COVID-19 and other zoonotic diseases – origins uncovered

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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*."

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.

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 that come from both of their parents.

Coronavirus disease symptoms vary depending on the species affected, in chickens coronaviruses can cause an upper respiratory tract disease, while in cows and pigs they can cause diarrhoea. In humans, they cause 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, previously known as 2019-nCov now called 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 an epidemic in the making.

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 emerging viruses!

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). In fact, SARS-CoV-2 is 96 per cent identical to bat coronavirus (Zhou *et al.*, 2020). However, it is thought to be a recombinant virus, with elements from bats and another unknown species (Ji *et al.*, 2020). The consensus is that SARS-CoV-2 originated in bats but passed to humans via an intermediate host (Salata *et al.*, 2019).

While SARS-CoV (and MERS-CoV) are genetically closely related to bat coronaviruses, scientists say that intermediate hosts are likely to be involved in the emergence and cross-species transmission of these novel human viruses (Chan and Chan, 2013).

Initially, snakes or bamboo rats were suggested as the intermediate host. However, recent research suggests that it may have been pangolins (Zhang *et al.*, 2020). Pangolins are the world’s most trafficked animals, presenting yet another potential level of risk. Coronavirus collected from caged pangolins obtained from an unspecified research organisation showed over 99 per cent genome sequence identity to SARS-CoV-2 (Sun *et al.*, 2020).

Alternatively, we 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.

STOP WILD MARKETS

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 intermediate 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!

MERS

Middle East respiratory syndrome or MERS is also caused by a coronavirus (MERS-CoV) and is thought to have originally spilled over from bats into camels, in which is it now endemic. It was first detected in a patient living in Jeddah in Saudi Arabia, in June 2012. MERS-CoV causes respiratory infection in humans, ranging from asymptomatic to severe pneumonia. In camels, the intermediate host, the virus only causes a mild infection but it spreads efficiently between animals (Widagdo *et al.*, 2019).

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 died from it (but the overall mortality risk could be lower as those with mild symptoms may be undiagnosed and therefore not counted).

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).

Avian influenza – bird flu

Avian influenza became commonly known as bird flu in the late 1990's when it spread through live-poultry markets in Hong Kong, infecting people and leading to six deaths. It was controlled only by slaughtering the entire poultry population in the affected region.

The natural hosts of bird flu viruses are wild water-birds 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. But now, these same viruses have been blamed for 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.

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).

Spanish flu

The 1918 Spanish flu pandemic was caused by an H1N1 virus with genes of avian origin (CDC, 2019). It's estimated that about 500 million people, around one-third of the world's population, became infected with the virus. The number of deaths was estimated to be up to 50 million worldwide making it one of the deadliest pandemics in human history. So far…

The pandemic affected 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. The mortality rate in Europe has been estimated to be just over one per cent (Erkoreka, 2009).

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!

Since 1918, the world has experienced three more influenza pandemics:

Asian flu

This flu pandemic outbreak of avian influenza caused by an H2N2 virus originated in China in early 1956 lasting until 1958. It originated from a mutation in wild ducks combining with a pre-existing human strain and is estimated to have killed from one to four million people.

Hong Kong Flu

The 1968 Hong Kong Flu pandemic was caused by a strain of H3N2 resulted in an estimated one million global deaths.

Swine flu

In 2009, a swine flu pandemic (caused by a swine-origin H1N1 virus called A/H1N1pdm09) was detected in Mexico and spread quickly across the world. Pigs are susceptible to infection with both avian and human influenza viruses and have thus been referred to as a ‘mixing vessel’ for viruses. The virus contained genetic material from human, avian and swine strains of the influenza virus.

It primarily affected children and younger adults, as many older people turned out to be immune. So it was less severe than previous pandemics, resulting in fewer than 300,000 deaths in its first year. 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.

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.

It is high time we start considering the fact that our increased consumption of animal protein isn’t just wreaking havoc on our health and the environment, it is sparking pandemics that kill thousands, potentially millions, of people. Some highly-pathogenic strains now threaten to cause serious infections in humans.

H5N1

The global spread of highly pathogenic H5N1 in birds is considered a significant pandemic threat. The virus has been infecting 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. Since then, high-pathogenic versions of H5N1 have spread from Asia to Europe and Africa, resulting in millions of poultry infections. 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).

During the 2005 outbreak, tens of millions of birds in south-east Asia were culled in an effort to contain the disease. 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*”.

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 and since then has affected over 1,600 people killing 40 per cent of them. 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 is 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?

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.

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 a perfect opportunity for mutation and infection. A perfect storm of our own making!

So the virus is changing and has begun to jump species. 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. In 2003-2004 a number of captive tigers and leopards in a zoo in Thailand who were fed fresh chicken carcases, died of H5N1 infection. Some tiger-to-tiger transmission is thought to have occurred (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 death rate if a highly pathogenic virus became able to spread in the air like the common flu!

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 could 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 stop factory farming.

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. 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, 2019a).

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 intermediate 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 contract 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

Human immunodeficiency virus (HIV) 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 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, known as simian immunodeficiency virus (SIV), which probably made the species-jump to humans as a result of chimpanzees being hunted and eaten. Scientists believe this happened in the 1920s, in Kinshasa (called Leopoldville until 1966) in what is now the Democratic Republic of Congo.

Before viruses in wildlife make a jump to infect humans, they usually accumulate a series of mutations enabling them to invade humans as a result of human occupation of their normal ecosystem or habitat, as exemplified with the story of initial human infection by HIV carried by chimpanzees in rainforests of West Africa (Chan and Chan, 2013).

Studies of natural chimpanzee populations indicate that there have been multiple transmission events of HIV-1 to humans (Keele *et al.*, 2006). 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.

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.

HIV continues 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).

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 up 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. 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).

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. 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 a 1,000 confirmed cases, and in 2019 the UK lost its eliminated status (Public Health England, 2019). According to the World Health Organisation, more than 140,000 people died from measles globally in 2018 – mostly children under the age of five, despite the availability of a safe and effective vaccine (WHO, 2019a).

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. 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 many 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. 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 greatest driver of AMR in people is the use of antibiotics in human medicine (European Medicines Agency, 2016), but the contribution from agriculture 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".

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, wet markets, slaughterhouses 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 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 7 2020) the number of confirmed cases worldwide has exceeded one million with over 76,000 deaths. In the UK, there have so far been over 5,000 deaths and we are not yet at the peak (Worldometer, 2020). Most of the world is in lockdown, experiencing restrictive measures usually only seen during wartime. This may be all because someone wanted to eat a pangolin!

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. It's time to go vegan!

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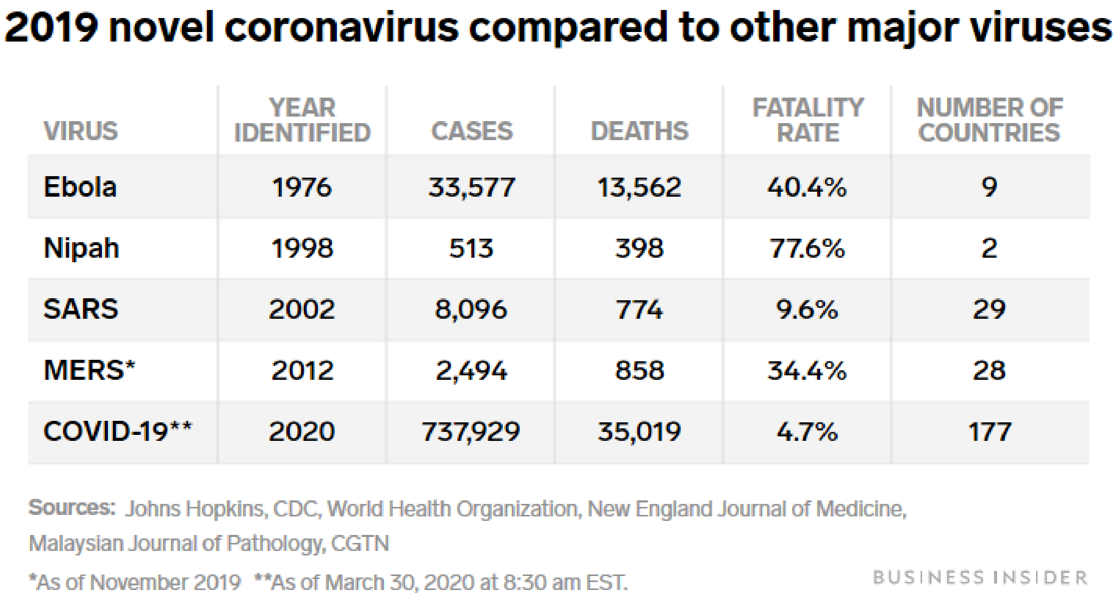

2019 novel coronavirus compared to other major viruses

VIRUS	YEAR IDENTIFIED	CASES	DEATHS	FATALITY RATE	NUMBER OF COUNTRIES
Ebola	1976	33,577	13,562	40.4%	9
Nipah	1998	513	398	77.6%	2
SARS	2002	8,096	774	9.6%	29
MERS*	2012	2,494	858	34.4%	28
COVID-19**	2020	737,929	35,019	4.7%	177

Sources: Johns Hopkins, CDC, World Health Organization, New England Journal of Medicine, Malaysian Journal of Pathology, CGTN

*As of November 2019 **As of March 30, 2020 at 8:30 am EST.

BUSINESS INSIDER

Source: Business Insider, 2020.