretions. It is not transmitted by kissing, hugging, shaking hands or sharing food and water (WHO, 2019).

There are two main types of HIV virus, HIV-1 and HIV-2, both derived from simian immunodeficiency viruses (SIVs) that circulate in at least 40 species of African non-human primates (Sharp and Hahn, 2010). Most SIVs infect monkeys and have been circulating in different species, causing them no problems, for many years.

HIV-1 was discovered first and is the most prolific and HIV-2 is most common in western Africa and is becoming more common in India. HIV-1 is a mutated version of a chimpanzee virus, which probably made the species-jump to humans as a result of chimpanzees being hunted and eaten. Chimpanzees, like humans, are apes and it is assumed they acquired SIVs from monkeys, most probably by predation (Sharp and Hahn, 2010). Scientists believe that the jump from chimpanzees to humans happened in the 1920s, in Kinshasa (called Leopoldville until 1966) in what is now



the Democratic Republic of Congo. HIV-2 comes from sooty mangabey monkeys and the crossover to humans in the 1960s is believed to have happened in a similar way, through the butchering and consumption of monkey meat. There have since been at least a dozen independent transmissions of SIVs to humans leading to HIV-1 and HIV-2 (Sharp and Hahn, 2010).

As we have seen, when normal ecosystems or habitats of wild animals are disturbed, by human occupation for example, random mutations in the viruses that they are natural hosts to can enable those viruses to jump host, as exemplified by the story of the HIV virus from chimpanzees in rainforests of West Africa (Sun *et al.*, 2020). It's the same story being replayed around the world with different host species and different viruses, the only constant is humans, disturbing the equilibrium at our peril.

Zoonoses a ticking time bomb

The opportunities for zoonotic transfer of SIVs from primates to humans have existed for hundreds if not thousands of years. However, only in the twentieth century did such viruses spread to detectable levels in humans. In west central Africa during the early part of that century, the destabilisation of social structures by invading colonial powers, the rapid growth of major cities and the widespread use of injections may have all contributed to provide an unprecedented opportunity for the spread of blood-borne viruses (Sharp and Hahn, 2010). Furthermore, in the 1960's, a 'perfect storm' of population growth, sex and railways allowed HIV to spread across Africa and the world, according to an international team of scientists (Faria *et al.*, 2014). They say a roaring sex trade, rapid population growth and unsterilised needles used in health clinics probably spread the virus.

Given the ongoing contact between infected primates and people through hunting and butchering, together with the increase of the bushmeat trade and logging, scientists say that it is likely that cross-transmissions are still occurring and human exposure to SIV has increased, as have the social and environmental conditions that support the emergence and spread of new zoonotic infections. One major public health implication is that, these SIV strains may not be recognised by HIV-1/HIV-2 screening tests and as a consequence, human infection may go unrecognised for several years and lead to another epidemic (Aghokeng *et al.*, 2010).

AIDS was first recognised as a new disease in the early 1980s when increasing numbers of gay men began falling ill with opportunistic infections and rare malignancies. HIV-1 was subsequently identified as the cause of what has since become one of the most

devastating infectious diseases to have emerged in recent history. HIV and AIDS continue to be a major global public health issue, having claimed over 32 million lives so far (WHO, 2019).

NIPAH VIRUS

The Nipah virus is another highly-pathogenic RNA virus that can spread from animals to humans. Infection may cause no symptoms, mild symptoms such as a cough, headache and breathlessness or more serious symptoms including acute respiratory infection and fatal encephalitis (inflammation of the brain). It is estimated that 40 to 75 per cent of those who are infected die (WHO, 2018).

Fruit bats are the natural host but pigs may become infected, possibly by consuming fruit contaminated with bat secretions, and the virus is highly contagious in pigs (WHO, 2018). The virus was first identified in 1999 during an outbreak of encephalitis and respiratory illness among pig farmers in Sungai Nipah, a village in Malaysia (CDC, 2014a). This virus emerged from pigs on farms in an area that harboured fruit bats.

During this first outbreak, which also affected Singapore, most human infections resulted from direct contact with infected pigs and contaminated meat (WHO, 2018). The outbreak caused a relatively mild disease in the pigs, but nearly 300 human cases with over 100 deaths were reported. In order to stop the outbreak spreading, more than a million pigs were killed (CDC, 2014). Subsequent outbreaks have occurred in India and Bangladesh with the latter experiencing outbreaks most years.

There are currently no specific drugs or vaccines for Nipah virus infection. In 2019, Richard Hatchett, chief



executive of the Coalition for Epidemic Preparedness Innovations said: *“Twenty years have passed since its discovery, but the world is still not adequately equipped to tackle the global health threat posed by Nipah virus”* (Kelland, 2019).

It's not just scientists that have been warning us of the threat of zoonotic disease outbreaks, terrifying yet plausible scenarios have been appearing in films and books for years. In the 2011 Steven Soderbergh film *Contagion*, MEV-1, the film's fictional virus, was based upon the Nipah virus. In the film, the director of the Centers for Disease Control and Prevention (Laurence Fishburne) tells the Department of Homeland Security: *“Someone doesn't have to weaponise the bird flu. The birds are doing that”*. A nod to how intensive factory farming methods provide a perfect breeding ground for emerging infectious diseases.

WHO say that if a Nipah virus outbreak is suspected, animal premises should be quarantined and culling of infected animals, with close supervision of burial or incineration of carcasses, may be necessary to reduce the risk of transmission to people. Or we could just stop pig farming!

MEASLES

Measles is a highly infectious disease that can lead to serious and potentially life-threatening complications in some people including pneumonia and encephalitis. According to the World Health Organisation, more than 140,000 people died from measles globally in 2018 – most of them were children under the age of five, despite the availability of a safe and effective vaccine (WHO, 2019a). About one in five children with measles experience complications such as ear infections, diarrhoea and vomiting, pneumonia, meningitis and eye disorders. One in 10 children with measles ends up in hospital. There is no treatment, vaccination is the only way of preventing it (NHS, 2017).

It's thought that each person with the common cold infects 2-3 other people, for seasonal flu, the number is 0.9-2.1 but each person with measles, on average, infects 12-18 others (Guerra *et al.*, 2017). The measles virus is contained in the millions of tiny droplets that come out of the nose and mouth when an infected person coughs or sneezes. You can easily catch measles by breathing in these droplets or touching a surface the droplets have settled on and then touching your eyes, nose or mouth (the virus can survive on surfaces for a few hours). People with measles are infectious from when the symptoms develop until about four days after the rash first appears (CDC, 2018).

Research suggests that the modern measles virus (MeV) emerged as a zoonotic disease from the rinderpest virus that caused 'cattle plague' around the 11th to 12th centuries (Furuse *et*

al., 2010). The virus required two conditions to emerge, firstly, humans had to live close to cattle infected with the rinderpest virus. This proximity became commonplace after the domestication of cattle 10,000 years ago. Secondly, to sustain an epidemic, measles requires a susceptible population of 250,000-500,000 or more, this became feasible in European cities in the later Middle Ages (Wertheim and Kosakovsky Pond, 2011). In June 2011, the United Nations FAO confirmed rinderpest virus was eradicated, but measles remains.

In 2017 the World Health Organisation declared that the UK had eliminated measles. WHO defines measles elimination as the absence of circulating disease, high vaccine coverage and good systems to identify cases. In countries that have eliminated measles, it can still occur, but these will be isolated cases that have limited spread within the community. However, because of suboptimal uptake of the vaccine, in 2018, there was a marked increase in the number of cases in England and Wales, with almost 1,000 confirmed cases, and in 2019 the UK lost its eliminated status (Public Health England, 2019).

Director-General of the World Health Organisation, Tedros Adhanom Ghebreyesus, says: *“The fact that any child dies from a vaccine-preventable disease like measles is frankly an outrage and a collective failure to protect the world's most vulnerable children”* (WHO, 2019a).

Measles is extremely contagious, much more so than seasonal flu or Covid-19, and should be taken as a warning of how highly infectious zoonotic diseases can be.



Antibiotic resistance

Viruses are not the only threat. Around three-quarters (73 per cent) of the world's antibiotics are used in animal agriculture, not for treating diseases in humans (Van Boeckel *et al.*, 2019). So as well as new emerging viruses coming from wild animals taken to markets, we have the serious global threat of antimicrobial-resistance (AMR). Neither viruses nor bacteria respect international borders so going vegan is the clear solution.

Antibiotics have been helping us fight infection since the 1940s. Before they were developed, even a small scratch could be fatal. Giving birth and having surgery were a lot riskier and sexually transmitted infections (STIs), such as syphilis and gonorrhoea, caused untold misery and could be a death sentence.

We now rely heavily on antibiotics to treat and prevent infection but they are also widely used in agriculture. The UK government says: *"As in humans, the sub-optimal use of antimicrobials in agriculture and veterinary practice contributes to the rise and spread of AMR all over the world"* (Global & Public Health Group, 2019).

The use of antibiotics in animals as growth promoters was banned in the EU in 2006 but huge quantities continue to be used globally. Antibiotic use in livestock outweighs human consumption in many countries, in the US, for example, 80 per cent of all antibiotics are used in animals (Martin *et al.*, 2015). In the UK, in 2017, 36 per cent of antibiotics were sold for use in animals (Veterinary Medicines Directorate, 2019), a lower proportion than in some other countries, but still a considerable amount at 226 tonnes in 2018 (UK-VARSS, 2019).

The overuse of antibiotics in humans and animals has led to the emergence of multidrug-resistant bacteria or 'superbugs'. AMR happens because random DNA mutations occur naturally in bacteria – these may help them prosper or have no effect. If a mutation helps a single bacterium survive antibiotic treatment while all others die, that one will reproduce, spread and take its new resistance gene with it, enabling it to survive the hostile environment – the genetic equivalent of a stab-vest!

If antibiotics fail, chest infections, urinary tract infections (UTIs), cuts, insect bites and even small scratches could develop into sepsis (blood-poisoning) which can be fatal if not treated quickly. In the UK, five people die from sepsis every hour and the number is rising (UK Sepsis Trust, 2020). The UK Sepsis Trust CEO, Dr Ron Daniels, says: *"...nearly 40 per cent of E. coli – the bacteria that causes a huge number of infections – is now resistant to antibiotics and these*

organisms account for up to one third of episodes of sepsis, showing the vital need for responsible use of antimicrobial drugs" (UK Sepsis Trust, 2019).

The idea of dying from a horsefly bite is unthinkable but is fast becoming a possibility, thanks to the overuse and abuse of antibiotics. Professor Colin Garner, chief executive of Antibiotic Research UK, says: *"Now we are in real danger that we could return to a pre-antibiotic past, where dirty wounds, bites and conditions like TB and typhoid might kill"* (Antibiotic Research UK, 2018).

The World Health Organisation (WHO) say that antimicrobial resistance is one of the main threats to modern medicine, with growing numbers of infections, such as pneumonia, tuberculosis, gonorrhoea and salmonellosis, becoming harder to treat (WHO, 2018a).

Lord Jim O'Neill's 2016 government-commissioned review on antimicrobial resistance warned that the 700,000 global deaths caused by AMR each year will rise to 10 million by 2050 if no action is taken (O'Neill, 2016). That means AMR could kill more people than cancer. In 2019, O'Neill, said: *"The case for having death certificates to include AMR as a cause of death is quite compelling"* (Newey, 2019).



O'Neill's review described the ways resistant bacteria in animals, created by the selective pressures of antibiotic use, could be transferred to humans – through direct contact with animals, from undercooked or unpasteurised animal foods, or via the spread of resistant bacteria into environmental reservoirs. The report says *"In light of this information, we believe that there is sufficient evidence showing that the world needs to start curtailing the quantities of antimicrobials used in agriculture now"* (O'Neill, 2016).

O'Neill's warnings are not being heard. Due to the increasing global demand for meat, it's predicted that antibiotic use in cattle, chicken and pigs worldwide will increase by 67 per cent by 2030 (Van Boeckel *et al.*, 2015). There have been improvements in the UK, with antibiotic sales for use in animals falling by 53 per cent between 2014 and 2018 (UK-VARRS, 2019). However, from 2013 to 2017, the number of antibiotic-resistant bloodstream infections (BSIs) in the UK increased by 35 per cent and continues to rise (APRHAI, 2019), and of course, the UK imports considerable quantities of meat thereby supporting antibiotic use abroad. It could be that the action being taken to reduce use in humans and animals is too little, too late!

Colistin is a 'last resort' antibiotic for humans but is still used widely in livestock, especially pigs, in some parts of the world and in 2015, bacteria carrying colistin-resistance genes were identified in China (Liu *et al.*, 2016). The genes were carried in such a way that bacteria are able to transfer them to other species of bacteria. This 'horizontal gene transfer' rang alarm bells among the scientific community as it heralds the breach of the last group of antibiotics available to humans and opens up the possibility of AMR spreading even faster.

Screening in areas of China, where colistin was routinely given to pigs, revealed resistant *E. coli* in more than 20 per cent of animals, 15 per cent of raw meat samples and one per cent of hospital patients (Liu *et al.*, 2016). Colistin-resistant bacteria have now been identified in over 50 countries, including the UK (Liu and Liu, 2018).

The use of this antibiotic in animals has been voluntarily restricted by livestock industries in the UK, decreasing by 99 per cent between 2015 and 2017 (Veterinary Medicines Directorate, 2019). It is unclear why there hasn't been a total ban, the European Medicines Agency suggests that last resort antibiotics used for treatment of life-threatening disease in humans should be excluded from veterinary use (European Medicines Agency, 2016).

UK policy to accept voluntary initiatives contrasts with other countries, such as Sweden, Denmark and the



Netherlands, where antibiotic use in animals is controlled through government legislation. China banned the use of colistin in 2016 in animals as a growth promoter, falling in line with the EU, US, Brazil and India. In their 2018 report, the World Organisation for Animal Health (known as OIE) found that 12 countries were still using colistin to fatten animals but said that some of them had committed to changing their legislation concerning growth promoters (OIE, 2018). Scientists are unsure if this late action can curb the spread of resistant genes – it could simply be a closing of the barn door after the horse has bolted!

Scientists point out the stark parallels between the AMR crisis and the climate crisis – both driven by the increasing global demand for cheap animal foods. The World Health Organisation talk about a 'One Health' solution because AMR does not recognise geographic or human-animal borders – we all share one planet (WHO, 2017). The most effective way to tackle antibiotic resistance is to change the way we live and eat, reducing antibiotic use in humans and animals.

The contribution from agriculture to AMR is significant and growing. Of course, livestock industries are inevitably resistant to change but the obvious solution is to drastically reduce consumption of animal foods. The widespread adoption of a vegan diet would remove the factory farms that are the breeding grounds for these superbugs.

AMR is a problem of our own making, in humans, and in animals as a direct consequence of the inappropriate use of antibiotics in a drive to produce cheap meat, fish and dairy foods on an industrial scale. Failure to act may result in the chilling prospect of an apologetic doctor saying to you: *"Sorry but there's nothing we can do for you"*.



Conclusions

Experts have been warning us about this for years. Most of the viruses causing new emerging diseases can be traced back to factory farms, slaughterhouses, wet markets and illegal animal trade such as bushmeat. While Chinese wet markets have taken the brunt of the blame, the increasing global demand for meat is fuelling these outbreaks.

The conditions in which we keep farmed animals today, packed into filthy, overcrowded sheds, standing on top of each other and in their own faeces, physically stressed, pushed to the limit – an ideal breeding ground for emerging viruses and antibiotic-resistant bacteria.

“SARS-CoV is only an example of emerging infections that we are going to face. In coming years, more cross-species infections are expected to happen. Factors influencing the chance of emergence of zoonotic infections are complex; and population density, ecology and proximity between animals and humans probably play a certain role” (Chan and Chan, 2013).

Experts are calling for the banning of wild animal markets worldwide – the sale of sometimes endangered species for human consumption is the cause of this new coronavirus outbreak and many past epidemics. Writing in the Telegraph, Adjunct Professor of Global Health at the Duke Global Health Institute, Dr Jonathan Quick, says: *“Traditional Chinese wet markets remain a threat to global health. China’s political and public health leaders must not fall into the cycle of short-lived commitments and long-term complacency following high-profile epidemics”* (Quick, 2020).

At the time of writing (April 28 2020) the global number of confirmed cases of Covid-19 has exceeded three million with over 200,000 deaths. In the UK, there have so far been over 20,000 deaths

(Worldometer, 2020). Most of the world is in lockdown, experiencing restrictive measures usually only seen during wartime. This could be all because someone wanted to eat a pangolin!

The next bird flu outbreak could become a pandemic on a similar scale – chicken isn’t cheap if it costs thousands of lives and leads to a global recession.

Not only are we decimating wild landscapes to clear the way for more intensively farmed animals, we are enclosing ever-increasing numbers of animals in filthy, overcrowded conditions, killing wild animals or caging them and sending them to market – all for the sake of our hunger for meat. Invading and disrupting ecosystems will inevitably shake viruses loose from their natural hosts just as factory farms are giving rise to superbugs. It’s time we listened to the warnings and put a halt to factory farming and wildlife markets.

Juliet Gellatley, founder and director of Viva! and zoologist says: *“We must have a societal shift in the way we view animals, the environment and our diets. We must stop eating animals. It is time to finally make the connection between animal agriculture and environmental destruction, antibiotic resistance and disease outbreak. We must stop tearing down forests to make way for animal farming or to grow animal feed. We must protect ecosystems and prioritise the safety and freedom of wild animals, leaving them to live their lives away from human contact. If we don’t take urgent and far-reaching action now, eating animals will be the death of us”*.

**Stop factory farming –
it’s time to go vegan!**

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“After the unprecedented challenges we all faced through Covid-19, this report helps us understand the huge threat we face from zoonoses – spreading due to our exploitation of animals. An excellent and timely report.”

Dr Michael Greger, physician, author and international speaker on nutrition, food safety and public health and author of How Not to Die.

The link between eating animals and pandemic risk is well-established scientifically, but the political will to curtail this risk is lacking. Viva!’s ground-breaking report describes zoonotic diseases from measles, Ebola, HIV and AIDS to bird flu and antibiotic-resistant superbugs and of course SARS, MERS and Covid-19. Where did all these diseases come from? What role do wet markets and factory farms play? Want to know what you can do to help avert another pandemic? This essential report reveals all.

Juliet Gellatley, Viva!’s founder and director says: *“We must have a societal shift in the way we view animals, the environment and our diets. We must stop eating animals. It is time to finally make the connection between animal agriculture and environmental destruction, antibiotic resistance and disease outbreak. We must stop tearing down forests to make way for animal farming or to grow animal feed. We must protect ecosystems and prioritise the safety and freedom of wild animals, leaving them to live their lives away from human contact. If we don’t take urgent and far-reaching action now, eating animals will be the death of us”.*

It’s time to end factory farming.

Viva!

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