WORLD HEALTH ORGANISATION

World Health
Organization

Background Guide

Agenda

Combating Zoonotic Diseases with Special Emphasis to COVID-19

LETTER FROM THE EXECUTIVE BOARD

Dear Prospective Members,

At the outset on behalf of the Executive Board, we extend a warm welcome to all of you and congratulate you on being a part of "**SXMUN 2020"**

The committee being simulated, would unlike most other simulations you must have heard of or been a part of; focus on political intellect and analytical application of thoughts and strategic application of thoughts in resolving impending politically sensitive bilateral issues.

Kindly note, we are not looking for existing solutions, that would be a copy paste of what the world leaders have already taken; instead we seek an out of the box solution from you, while knowing and understanding your impending political and ideological limitations.

This Introductory guide would be as abstract as possible, and would just give you a basic perspective on what you can expect from the committee and areas wherein which your research should be focused at this given point in time. Given, the extremely volatile nature of this committee, your presence of mind and politico-analytical aptitude is something which we at the executive board would be looking to test.

That being said, kindly do not limit your research to the areas highlighted further but ensure that you logically deduce and push your research to areas associated with the issues mentioned.

Kindly note, that unlike most conventional/unconventional committees you have attended, this committee shall have "substantive" intervention by the Executive Board.

The objective of this background guide is to provide you with a ‘background’ of the issue at hand and therefore it might seem to some as not being comprehensive enough. If you feel that the Guide does not cover all the issues and it could have been compiled in a better way by giving more information or links or better arguments ‘for’ and ‘against’, we think that would be the appropriate time to pat our backs for we successfully managed to compile a ‘Background Guide’ and not a ‘Study Guide’ which most of the Executive Board members fail to differentiate. We feel that ‘study guides’ are detrimental to the individual growth of the delegate since they overlook a very important part of this activity, which is- Research. We are sure however that this background guide gives you a perfect launching pad to start with your research.

Wishing you all a very warm good luck and hoping to see you all at this conference discussing imperative issues of national trust.

Warm Regards,

Girik Kashkari	Manan Sehgal
Chairperson	Vice-Chairperson

Following Is A Suggested Pattern for Researching (If Required):

- Research on the allotted nation, understanding their thinking about the topic.
- Comprehending the foreign policy of the allotted country. It includes understanding the ideology and principles adopted by the nation on the agenda. It further includes studying past actions taken by the nation on the agenda and other related issues – specifically analyzing their causes and consequences.
- Reading the background guide thoroughly.
- Researching further upon the agenda using sources such as academic papers, institutional reports, national reports, news articles, blogs etc.
- Understanding policies adopted by different stakeholders involved in the agenda. Including their position, ideology and adopted past actions.
- Characterizing the agenda into sub-topics and preparing speeches and statements on them. It is the same as preparing topics for the moderated caucuses and their content.
- **Preparing a list of possible solutions and actions that can be adopted on the issue as per your country's policies.**
- Assemble proof/evidence for any important piece of information/allegation you are going to use in committee
- Keeping your research updated using various news sources, especially news websites given in the proof/evidence section.
- Lastly, we would request all the delegates to put sincere efforts in preparation and research for the simulation and work hard to make it a fruitful learning experience for all. Feel free to contact if you have any queries or doubts.
- A lot of members have doubts such as what they are supposed to write or how should they should structure their speech. This is completely up to the member. The maximum we can do is to tell you according to our experiences about how speeches are structured and content chosen for them accordingly.

These are:

- Premise – Analysis – Example
- Problem – Solution – Benefits
- Past – Present – Future Scenario
- What – So what – Now what
- There can be more structures. These are some of them which the members of the Executive Board have seen.

The best way to debate in any format is to clearly state your opinion and justify it with substantive rational sources.

Reiterating, kindly do not limit your research only to these points and feel free to broaden your horizons of the research. This is just a list of topics you should cover and is a reflection of the direction in which we intend to see the flow of debate in the committee.

INTRODUCTION TO WHO

The World Health Organization (WHO) is a specialized agency of the United Nations responsible for international public health. The WHO Constitution, which establishes the agency's governing structure and principles, states its main objective as "the attainment by all peoples of the highest possible level of health." It is headquartered in Geneva, Switzerland, with six semi-autonomous regional offices and 150 field offices worldwide.

The WHO was established by constitution on 7 April 1948, which is commemorated as World Health Day. The first meeting of the World Health Assembly (WHA), the agency's governing body, took place on 24 July 1948. The WHO incorporated the assets, personnel, and duties of the League of Nations' Health Organisation and the Office International d'Hygiène Publique, including the International Classification of Diseases (ICD). Its work began in earnest in 1951 following a significant infusion of financial and technical resources.

The WHO's broad mandate includes advocating for universal healthcare, monitoring public health risks, coordinating responses to health emergencies, and promoting human health and wellbeing. It provides technical assistance to countries, sets international health standards and guidelines, and collects data on global health issues through the World Health Survey. Its flagship publication, the World Health Report, provides expert assessments of global health topics and health statistics on all nations. The WHO also serves as a forum for summits and discussions on health issues.

The WHA, composed of representatives from all 194 member states, serves as the agency's supreme decision-making body. It also elects and advises an Executive Board made up of 34 health specialists. The WHA convenes annually and is responsible for selecting the Director- General, setting goals and priorities, and approving the WHO's budget and activities. The current Director-General is Tedros Adhanom, former Health Minister and Foreign Minister of Ethiopia, who began his five-year term on 1 July 2017.

The WHO relies on contributions from member states (both assessed and voluntary) and private donors for funding. As of 2018, it has a budget of over $4.2 billion, a large part of which comes from voluntary contributions from member states. Contributions are assessed by a formula that includes GDP per capita. In 2018–19, the US contributed 15.9% of the WHO's $5.6 billion budget (additionally, American philanthropist Bill Gates provides 9.4% of the funding through his foundation), the EU and its member states contributed 11%, while China contributed 0.2%. The agency is part of the United Nations Sustainable Development Group.

SECTION-1

UNDERSTANDING ZOONOSES

What are emerging diseases and what are zoonoses?

People and other animals share many microorganisms and diseases; such co-existence is natural, common and important to health. Only a few of these cause diseases. Considering the millions of species of microorganism on Earth, pathogens (microorganisms that harm the host) are extremely unusual. Only about 1,400 microorganisms are known as potential causes of human infections. New diseases in humans can emerge either as a result of a change in the nature or behavior of commensal microorganisms that cause disease, or through infection by novel organisms, usually through contact with animals and the environment, where most microorganisms exist.

About 60 per cent of human infections are estimated to have an animal origin, and of all new and emerging human infectious diseases, some 75 per cent "jump species" from (non-human) animals to people. In high-income countries, direct infection with a zoonosis is probably a rare event, with most described zoonoses happening indirectly, e.g. through insect vectors or, more frequently, via the food system. Domesticated animal species share an average of 19 (range of 5–31) zoonotic viruses with people, and wild animal species share an average of 0.23 (range of 0–16) viruses with people.

So, unsurprisingly, the vast majority of animals involved in historic zoonotic events or current zoonosis are domestic. (livestock, domesticated wildlife and pets), which is logical as the contact rates are high. The emergence of a new wildlife zoonosis is extremely rare, but can be very significant. Around 80 per cent of pathogens infecting animals are "multi-host," meaning that they move among different animal hosts, including occasionally humans. Domestic animals and peri-domestic wildlife also act as bridges for the emergence of human diseases; this can occur in an evolutionary sense, or the animal could serve as a physical transmitter.

Some of these viruses generated in bio-insecure industrial and intensive agricultural systems result in zoonotic forms of the virus. An example is the highly pathogenic avian influenza (HPAI), an important economic disease of domestic poultry that evolves from low-pathogenic viruses that circulate commensally in the environment in wild bird populations. True human pandemic influenza viruses (rather like COVID-19) have a more complex evolution with mixing of viruses in different domestic animal compartments, usually pigs and poultry and interacting with human influenzas to produce highly pathogenic human influenza pandemics.

While we are in the midst of an ongoing pandemic of COVID-19, recent decades have seen other headline-hitting and dramatically destructive novel diseases. Amongst the more prominent examples are: zoonotic influenza (Bird Flu), pandemic human influenza (H1N1), Middle East respiratory syndrome (MERS), and severe acute respiratory syndrome (SARS), most of which have a proven or suspected domestic animal involvement in transmission; only SARS has a suspected peri-domestic wildlife reservoir, though yet unproven. Other diseases, such as re-emerging West Nile fever, yellow fever and Zika virus diseases are indirect zoonoses. In recent decades, emerging diseases of zoonotic origin have had direct costs of more than USD100 billion; it was earlier estimated that if these outbreaks had become human pandemics, the losses would have amounted to several trillion dollars. And this is likely to be the case for the current COVID-19 pandemic. Despite the massive real and potential socio- economic impacts of emerging zoonotic diseases, and despite the general consensus that prevention is better than cure, investments and political will to control them at their source have been insufficient to date.

Emerging diseases are of course hugely problematic, with some becoming *epidemic* (affecting a large number of people within a region), others becoming *pandemic* (spread over several countries and continents and affecting large numbers of people around the world). COVID-19 is now a pandemic spread across the planet, sickening and killing people and sending billions into lockdowns of various kinds as health services struggle to cope and killing hundreds of thousands by June 2020. Also, of great importance to some countries and regions of the world are *endemic* zoonotic diseases.

The so-called “neglected zoonoses” are continuously present in affected (mainly impoverished) populations, yet receive much less international attention and funding than emerging zoonotic diseases. Among the important neglected zoonoses widespread in developing countries are anthrax, bovine tuberculosis, brucellosis, rabies, cysticercosis (pig tapeworm), echinococcosis (hydatid disease), Japanese encephalitis, leptospirosis, Q fever, rabies, Lassa fever virus and trypanosomiasis (sleeping sickness). Most of these are spread by domestic animals, but several have a wildlife interface, or wildlife is of occasional importance (brucellosis, leptospirosis, rabies, alveolar echinococcosis and bat- associated rabies). Only Lassa fever has exclusively a wildlife host (the multi-mammate rat). Neglected zoonoses persist in communities experiencing complex development problems—typically a mix of poverty, poor sanitation, poor access to water and waste removal services, isolation, socio-political insecurity, political marginalization, low literacy levels, gender inequality and degraded natural resources.

These communities often have a high dependence on livestock and high contact with wild or peri-domestic wildlife, which increases their exposure to pathogens. Another often neglected category of diseases with mainly domestic animal origins are those that are foodborne. For poor people, some of the responses made to control outbreaks may inadvertently cause harm, for example by reducing access to animal source food, important for nutrition, as a result of large-scale culling of domestic animals.

Remarkably, a recent study by the World Health Organization (WHO) found the burden of a selection of important food-borne diseases to be comparable to that of “the big three” major infectious diseases: HIV/ AIDS (human immunodeficiency virus-acquired immune deficiency syndrome), malaria and tuberculosis. Between 2018 and 2019, for example, South Africa experienced the world’s largest outbreak of listeriosis, with more than 1,000 laboratory- confirmed cases and more than 200 fatalities of people who got infected after eating contaminated food products

When do zoonoses become human disease outbreaks?

Historically, the emergence of new human diseases from animals has been associated with major societal change. For example, during the Neolithic transition from hunter-gathering to agricultural societies, humans lived shorter lives, ate less and poorer-quality foods, were smaller in size and were sicker than their hunter-gatherer ancestors. With the advent of agriculture, the dramatic rise in population and the settlement of people in close proximity to their waste led to increases in human disease; the domestication of animals led to livestock pathogens jumping species into people, where they became the probable cause of diseases such as diphtheria, influenza, measles and smallpox. Subsequent major plagues or outbreaks, associated with major societal stresses and upheavals, were linked with zoonoses or diseases that had originally jumped species from animals to people, but had subsequently become transmitted mainly from person to person.

The global human population has increased from about 1.6 billion in 1900 to about 7.8 billion today. The population of the domesticated animals that provide people with food, and of pests or “peri-domestic animals” (such as rats) that thrive in new environments created by people, increased in parallel. In general, these exploding human, livestock and pest populations have reduced the size of wildlife populations while paradoxically increasing contacts among people, livestock and wildlife (with more people hunting fewer wild animals in diminished and degraded ecosystems, and an increasing number of human-wildlife conflicts worldwide).

However, this broad-brush picture conceals some great regional and local differences. Some countries have declining rather than expanding human populations. And over the last century, “natural environments” have returned to depopulated rural areas (e.g., parts of the north eastern United States) as small farms proved unviable and farmlands reverted to forested lands.

Despite these exceptions, overall, there have been significant increases in human populations, encroachment of humans and livestock into wildlife habitats, and concurrent massive decreases in natural environments. These changes have important implications for ecosystem, animal and human health alike. One of these consequences is an increase in emerging zoonoses. Many of these diseases are emerging in high-income settings, but there is an increasing trend for these diseases to emerge in low- and middle-income countries.

While still imperfect, our understanding of the factors favouring emerging diseases is growing. For example, one study makes the case that the risk of zoonotic emerging infectious diseases is elevated in forested tropical regions where land use is changing and wildlife diversity, in terms of mammalian species richness, is high.

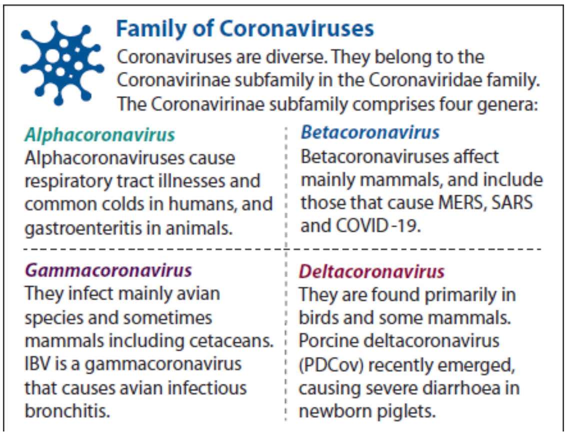
Seven major anthropogenic drivers of the emergence of zoonotic disease

A broad range of studies on zoonotic disease emergence implicates the following seven main drivers of their emergence. Many of these drivers are now occurring in the same places, amplifying their impact. A list of these drivers is provided below.

1) Increasing demand for animal protein
2) Unsustainable agricultural intensification
3) Increased use and exploitation of wildlife
4) Unsustainable utilization of natural resources accelerated by urbanization, land use change and extractive industries
5) Travel and transportation
6) Changes in food supply chains
7) Climate change

SECTION-2

CONORAVIRUSES



Family of Coronaviruses

Coronaviruses are diverse. They belong to the Coronavirinae subfamily in the Coronaviridae family. The Coronavirinae subfamily comprises four genera:

Alphacoronavirus
Alphacoronaviruses cause respiratory tract illnesses and common colds in humans, and gastroenteritis in animals.

Betacoronavirus
Betacoronaviruses affect mainly mammals, and include those that cause MERS, SARS and COVID-19.

Gammacoronavirus
They infect mainly avian species and sometimes mammals including cetaceans. IBV is a gammacoronavirus that causes avian infectious bronchitis.

Deltacoronavirus
They are found primarily in birds and some mammals. Porcine deltacoronavirus (PDCov) recently emerged, causing severe diarrhoea in newborn piglets.

What are coronaviruses?

Coronaviruses are a large group of viruses that infect many animals and humans and are responsible for numerous diseases. They are named “corona” for the crown-like arrangement of the spike-shaped proteins on the surface of their membranes. Some human coronaviruses usually cause mild upper respiratory illness like the common cold. They can also cause serious diseases such as infectious peritonitis in cats and respiratory and enteric infections in cattle. The only known serious human coronavirus diseases are SARS, MERS, COVID-19, and possibly the Asian Flu from the late 19th century; all are likely to have zoonotic origins. In addition to these well-known, sporadic, locally important and long-established diseases, there have been at least six major outbreaks of novel coronaviruses in the last century, all of which imposed high costs across several continents:

1. **Infectious bronchitis virus (IBV)** causes infectious bronchitis in poultry. It emerged in the 1930s and is still one of the main causes of economic losses in the poultry industry, with repeated waves of disease caused by different strains.

2. **Transmissible gastroenteritis (TGE)** virus was first reported in the United States in 1946 and subsequently spread to Europe, Africa, South America and China.

3. **Porcine epidemic diarrhea (PED)** virus emerged in 1971 as a pig disease causing a global pandemic of enormous cost and is still a major

problem in piglets. Since then different strains have caused waves of disease in Asia, Europe and the Americas.

4. **SARS-CoV**, the coronavirus that causes severe acute respiratory syndrome, or SARS, was first reported in China in February 2003 and likely originated from bats, probably then spreading to other animals (likely civet cats) and then to humans. The illness then spread to more than two dozen countries in North America, South America, Europe and Asia before it was contained. Over 8,000 cases were reported and nearly 800 people died of the disease. Since 2004 there have not been any reported cases.

5. **MERS-CoV**, the coronavirus that causes Middle East respiratory syndrome, or MERS, was first reported in Saudi Arabia in 2012 and has a higher mortality rate than SARS. MERS-CoV can occur zoonotically from human contact with camels but has secondary cycles of spread from ill people to other people through close contact. To date, there have been around 2,500 laboratory confirmed cases mostly human to human, of which more than one third proved fatal. Sporadic cases continue to occur as the infection remains present in dromedary camels.

6. **SARS-CoV-2**, the coronavirus that causes a severe acute respiratory syndrome known as COVID-19, already has had its genome compared to the genetic sequences of more than 200 other coronaviruses from around the world that infect various animals. SARS- CoV-2 appears to be a recent mix, or genetic recombination, of coronaviruses.57 As a result of this recombination, one of the proteins of SARS-CoV-2 enables the virus to enter the cells of humans. Other research has shown the virus to be 96 per cent identical to a previously identified bat coronavirus, with a common ancestor about 50 years ago. It is hypothesized that this is the origin of the unknown pathway that resulted in the transmission of SARS-CoV-2 to humans in 2019

Common elements and origins of coronavirus pandemics

The six coronavirus pandemics share some of the following common elements.

1. **Bats**: - Bats are natural reservoir hosts as well as vectors of many microbes that can affect animals and people. Contact between bats and other animals, including humans, allows for inter-species transmission of the pathogens they harbour, potentially resulting in disease outbreaks. Most of the recent coronavirus pandemics have been hypothesized to have an initial origin in bats. More than 200 novel coronaviruses have been found in bats and they are likely the source and natural hosts for all coronavirus lineages. Bats are also associated with many other important zoonoses such as Ebola, Nipah (via bridging with pigs or indirectly through contamination of domesticated plants) and very rarely rabies. Bat species harbour at least 61 potential zoonotic viruses

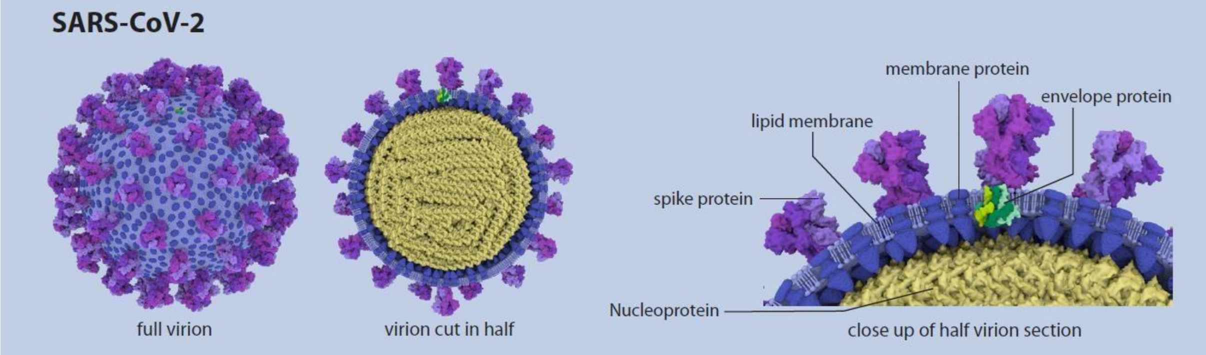
2. **Agricultural intensification and increased demand for animal protein: -** These coronavirus disease outbreaks followed rapid intensification of agricultural practices and systems, and dramatic changes in the ways animals were kept or farmed, many of which were made without proper precautionary measures being taken. SARS-CoV and SARS-CoV-2 may be associated with wildlife harvest, trade practices and the intensification of wildlife farming in East Asia. The latter has been actively encouraged in some countries; by 2006, nearly 20,000 wildlife breeding and farming ventures were established in China. As wealthy consumers tend to prefer wild-caught animals, the meat from these farms is often consumed by China's rapidly growing middle class. MERS-CoV was associated with increases in dromedary camel numbers and a shift from extensive to intensive camel production systems. An analysis of potential drivers of MERS-CoV emergence in Qatar suggests that the socio-economic transformation in the last three decades and the growing popularity of camel racing triggered major changes in camel

farming practices. Camels were raised in designated camel complexes in a high-density environment alongside the workers who fed and took care of them. Races and contests in the Gulf region also required camels to travel frequently and extensively, both across borders and within the country. These factors played an important role in the transmission of MERS-CoV from camels to humans.

3. **Traditional markets:-** Both SARS-CoV and SARS-CoV-2 have been associated with traditional informal markets or fresh produce markets (sometimes called wet markets). SARS-CoV was associated with civet cats sold in informal markets. SARS-CoV-2 has been associated with a traditional food market where wildlife was purported to be sold.

4. **High economic costs: -** All six coronavirus pandemics (IBD, PED, TGE, SARS, MERS, COVID-19) have had high economic costs and, for some diseases, very high animal mortality rates. The huge health impacts of this new coronavirus necessarily imply enormous economic impacts. The International Monetary Fund predicts that the global economy will shrink by 3 per cent in 2020, a downgrade of 6.3 percentage points from estimates in January 2020. The Fund also estimates that over the next two years, cumulative output losses from the COVID-19 pandemic could reach USD9 trillion.

Understanding SARS-CoV-2



SARS-CoV-2 is an enveloped virus, meaning that its RNA is packaged within an outer **lipid (fatty) membrane**. The lipid membrane is stable enough to protect the RNA from the surrounding environment, but also able to break open inside the host cell to release the RNA. This balance means the membrane is susceptible to being destroyed by detergent.
The membrane contains several virus proteins.

The large **spike (S) proteins** allow the virus to bind to and enter host cells. The distinctive 'corona' of spikes gives the virus its name. Seven human coronaviruses have been identified so far, of which three are capable of invading deep into the lungs and causing more severe disease. One possible reason is that the S protein of SARS-CoV-2, like SARS-CoV (the virus responsible for SARS), binds to ACE- 2 receptors on human cells. ACE-2 receptors are found throughout the body but are particularly concentrated in the upper and lower airways of the lungs. SARS-CoV-2 also binds to ACE2 particularly well. It is 10–20 times more likely to bind ACE2 than SARS-CoV.

The **membrane (M) proteins** give shape and integrity to the virus particle. They are also thought to help assemble new virus particles inside the host cell. The **envelope (E) proteins** are thought to assist virus growth and ability to cause disease. They may form small pores that alter the properties of the host membranes, prevent M protein from clumping together, and assist in assembly of new viral particles inside the host cell.

Inside the viral envelope is the viral RNA, which is bound to the nucleoprotein (N). N proteins form a tight spiral that wraps and coils the RNA, protecting it from damage. When the RNA is first released into the host cell, the N protein also reduces the host cell's natural defences against the virus.

The coronavirus **RNA** molecule is 30,000 'letters' long, making it one of the largest RNA viruses discovered. While RNA viruses have a high mutation rate, coronaviruses also possess a genomic proofreading mechanism. This can keep them from accumulating negative mutations that would weaken them. Coronaviruses can also swap blocks of RNA with each other, potentially trading useful mutations.

While the new coronavirus likely originated from bats, it is not yet known whether or which mutations allowed this jump from animals to humans. The RNA of SARS-CoV-2 is 96% similar to a virus found in a bat in China. However, the bat virus contains key differences in its S protein, and is not able to infect humans. It is also likely that SARS-CoV-2 viruses will contain **host cell proteins** from previous host cells. The virus also makes additional proteins following host cell entry that allow it to multiply and make new virus particles. In addition to vaccine efforts targeting the S-protein on the virus particle, these intra-cellular proteins are potential targets for intervention.

1931

Avian infectious bronchitis

Pathogen: Infectious bronchitis virus (IBV)
Genus: *Gammacoronavirus*
Host: Chickens
Place of emergence: North Dakota, USA

IBV causes an acute, highly contagious respiratory disease in chickens. It can also damage the reproductive tract, causing decreased egg quality and production. First documented in USA, the disease is now prevalent in all countries with an intensive poultry industry.

1971

Porcine epidemic diarrhoea (PED)

Pathogen: Porcine epidemic diarrhoea virus (PEDV)
Genus: *Alphacoronavirus*
Host: Pigs
Place of emergence: United Kingdom

Following the first appearance in the UK, it spread to other European countries and Asia. A highly virulent PEDV strain emerged in 2013 and caused nationwide outbreaks in the US, and rapidly spread to North, Central and South American countries. The virus is not zoonotic and poses no risk to humans, or food safety.

2003

Severe acute respiratory syndrome (SARS)

Pathogen: SARS coronavirus (SARS-CoV)
Genus: *Betacoronavirus*
Natural reservoir: Horseshoe bats
Intermediate host: Masked civet cats
Place of emergence: Guangdong, China

This pneumonia-like infection spread from Guangdong, China, to more than 26 countries in Asia, Europe, North America and South America before it was contained. SARS-like coronavirus has been found in horseshoe bats, suggesting that bats are natural reservoirs.

2012

Middle East respiratory syndrome (MERS)

Pathogen: MERS coronavirus (MERS-CoV)
Genus: *Betacoronavirus*
Natural reservoir: Probably bats
Intermediate host: Dromedary camels
Place of emergence: Saudi Arabia

First reported in Saudi Arabia, MERS has spread to 27 countries with a large outbreak in Korea in 2015. A study in 2018 shows high prevalence of MERS-CoV strains in local camels in Saudi Arabia, compared to imported camels from Africa.

2016

Swine acute diarrhoea syndrome (SADS)

Pathogen: SADS coronavirus (SADS-CoV)
Genus: *Alphacoronavirus*
Natural reservoir: Probably bats
Host: Pigs
Place of emergence: Guangdong, China

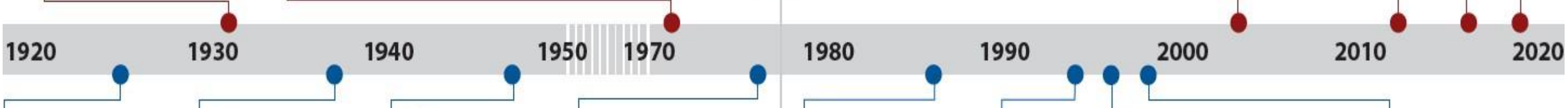
SADS-CoV caused severe and acute diarrhoea and vomiting in newborn piglets. The outbreak killed nearly 25,000 piglets in Guangdong. Case fatality ratio: 90% in piglets less than five days old. This coronavirus did not appear to jump to humans.

2019

Coronavirus disease 2019 (COVID-19)

Pathogen: SARS-CoV-2
Genus: *Betacoronavirus*
Natural reservoir: Probably bats
Intermediate host: Unknown
Place of emergence: Wuhan, China

SARS-CoV-2 appears to be a recent mix, or genetic recombination, of two coronaviruses. Genome sequencing suggests that SARS-CoV-2 is 96% identical to a coronavirus in horseshoe bats.



1920s

Human Immunodeficiency Virus (HIV) infection

Pathogen: HIV
Genus: *Lentivirus*
Natural reservoir: Chimpanzee for HIV type 1, and Sooty Mangabey for HIV type 2
Place of emergence: Kinshasa, Democratic Republic of Congo

Based on genetic sequencing and historical records, the emergence of HIV is traced back to 1920s in Kinshasa, DRC. It is thought that simian immunodeficiency viruses (SIVs) in primates crossed over to humans at the time, presumably as a result of hunting and meat consumption. SIVs then adapted to the new human host to become HIV.

1937

West Nile fever

Pathogen: West Nile virus
Genus: *Flavivirus*
Host: Birds
Place of emergence: West Nile district, Uganda

Mosquitoes serve as disease vectors carrying the virus from infected birds to people and some mammals. Humans are usually incidental and dead-end hosts for the virus. The first recognized outbreak occurred in Israel in 1951, then Egypt. The virus re-emerged in Romania in 1996, and has established itself in the US since 1999. West Nile virus belongs to the same genus as dengue virus and yellow fever virus.

1947

Zika virus disease

Pathogen: Zika virus (ZIKV)
Genus: *Flavivirus*
Natural reservoir: Primates including humans
Place of emergence: The Zika forest, Uganda

ZIKV was first discovered in a febrile sentinel rhesus monkey from the Zika forest, and in the *Aedes africanus* mosquito from the same forest a year later. The first human cases were detected in Uganda and Tanzania in 1952. An outbreak occurred in the Yap Islands, Federated State of Micronesia in 2007, followed by a major epidemic in the Americas in 2015-16.

1976

Ebola virus disease

Pathogen: Ebola virus
Genus: *Ebolavirus*
Natural reservoir: Unconfirmed but likely to be African fruit bats of the *Pteropodidae* family
Intermediate host: Apes and monkeys
Place of emergence: Two simultaneous outbreaks in Democratic Republic of Congo (DRC) and South Sudan

The largest outbreak in history occurred primarily in Guinea, Liberia and Sierra Leone from 2014 to 2016, killing 11,323 people. The virus also recently re-emerged in eastern DRC from 2018 to 2019. Case fatality ratio of Ebola varied from 25% to 90%.

1986

Bovine spongiform encephalopathy or mad cow disease

Agent: Pathogenic prions
Host: Cattle
Place of emergence: United Kingdom

Mad cow disease is a progressive, fatal neurological disorder in cattle. The human form of the mad cow disease known as variant Creutzfeldt-Jakob disease is linked to consumption of beef from cattle infected with the disease.

1994

Hendra virus infection

Pathogen: Hendra virus
Genus: *Henipavirus*
Natural reservoir: Large fruit bats (*Pteropus* spp.) or flying fox
Host: Horses
Place of emergence: Hendra, Australia

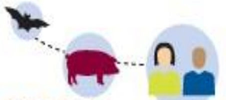
Sporadic outbreaks have occurred in Australia over the years since its initial appearance in 1994. So far, no cases have been reported outside Australia. Case fatality ratio is 75% in horses, and 50% in humans. Hendra virus belongs to the same genus as Nipah virus.

1996

Highly pathogenic avian influenza (HPAI) or bird flu

Pathogen: HPAI virus subtype H5N1
Genus: *Alphainfluenzavirus*
Natural reservoir: Wild waterfowl
Host: Poultry
Place of emergence: Guangdong, China

First human cases found in Hong Kong in 1997 were traced back to wild and domestic waterfowl in Guangdong in 1996. Re-emerging in Hong Kong in 2002, the virus spread rapidly to South East Asian countries. Over 100 million domesticated chickens and ducks either died of the disease or were culled to stop the outbreak in Asia.



1998

Nipah virus infection

Pathogen: Paramyxovirus
Genus: *Henipavirus*
Natural reservoir: Large fruit bats (*Pteropus* spp.) or flying fox
Host: Pigs
Place of emergence: Guangdong, China

Nipah virus emerged as a respiratory and neurologic disease in pigs, and then spread to humans. A large outbreak in Malaysia from 1998 to 1999 was followed by five outbreaks in Bangladesh from 2001 to 2005. To control the outbreak in Malaysia, at least one million pigs were culled.

SECTION-3
COMBACTING ZOONOSES

The 3 Approaches

One Health approach can be defined as the collaborative effort across multiple disciplines to attain optimal health for people, animals and the environment. This approach has emerged as a key tool for preventing and managing diseases occurring at the interface of human, animal and environment health. At the same time, a closely related approach, known as "EcoHealth" has been defined as a set of systemic, participatory approaches necessary to understanding and promoting both health and well-being in the context of social and ecological interactions. Both the One Health and EcoHealth approaches emphasize multidisciplinary collaboration for holistic interventions that attain not only human health goals but also animal and environment health targets, the latter two of which are central to improving the control of neglected and emerging infectious diseases, many of which are zoonoses. A third concept, "Planetary Health," focuses on human health in relation to global sustainability.

One health aspects of zoonoses control and prevention

Controlling and preventing zoonotic outbreaks requires coordinated interdisciplinary responses across human, animal and environment health. zoonoses are complex; responsibility for their prevention and control falls across several sectors— environment, agriculture, health, trade and commerce. Approaches to dealing with these diseases to date have been inadequately coordinated across these multiple dimensions. Institutionally speaking, zoonoses can find themselves outside conventional health fields (falling between different siloed sectors of human and veterinary health) and, in the worst cases, ignored. One Health thinking and research offers an approach to break down. traditional sectoral barriers to achieve effective control of zoonoses. A promising development in the wake of the bird flu pandemic is the establishment of joint zoonoses working groups in many countries and other international collaborations. Successful control of zoonoses requires strong policy frameworks and judicious legal mechanisms to accompany policy frameworks. It also demands well-functioning institutions that have adequate capacity, adequate financing and a clear plan for implementing interventions.

In the case of emerging diseases, up-front investments in surveillance and in coordinated human, animal and environment health services are needed to ensure that 'emergence events' do not turn into full-scale epidemics, or pandemics. In economic terms, the World Bank estimated eight years ago that an annual investment of USD3.4 billion in animal health systems worldwide would avert losses incurred through delayed or inadequate responses to zoonoses— losses estimated at almost double the preventative investment.

The loss of human life, and economic and social costs of the COVID-19 crisis clearly indicate the value—and the necessity— of increased investment in surveillance, prevention measures and coordinated cross-sectoral early response to ensure we do everything possible to prevent this from happening again. Improved interdisciplinary science will help to inform the prevention and control of zoonotic diseases. It is important not to study pathogens in isolation, but rather to better understand how human social behavior impacts the natural world, as well as the emergence and spread of disease. These relations are non-linear and involve complex systemic relationships that must be factored into both research and effective decision-making.

Success will require addressing the root causes and drivers of disease emergence, which in turn will require changing our behavior and our actions in relation to ecosystems. While some of the basic ecological factors of disease emergence are known, these factors need to be integrated fully into country-level surveillance and response programmes with relevant expertise included in inter-sectoral teams. Many zoonotic diseases can occur along with other infectious diseases within a given environment or host. This can complicate disease management if each pathogen requires a different measure to control it. It is also critical to understand these interactions and identify opportunities to control multiple pathogens or vectors with a single intervention.

Interventions at the human-livestock interface

Many zoonoses can be best tackled through interventions involving the livestock hosts of the disease pathogens. Improved and sustained collaboration between medical, veterinary and wildlife authorities is necessary to improve surveillance and control of zoonotic diseases.

While these authorities may come together during a crisis to collaborate and share resources, as is the case now where many veterinary laboratories are supporting testing for the current novel coronavirus, these collaborations are not fully institutionalized and often discontinue in non- crises periods. Intensive livestock production systems would benefit from stringent biosecurity and veterinary control measures. Extensive livestock production systems, including pastoralism, can provide proteins efficiently while also providing environmental co-benefits and reduced zoonotic disease risk.

The control of coronavirus and other zoonotic infections in farmed domestic animals, captured wild animals and companion animals is difficult in many developing countries. This generally requires combined applications of vaccines, biosecurity protocols, movement controls, slaughter of affected animals and quarantine of premises, and husbandry management, among other measures.

Early warning systems and monitoring wildlife

Animal and environmental indicators can provide a valuable tool for disease early warning systems:

- Monitoring microbial diversity in wildlife, either in a given region or certain species, can be a good indicator for detecting potential disease outbreaks, particularly for coronaviruses, filoviruses and paramyxoviruses.

- Consistent monitoring of wildlife morbidity or mortality events can also provide indicators of active circulation of disease or outbreaks. For example, an investigation of dead howler monkeys found near a wildlife sanctuary in Bolivia led to the detection of yellow fever virus. This provided vital alert information and activation of vaccination campaigns to prevent human cases.

- Sentinel surveillance approaches that select a smaller and targeted group of health workers to gather data have been utilized effectively to get ahead of potential spillover events for the detection of West Nile virus in birds and equids, Ebola virus in great apes, and monkeypox in chimpanzees in Cameroon.

- Targeted environmental indicators may also be useful for forecasting risk alerts. Examples have included prolonged periods of rainfall, which are associated with elevated risk of Rift Valley fever outbreaks in some regions, or flooding events, which are associated with leptospirosis.

- As certain species are known to serve as hosts or transmitters of zoonotic diseases, monitoring species distribution can offer important indications of potential risks to human health. For example, a change in species range or introduction of invasive species that has the potential to serve as a host can signal potential risks.

- Consistent monitoring and sharing of this information among wildlife, livestock and human health agencies is important to improve risk assessment and prevention for zoonotic disease threats.

Some Key Policy Recommendations

- **AWARENESS:** Raise awareness and increase understanding (knowledge) of zoonotic and emerging disease risks and prevention (where appropriate), at all levels of society to build widespread support for risk-reduction strategies.

- **GOVERNANCE:** Increase investments in interdisciplinary approaches including the One Health perspective; strengthen the integration of environmental considerations in the World Health Organization (WHO)/Food and Agriculture Organization (FAO)/World Organization for Animal Health (OIE) Tripartite Collaboration.

- **SCIENCE:** Expand scientific enquiry into the complex social, economic and ecological dimensions of emerging diseases, including zoonoses, to assess risks and develop interventions at the interface of the environment, animal health and human health.

- **FINANCE:** Improve cost-benefit analyses of emerging diseases prevention interventions to include full-cost accounting of societal impacts of disease (including the cost of unintended consequences of interventions) so as to optimize investments and reduce trade-offs. Ensure ongoing and well-resourced preparedness and response mechanisms.

- **MONITORING AND REGULATION:** Develop effective means of monitoring and regulating practices associated with zoonotic disease, including food systems from farm to fork (particularly for removing structural drivers of emergence) and improving sanitary measures, taking into account the nutritional, cultural and socio-economic benefits of these food systems.

- **INCENTIVES:** Include health considerations in incentives for (sustainable) food systems, including wildlife source foods. Augment and incentivize management practices to control unsustainable agricultural practice, wildlife consumption and trade including illegal activities). Develop alternatives for food security and livelihoods that do not rely on the destruction and unsustainable exploitation of habitats and biodiversity.

- **BIOSECURITY AND CONTROL:** Identify key drivers of emerging diseases in animal husbandry, both in industrialized agriculture (intensive husbandry systems) and smallholder production. Include proper accounting of biosecurity measures in production-driven animal husbandry/livestock production to the overall cost of One Health. Incentivize proven and under-used animal husbandry management, biosecurity and zoonotic disease control measures for industrial and disadvantaged smallholder farmers and herders (e.g. through the removal of subsidies and perverse incentives of industrialized agriculture), and develop practices that strengthen the health, opportunity and sustainability of diverse smallholder systems.

- **AGRICULTURE AND WILDLIFE HABITATS:** Support integrated management of landscapes and seascapes that enhance sustainable co-existence of agriculture and wildlife, including through investment in agro-ecological methods of food production that mitigate waste and pollution while reducing risk of zoonotic disease transmission.

  Reduce further destruction and fragmentation of wildlife habitat by strengthening the implementation of existing commitments on habitat conservation and restoration, the maintenance of ecological connectivity, reduction of habitat loss, and incorporating biodiversity values in governmental and private sector decision-making and planning processes

- **CAPACITY BUILDING:** Strengthen existing and build new capacities among health stakeholders in all countries to improve outcomes and to help them understand the human, animal and environment health dimensions of zoonotic and other diseases.

- **OPERATIONALIZING THE ONE HEALTH APPROACH:** Adequately mainstream and implement the One Health approach in land-use and sustainable development planning, implementation and monitoring, among other fields.