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LEARNING OBJECTIVES

1. Identify characteristics of emerging infectious diseases (EIDs).
2. Identify the most important variable driving EIDs.
3. Identify 11 major factors associated with EIDs.
4. Recognize the role of travel and trade in EIDs.
5. Match animals to the organism or disease transmitted by them.
6. Match the mortality rates for each EID.
7. Recognize the economic impact of infectious disease.
8. Identify the agent likely to cause the next pandemic and the suggested mechanism for its pathogenicity.

The nature of emerging zoonotic diseases: ecology, prediction, and prevention

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 and **Lisa M. Schloegel, BA**

The world is experiencing a period of unprecedented infectious disease emergence.^{1,2} Nearly half of all human infectious diseases known today can be classified as emerging.³ These are diseases that 1) have been newly discovered; 2) have recently increased in incidence or prevalence; 3) have recently expanded in geographic or climatologic range; or 4) have jumped from animal populations into humans. This differs somewhat from re-emerging infectious diseases, which are diseases that have been discovered previously in a species and are often at enzootic levels in that species but, for some reason, have significantly increased in incidence at a given point in time or in a specific geographic region. Of those pathogens classed as emerging, approximately 75% are zoonotic, or of animal origin.³ HIV, SARS (severe acute respiratory syndrome), monkey pox, Nipah virus, Avian influenza, and West Nile virus are examples of emerging infectious diseases (EIDs) that have spilled over from animal reservoirs into humans.

The human dimension

Regarding drivers of EIDs, a multitude of important variables can play a role; however, the most important variable is a change in the pathogen-host relationship — a change often associated with anthropogenic activities or a result of increasing human population densities.⁴⁻⁷ Major factors associated with emergence of diseases include 1) human population expansion; 2) human encroachment on natural habitats; 3) international travel and commingling of humans and wildlife; 4) modification of ecological systems and habitats; 5) deforestation; 6) intensification of agricultural practices; 7) cohabitation of agricultural species and wildlife; 8) inadvertent or

intentional movement of wildlife species or pathogens from natural habitats to different geographic locations — both natural or urban centers where wildlife trade exists; 9) global climate change; 10) weather patterns; and 11) extensive antimicrobial use and resistance.^{4,5,8-19}

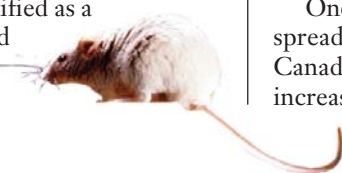
The use of antimicrobial agents over time has selected for resistant pathogens, which are increasingly difficult to treat (e.g., multidrug-resistant tuberculosis, *Staphylococcus*, and HIV).²⁰⁻²² Deforestation has facilitated disease emergence both through increased “bush-meat” trade and by creating altered habitats that promote insect vector proliferation (e.g., mosquitoes) and transmission of malaria.^{23,24} Logging routes carved into primary forest habitats have provided easier access for hunters in search of animals to eat or sell. The local and international trade in bush meat has led to the spillover of various zoonotic viruses, some of which are known to cause significant human mortality (e.g., HIV, Ebola virus, and SARS).²⁵⁻²⁷

Genetic analysis points to an animal reservoir for SARS CoV, but the true wildlife reservoir remains to be identified.

Many EIDs today, although only recently discovered, have likely existed for hundreds or even thousands of years (e.g., HIV, SARS CoV, Nipah virus, and Ebola virus). Many of these pathogens probably coevolved with their natural host species to the point of mutualism, where they are transmitted readily between individuals within a population but do not cause significant morbidity or mortality to that species. These pathogens often have lethal consequences once they spill over into naïve species. This highlights the dangers of one of the most pervasive human activities that can facilitate disease emergence: global travel and trade. People, animals, and pathogens can travel across the world in less than 24 hours, bringing together species of animals and microbes that have never before met, allowing for transmission from one species to another. The live markets in Guangdong, China, where SARS emerged, are a perfect illustration of what can happen when a variety of different species from points both within and outside the local area are brought together, densely housed, and commingled with humans. This outbreak occurred in China, but the same market conditions exist in many other countries around the world, providing meeting places for many pathogens and novel host species, including humans.

SARS: Wildlife trade, wet markets, and global travel lay the groundwork for a potential pandemic

The 2003 SARS outbreak provides an example of a virus that emerged from an animal reservoir, spread globally, and might have resulted in an even greater pandemic had scientists not acted in concert to identify and control the spread of this lethal pathogen. SARS was identified as a coronavirus and traced back to masked palm civets (*Paguma larvata*) sold in live animal markets in southern China.²⁷



Outbreak response vs. prevention: Discovering emerging pathogens is only half the battle. Predicting disease outbreaks and protecting human and animal health is the ultimate goal.

How do epidemiologists handle an outbreak of a disease that has never been seen before? There have been many lessons learned over the years, but SARS may be the best example of a disease that recently emerged with the potential to become a global pandemic. When SARS emerged in China, followed by Canada, it took a global collaboration of epidemiologists, molecular biologists, diagnosticians, and virologists to identify the coronavirus that causes this disease. Subsequently, this team of experts needed to break the chain of transmission between animals and humans and among people in China and Toronto. The search is still ongoing for the natural reservoir of the SARS coronavirus — a key piece of information necessary to prevent future outbreaks of this lethal pathogen.

Disease ecologists working in the field of conservation medicine draw on a multitude of scientific disciplines (e.g., human and veterinary medicine, ecology, mathematics, virology, epidemiology, and climatology, to name a few) to study the reasons *why* pathogens have emerged in both human and wildlife populations.^{47,50,51} Some major drivers of disease emergence are related to human or anthropogenic factors: antimicrobial use (leading to resistant pathogens), agricultural expansion, deforestation and habitat destruction, urbanization, and bush-meat and wildlife trade. Many of these activities alter the natural habitat and ecology of animals and increase the interface between humans, domestic animals, and wildlife.

Pathogens that evolved with wild animal hosts typically do not cause disease in these animals, making them natural reservoirs. When these species interact with other species that are naïve to the pathogens, the result can be devastating. Conservation medicine scientists at the Wildlife Trust and the Consortium for Conservation Medicine focus on the health of ecosystems, wildlife, and humans, with an emphasis on the ecology of pathogens like SARS, Nipah virus, West Nile virus, and Avian influenza.

How these pathogens jump from wildlife — their natural host species — to humans is a major focus of research. By understanding how pathogens behave in nature, we are starting to learn how human behavior, land-management decisions, and ecological degradation are contributing to increased prevalence of disease in both humans and wildlife. The goal of our research is to understand disease emergence and drivers of disease. Equally important is the need to identify how to prevent diseases, prevent further ecological damage that contributes to emergence of new infectious diseases, and at the same time, balance the needs of wildlife and humans in a world of limited resources and increasing human densities.

Although the civets were originally implicated as the reservoir for SARS, scientists now believe that they were only incidental hosts, having been infected with SARS CoV around the same time as humans.^{27,28} Genetic analysis points to an animal reservoir for SARS CoV, but the true wildlife reservoir remains to be identified.^{28,29}

Once SARS CoV entered the human population, it quickly spread within Guangdong province and beyond China to Canada. Public health measures, including quarantine and increased surveillance at airports and hospitals, allowed the

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Anthropogenic threat to wildlife populations

In recent years, scientists have begun to pay particular attention to the threats EIDs pose to wildlife populations in addition to human populations. Infectious diseases are thought to be linked to the extinctions of various endemic Hawaiian bird species, the thylacine and, indirectly, the eelgrass limpet.^{52,56} Population crashes of the black-footed ferret, African wild dogs, and amphibian populations worldwide are also attributed to EIDs — contributing to a significant loss of biodiversity in those species.^{57,58} It has become increasingly clear that anthropogenic factors altering natural ecosystem processes threaten the health of both the human and wildlife communities.

outbreak to be slowed and eventually contained, but not without great economic cost to China, Canada, and the airline industry (Figure 1).³⁰⁻³² The SARS outbreak illustrates both the increased risk of pathogen exchange when wild and domestic animals are brought together at high density and the significant economic costs of emerging diseases.

Nipah virus: Agricultural intensification, coupled with habitat loss, increases the human to domestic animal to wildlife interface

Agricultural expansion and intensification is another anthropogenic factor that can facilitate disease emergence, as it brings domestic animals and humans in closer contact with wild animals and their pathogens.⁷ The emergence of Nipah virus in Malaysia in 1998 is an example of domestic animals playing an integral role in the transmission of a lethal zoonotic pathogen. Nipah virus emerged as a respiratory and neurological disease in pigs in northern Malaysia in 1998 and spread rapidly throughout Malaysia and Singapore through the movement of infected pigs between farms.^{33,34} Nipah virus infected over 265 people, most of whom worked on pig farms or had contact with infected pigs.³⁵ Forty percent of those infected with Nipah virus died, making it one of the more lethal EIDs (SARS carries a case fatality rate of 9.6%, Ebola up to 80%).^{36,37}



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Pig farming is not a new practice in Malaysia; however, the majority of farms have been small operations, generally consisting of fewer than a thousand head of pig (Jamaluddin, personal communication). The farm on which Nipah virus emerged was among the largest in Malaysia, with over 30,000 head of pig. Nipah virus is a density-dependent pathogen, requiring a minimum, or “threshold,” density of susceptible individuals to persist within a population. The population size and density of the pigs on the index farm, as well as the high rate of immigration of young, immunologically naïve pigs

from other farms, played a significant role in maintaining the virus in this population (Pullium, unpublished). The Nipah virus outbreak was devastating to the Malaysian pig industry, as over 1 million pigs were culled and hundreds of farms were closed in order to contain the spread.³³ But how did Nipah virus infect the pigs in the first place?

The reservoir for Nipah virus was determined to be two native species of large fruit bats, or, “flying foxes,” from the genus *Pteropus* (Abdul Rahman, unpublished data).^{38,39} Pteropid bats feed on pollen, nectar, and fruit, and are important seed dispersers and pollinators of rain forest trees.^{40,41} Flying foxes utilize orchards as food resources, particularly where native fruit availability may be limited due to deforestation or drought.^{42,43, 44} The index farm where the first porcine cases occurred also contained large fruit orchards, which provided a ready food resource for flying foxes and other fruit bats. The farm is located in a valley adjacent to primary rain forest in which there are seasonal roosts of flying foxes (Epstein, unpublished). Some of the fruit trees grew over the open enclosures where pigs were housed. Bats infected with Nipah virus most likely fed in these trees and dropped pieces of fruit covered with their saliva (one of the main routes of excretion for Nipah virus) into the pigs’ stalls.⁴⁵ Although Nipah virus does not cause clinical disease in flying foxes, it caused a severe respiratory and neurological disease in the domestic pigs. The pigs amplified and aerosolized the virus, allowing it to subsequently infect farm workers.^{34,35,46} Thus, agricultural expansion into wildlife habitat, high densities of domestic animals, and the general loss of native food resources due to deforestation all contributed to the emergence of one of the most lethal zoonotic viruses yet discovered.



Viral adaptations to invade new hosts

In addition to ecological changes or anthropogenic-associated drivers of disease, EIDs can also result from genetic mutations in viruses or a recombination of genetic material of similar viruses. According to Burke, many recent human viral epidemics and pandemics have resulted from genetic recombination or genetic reassortment of RNA viruses. Viral diseases such as HIV/AIDS, hemorrhagic fever, and hantavirus pulmonary syndrome are all human diseases that likely resulted from viruses spilling over from animal hosts into humans.² Once a pathogen jumps from its natural host species to a new species, it may or may not adapt to include humans in its life cycle (e.g., HIV).⁴⁷ There is a vast pool of zoonotic pathogens in wildlife. In fact, we only know of about 1% of the viruses in animals that may infect humans.⁴ While some zoonotic pathogens will cause small-scale outbreaks when they jump into humans, some have the potential to create major pandemics (see sidebar, “Anthropogenic threat to wildlife populations”). The challenge for conservation medicine scientists is to understand whether a



specific pathogen has the necessary properties to establish itself in a human population.

Avian influenza: Is it a matter of time before our next pandemic?

One RNA virus of concern is the Avian influenza virus, from the family *Orthomyxoviridae*, which has caused historic pandemics (strains H3N2 and H1N1) and is the virus most likely to cause the next global pandemic, specifically the highly pathogenic H5N1. Outbreaks of H5N1 influenza occurred among poultry in eight countries in Asia (Cambodia, China, Indonesia, Japan, Laos, South Korea, Thailand, and Vietnam) during late 2003 and early 2004. More than 100 million birds either died from the disease or were killed to try to control the outbreak — economically significant in the poultry industry. In June 2004, new deadly outbreaks of H5N1 influenza among poultry were reported in Cambodia, China, Indonesia, Malaysia, Thailand, and Vietnam.⁴⁸

Currently, H5N1 is believed to be carried by migratory waterfowl that are not affected by the disease but can transmit it to domestic birds, such as chickens, ducks, and turkeys, in which it is quite debilitating and lethal. Infected birds shed

the virus in their saliva, nasal secretions, and feces; when other susceptible birds become exposed to these secretions, they become infected, providing for rapid disease spread through

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heavily concentrated poultry flocks. Most human cases of Avian influenza have probably resulted from contact with infected poultry or contaminated surfaces, resulting in a 50% case fatality rate. A few sporadic cases of human-to-human disease transfer may have occurred; however, conclusive evidence is not yet available.⁴⁸

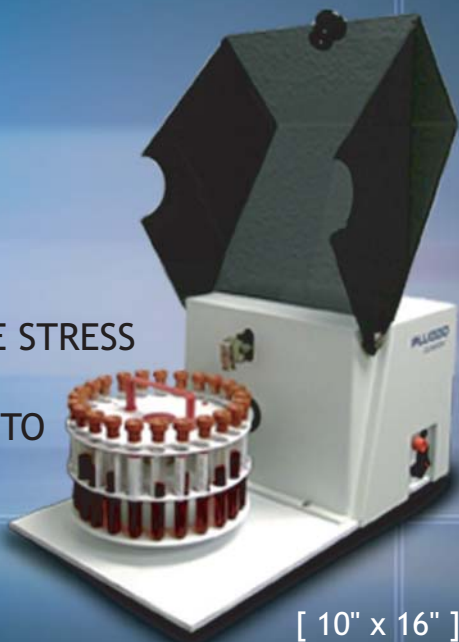
Historically, Avian influenza has impacted millions of humans and is the candidate most likely to result in the next human pandemic for a variety of reasons. What makes it so dangerous to humans is that Avian flu is capable of mixing genetic material from both animal influenza viruses and human



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influenza viruses. If this occurs in the case of H5N1, the resulting virus could be transmitted among people and therefore could result in a global pandemic.⁴⁹ Furthermore, spontaneous mutations that occur in human influenza viruses often evade immunization efforts. If genetic recombination occurs, the resulting disease potentially could be transmitted among humans who likely will have no previously acquired immunity to the new strain. Transmission would be rapid, and expected morbidity and mortality rates would be high. In fact, the Centers for Disease Control and Prevention in Atlanta predict that a pandemic would likely result in 2 to 7.4 million deaths globally, with a demand for 134

to 233 million outpatient hospital visits and 1.5 to 5.2 million hospital admissions.

The economics of EIDs

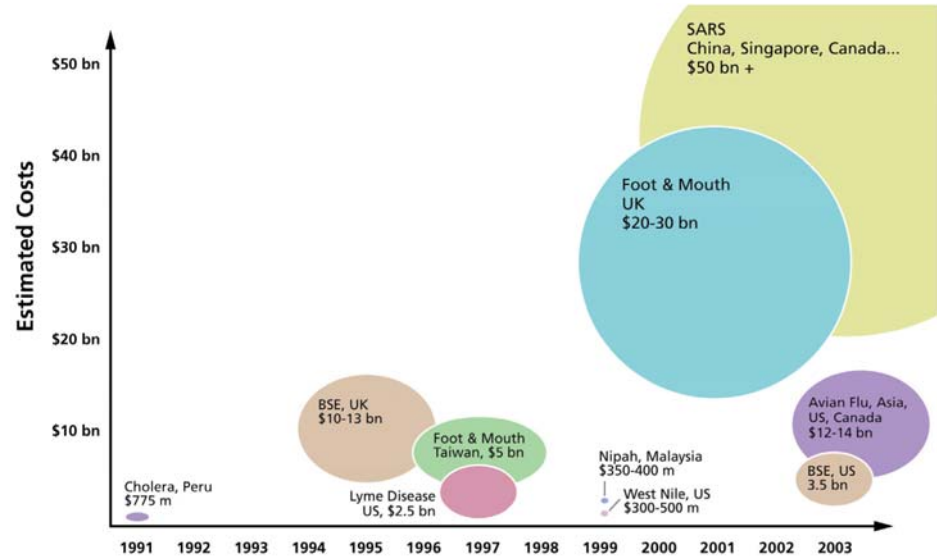
Given the increasing prevalence of EIDs globally in both animals and humans, it has become clear that using surveillance and prevention is a more financially sound manner of addressing future EIDs. Not only are infectious diseases responsible for the greatest portion of the global public health burden, they also significantly impact national and global economies (Figure 1). There is more need than ever to develop better surveillance protocols and diagnostic reference laboratories in regions of the world that may be particularly vulnerable to emerging disease so that rapid identification and response to outbreaks can be achieved. This strategy is crucial to the protection of human and animal health, and also serves to protect local and global economies.

SARS cost the Chinese and Canadian economies over \$50 billion U.S. dollars associated with medical treatment, disease control, and lost revenue associated with the abrupt halt of their tourism industries. Foot-and-mouth disease and bovine spongiform encephalopathy (“mad cow” disease) cost the British economy a combined \$30 to \$40 billion U.S. dollars in lost revenue resulting from farm closures and trade restrictions. Even today, the potential threat of exposure to mad cow disease continues to prevent some people from eating beef, a cost that cannot be appropriately calculated. Costs to respond to the Avian influenza outbreak continue to increase on a daily basis; if this disease becomes the next pandemic, costs will soar to unprecedented levels.

Disease outbreaks also result in intangible costs, (e.g., the psychological impact of losing one’s farm or livelihood after an outbreak and the loss of human lives from the disease itself). There is also the continued economic burden that chronic infectious diseases place on healthcare systems (e.g., HIV/AIDS) and the ongoing emotional stress on healthcare workers.

The economic and public health costs of infectious disease

Figure 1: Economic impacts of selected emerging and re-emerging infectious diseases. Source: *Bio-Era*, 2004.



Figures are estimates and are presented as relative size.

are so great globally that preventive strategies are not only cost-effective, but imperative. Using the multidisciplinary approach of conservation medicine to understand the drivers of disease emergence, host-pathogen relationships, transmission mechanisms, and appropriate control and prevention measures, we are moving towards a new era. The new era will offer increased collaborative studies between scientists globally; more sensitive surveillance with better laboratory preparedness; improved decision making to ensure that choices about land management do not result in ecological changes that promote disease emergence; and finally, a greater ability to predict and prevent future outbreaks. □

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Jonathan H. Epstein, DVM, MPH, is a certified international veterinary medicine senior research scientist at the Consortium for Conservation Medicine, NY. His fieldwork ranges from conducting a feasibility study for re-introducing the Eastern Bongo to Mount Kenya’s forests, to the study of Australian Bat Lyssavirus, a newly emergent zoonotic disease. His analysis of Queensland, Australia’s public health experience with potential human exposure to the bat was published in the CDC’s *Journal of Emerging Infectious Diseases*. He has also investigated the potential disease-transmission risk from the Australian White Ibis to humans and food production animals in Queensland. He is a recipient of the Sylvia Mainzer Public Health Achievement Award and the Hill’s

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"Buddy" award for excellence in small animal clinical nutrition. His research interests include the human-wildlife interface as a point of zoonotic disease transmission and anthropogenic changes to the environment that drive disease emergence. He received his Doctor of Veterinary Medicine and Masters of Public Health degrees from Tufts University's School of Veterinary Medicine, and was the first recipient of its certificate in international veterinary medicine.

Lisa Marie Schloegel, BA, is a PhD Candidate at Kingston University, England, and a program assistant at the Consortium for Conservation Medicine, NY. During her college career, she studied abroad at James Cook University, Townsville, Australia, and participated in a census of monkey populations inhabiting the rain forests of Bioko Island, Equatorial Guinea, Africa. Following graduation, she studied the ecology and intraspecific relationships of howler monkeys at the Ometepe Island, Nicaragua, field station. She then interned at Defenders of Wildlife before accepting a position at Central Montgomery MH/MR Center as an intensive case manager. She is currently enrolled in a PhD program at Kingston University, studying the role of the wildlife trade in the spread of amphibian chytridiomycosis, a fungal pathogen linked to the declines and extinctions of amphibian populations worldwide. She received her BA in Psychobiology, along with a minor in Professional Writing, from Arcadia University.

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GLOSSARY

Epidemiology is the study of disease dynamics in human populations and understanding the factors that are associated with disease occurrence, and involves learning about these disease dynamics through performing quantitative science on data collected during a disease event. This information is applied to understand the cause of the disease, the disease significance, or methods to control and prevent transmission. Epidemiology describes and characterizes variables associated with disease, including comparisons among groups of infected individuals.

When diseases affect animals, we call the study of the disease outbreak **epizootiology**.

Disease prevalence pertains to the occurrence of disease at a specific point in time, or the

- # of diseased animals
- # of animals in the group or population

Disease incidence is the number of new cases of a disease, or

- # of animals developing disease per unit of time
- # of animals at risk in the group or population

Disease prevalence or incidence can be used to describe both human and animal diseases. These terms, however, are often confused with the terms **epizootic** and **epidemic**, which are characterized by case frequencies that are in excess of the expected or background levels of disease in humans and animals, respectively.

A **pandemic/panzootic** disease has spread across large regions or continents and affects a significant portion of the human/animal population. Pandemic diseases may initially begin through disease transmission from an animal to a human (**zoonotic** transmission), as is the case with HIV/AIDS, which originated from nonhuman primates. Human-to-human transmission is generally necessary for a pathogen to cause a pandemic, and the population of susceptible individuals must be large enough to maintain the infection within that population. Furthermore, a pathogen must not kill its host before it has time to transmit the pathogen to another susceptible individual (this is why SARS made it from China to Canada, but Ebola outbreaks tend to be confined to a small radius). If these conditions do not exist, outbreaks are generally self-limiting.

In contrast to pandemics, epidemics, and epizootics, **enzootic** or **endemic** levels of diseases are characterized by case frequencies at expected levels in animals and humans, respectively. **Enzootic/endemic** and **epizootic/epidemic** characterizations are dependent on prior knowledge of disease occurrence in a specific area. Therefore, these terms are usually used only after a disease has been documented, whereas **prevalence** and **incidence** can be used during an ongoing outbreak.

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