REVIEW ARTICLE

Emerging Zoonotic Diseases: Epidemiology, Public Health Impact, and the Urgent Need for a Unified "One Health" Approach

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ABSTRACT

Emerging zoonotic diseases (EZDs) pose significant and growing threat to global public health, driven by complex interactions among humans, animals, and the environment. These diseases, often arise from infections of bacteria, viruses, parasites, or fungi, and are capable of causing widespread health crises. In recent decades, there has been an alarming increase in zoonotic outbreaks, driven by anthropogenic activities such as deforestation, wildlife trade, climate change, and agricultural intensification. Notable examples include Monkeypox (Mpox), COVID-19, Ebola, Nipah, and H1N1 influenza pandemic, which firmly bring zoonoses into the realm of large-scale epidemics among human populations. This review discusses the epidemiology of EZDs, focusing on etiology, transmission pathways, and pathology, with a view to the control strategy of the important zoonotic infections. Special emphasis is placed on the public health concerns associated with emerging zoonoses, particularly in hotspots such as Southeast Asia, where rich biodiversity and human-animal interactions provide suitable environment for zoonotic spillovers. The critical need for a coordinated "One Health" approach, which integrates human, animal, and environmental health, is underscored as essential in controlling and preventing future outbreaks. By integrating innovations in molecular diagnostics and predictive analytics, including machine learning, global surveillance systems can enhance their ability to swiftly identify and respond to zoonotic threats. A unified approach involving strong surveillance, vaccination of animals, food safety measures, and public education is essential to protecting global health and slow down the rise of new zoonotic diseases.

INTRODUCTION

Zoonotic diseases, more commonly known as zoonoses, are infections that can be transmitted from animals to humans, emphasizing the strong interrelation between human and animal health. Newly emerging zoonotic diseases are described as infectious diseases that have either recently appeared within a population or are

rising in incidence or geographic range, originating from an animal source to cause infections in human populations (Elsohaby and Villa, 2023). Zoonoses are classified by the World Health Organization as diseases that can be naturally transmitted from vertebrate animals to humans, and such diseases may be caused by a variety of pathogens including bacteria, viruses, parasites, and fungi (Rahman *et al*., 2020; Elsohaby and Villa, 2023). The impacts of zoonotic diseases are very large and varied, ranging from negligible to very serious and sometimes fatal. These diseases can be transmitted through various routes: direct contact with infected animals; contaminated food and water; or vectors like mosquitoes and ticks (Rahman *et al*., 2020).

Zoonotic diseases have significantly influenced the course of human civilization throughout the course of history, most amply illustrated by the Black Death catastrophe in the 14th century and the 1918 influenza pandemic (Bennasar-Figueras, 2024). All these diseases together show a real, ongoing, and dynamic danger. The occurrence and severity of zoonotic epidemics have increased significantly in the twenty-first century, owing mostly to anthropogenic activity. Deforestation, wildlife trade, agricultural intensification, urbanization, and climate change collectively increased the interfaces between human populations and wild animals, promoting pathogen transmission from animal reservoirs to human hosts (Nelson and Worobey, 2018; Markotter *et al*., 2023).

The emergence of novel zoonotic diseases or their significant rise in incidence is a major concern, as these diseases have the potential to cause pandemics. Most notably, Mpox and COVID-19 pandemics are both likely to have zoonotic origins, and the outbreaks clearly represent very serious global health risks from such pathogens (Ashour *et al*., 2020). Ebola, with its relentless outbreaks and intricate links to human interactions with wildlife in Africa, is a very sobering example of the dangers represented by emerging pathogens (Sultana Runa *et al*., 2018; Dhama *et al*., 2020). Southeast Asia is at the forefront of regions rich in biodiversity and has gained global recognition for its critical role in zoonotic disease surveillance and intervention (Saba Villarroel *et al*., 2023).

Moreover, public health concern in regard to these emerging zoonoses is further heightened by the speed at which many diseases cross international borders. In fact, the globalization of human society, aided by increased travel, trade, and interconnectivity, has given an accelerated potential for zoonotic pathogens to initiate wide-based epidemics (Dhama *et al*., 2020). For example, diseases such as Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS), on one hand, serve as examples of rapid outbreaks that rolled across continents and brought fatal outcomes to the concerned populations (Markotter *et al*., 2023). However, these have also helped raise concern for the need for a coordinated global effort toward prevention and control of these threats. Zoonotic diseases, in their spread, call for a "One Health" unified approach-one where human, animal, and environmental health come into one umbrella to engage with the cross-boundary natures of risks. This would seek to bring collaboration between veterinary sciences, human medicines, environmental studies, and public health in the strongest possible efforts toward surveillance, early detection, and appropriate response to zoonoses outbreaks (Elsohaby and Villa, 2023). The expanding function of technology-molecular diagnostics and predictive tools like machine learning-in identification and controlling sources of zoonotic pathogens will, within the next few years, show further growth (Rahman *et al*., 2020; Saba Villarroel *et al*., 2023).

Despite these, there remains wide gaps in the global surveillance systems, research infrastructure, and public health preparedness. The rising menace of zoonoses calls for investments in zoonotic research, vaccine development, and public education (Rahman *et al*., 2020). It is not in doubt that in the near future, stronger surveillance systems, improvement in food safety, and increased public awareness will be crucial in mitigating the impact of zoonotic outbreaks on global health. Epidemiology, etiology, transmission, and pathology of the EZDs are discussed here, as well as public health implications especially in the face of increasing interactions between humans and animals. Its control and preventive strategies are discussed in detail; also, how necessary a coordinated approach at a global level is, to mitigate the risks associated with zoonotic diseases and prevent future pandemics.

Review Methodology: The current review of these EZDs is based on an extensive review and critical analysis of the literature showing the interplay between human, animal, and environmental health. For this purpose, articles were sourced systematically from reputed academic databases, including Scopus, PubMed, Google Scholar, Web of Science, and ScienceDirect. For developing the search strategy, a set of targeted keywords on the review topic, its epidemiology, zoonoses, EZDs, mode of transmission, and impact on public health was used. A total of 84 articles were selected that substantially provided information on the etiology, transmission route, and pathology of some important zoonotic infections like Mpox, COVID-19, Ebola, SARS, MERS, Dengue, Chikungunya, Avian Influenza, Rift Valley Fever Virus, and Nipah virus. The bibliometric analysis was accomplished using the VOSviewer software (VOSviewer version 1.6.20), which allowed clustering of these articles into different groups on the basis of their thematic relatedness. Using this approach, the analysis detected 1,186 links amongst the articles with a cumulative link strength of 3,795, representing the depth and interlink between researches in this critical thematic area (Fig. 1). The map used in this study, was primarily generated using ArcMap 10.8. After constructing the base map, we manually added the "country names" and the "first identified year" of the disease's occurrence. Additionally, BioRender (www.biorender.com) was used to illustrate the disease transmission pathway. All other graphs were generated using MS PowerPoint 2016.

Etiology, Host/Vector and Pathology of EZDs: In recent years, EZDs have gained significant attention due to their impact on public health, animal health, and economies worldwide. These diseases, caused by pathogens that can be transmitted from animals to humans, often arise from changes in ecological systems, urbanization, and increased human-animal interactions. The details regarding several notable EZDs, their etiologies, characteristics of their causative agents, animal hosts or vectors, and the associated pathologies are summarized in Table 1.

Historical Landscape of Emerging Zoonoses: The EZDs has significantly impacted global health, with various pathogens originating from distinct geographical regions.

As depicted in the global map (Fig. 2), diseases such as Ebola virus, first identified in 1976 in Zaire, and Nipah virus, recognized in 1998 in Malaysia, highlight the diverse origins of these threats (Bwaka *et al*., 1999; Halpin *et al*., 2000; Singh *et al*., 2019; Garbuglia *et al*., 2023). Monkeypox, emerging from the Democratic Republic of the Congo in 1958, alongside SARS and MERS, which were first identified in China and Saudi Arabia, respectively, underscore the interconnectedness of human and animal health (Petersen *et al*., 2019; Peiris and Poon, 2021; Bunge *et al*., 2022; Kaler *et al*., 2022). The rest of the significant pathogens, like Zika virus and chikungunya, are from Africa, and other diseases like avian influenza and Rift Valley fever are attributed to particular regions like Italy and Kenya respectively (Musso and Gubler, 2016; Peiris and Poon, 2021; Chagas *et al*., 2022; Kimble *et al*., 2024). Determining the geographical and historical backgrounds of this emerging diseases will definitely promise a good outcome in developing efficient surveillance and response.

Transmission of Zoonoses (Direct and Indirect Pathway): Zoonotic diseases reside in a diversity of animal hosts and can be transmitted to humans through many direct and indirect routes (Webster, Borlase, and Rudge, 2017) (Fig. 3). Arboviruses - those viruses that are spread by arthropod vectors - typically mosquitoes - have a lower pandemic potential than viruses spread directly via aerosols, even though the two routes of transmission are likely to occur with either type of virus roughly and equally (Loh *et al*., 2015) . One of the key limitations of

Fig. 1: A bibliometric analysis of the selected study. This figure represents a bibliometric analysis of EZDs, illustrating key research themes and their interconnections. The network visualization is based on keyword co-occurrence, with node size corresponding to keyword frequency and link strength indicating co-occurrence relationships. The largest and most prominent nodes, such as "humans," "animals," "zoonoses," "disease outbreaks," and "COVID-19," indicate major research focuses in the field of zoonotic diseases. Different colors cluster represent distinct research areas.

Table 1: Etiology, characteristics, animal host/vector and pathology of emerging zoonotic diseases (EZDs)

| Emerging disease	Etiology	Characteristics of Etiological Agent	Animal host/Vector	Pathology & Organ Involvement in Human	References
Ebola Virus	Ebola viruses from Filoviridae family	Shape: Long, thread-like, or filamentous; Size: 80nm in diameter, 14000 nm in length; enveloped virus with single-stranded RNA	Bats	Malaise, exhaustion, and muscle weakness and/or myalgia that occur before or at the same time as a fever (>38°C) are among the initial signs. Meningoencephalitis, or malfunctioning of the central nervous system (CNS), symptoms of upper motor neurons including prolonged clonus and hyperreflexia, electrolyte problems, hypoglycemia, uremia, or hyperammonemia	(Bwaka et al., 1999; Chertow et al., 2014; Hunt et al., 2015; Garbuglia et al. 2023)
Nipah Virus	Henipavirus and family Paramyxoviridae	Pleomorphic, spherical, or thread-like, with an average between 40 and 1900 nm in diameter. Enveloped virions, Negative-sense, single-stranded RNA genome Helical nucleocapsid, Size ranging from 150-350 nm in diameter, Genome length of 15-19 kb, have Six structural proteins.	Fruit bats	Humans are susceptible to severe and rapidly spreading viruses, which primarily damage CNS and respiratory system. The first symptoms of NiV which include feeling dizzy, having a headache, fever, and vomiting, are similar to those of viral infections.	(Halpin et al., 2000; Hossain et al., 2008; Breed et al., 2010; Sharma et al., 2019; Singh et al., 2019; Thakur and Bailey, 2019; Skowron et al., 2022)
Monkeypox (Mpox)	Mpox virus from Orthopox virus genus of the Poxviridae family	Double-stranded, large, DNA viruses. The West African clade and the Central African (Congo Basin) clade are the two separate genetic lineages into which the virus that causes Mpox is divided.	Rodents & non-human primates especially Monkey	Fever, malaise, and swollen lymph nodes; Systemic involvement may occur, resulting in complications such as pneumonia, encephalitis, and, in severe cases, multi-organ failure.	(Petersen et al., 2019; Peiris and Poon, 2021; Bunge et al., 2022; Kaler et al., 2022; Zinnah et al., 2024)
SARS & MERS	Coronaviruses SARS-CoV and MERS-CoV	Enclosed, positive-sense, single-stranded RNA viruses, genomic size of about 30 kb, diameter of around 100–140 nm and a characteristic corona of petal-shaped spikes.	Bats, Dromedary camels	Fever, cough, headache, myalgia, nausea, diarrhea, and malaise; Difficulty in breathing, respiratory distress, organ failure, lymphopenia	(Kaler et al., 2022)
Zikah Virus	The Zika virus (ZIKV), genus Flavivirus and the family Flaviviridae	Icosahedral-like arrangement, spherical, enclosed, and around 50 nm in diameter.	Monkey and Apes	Significant neurological complications, congenital Zika syndrome, microcephaly, In adults, Guillain-Barré syndrome, a neuropathy and myelitis, further contributing to its neurological disorder.	(GW et al., 1952; Faye et al., 2014; Ahmad et al., 2016; Majumder et al., 2016; Musso and Gubler, 2016)
Chikungunya	Chikungunya virus, Family: Togaviridae, Genus: Alphavirus	Enveloped virus: Contains a lipid membrane; Nucleic acid: Single-stranded RNA, Multiple genotypes exist,	Aedes mosquitoes, Human and Non-human primates	Infection typically leads to fever, severe joint pain, rash, and fatigue. The virus can persist in the body, leading to chronic joint pain in some individuals.	(Rama et al., 2024)
Dengue	Dengue virus, Family: Flaviviridae, Genus: Flavivirus	Enveloped virus: Surrounded by a lipid membrane. Nucleic acid: Single-stranded RNA. Serotypes (DENV-1, DENV-2, DENV-3, DENV-4)	Aedes mosquitoes, Human and Non-human primates	High fever, hemorrhagic fever, headache, muscular pain (breakbone fever), Rash, pain behind eye and also in joints, shock syndrome. Severe cases can result in bleeding (e.g., nosebleeds, gum bleeding), organ failure.	(Chagas et al., 2022)
Avian Influenza	Avian Influenza virus from Orthomyxoviridae.	Shape: Spherical or pleomorphic, Size: 80-120 nm in wide, enveloped virus, eleven viral proteins are encoded by eight RNA segments; antigenic drift and antigenic shift also occurred.	Water fowl	The most typical side effects of an infection are symptoms like the flu or conjunctivitis. All series shared the same general findings of lymphopenia and thrombocytopenia, which were predictive markers for ARDS and death	(Taylor and Turner, 1977; RG et al., 1981; Hien et al., 2004; Wong and Yuen, 2006; Kimble et al., 2024; Subedi et al., 2024)
Rift Valley Fever	Rift Valley Fever virus, Family Bunyaviridae and genus Phlebovirus	Enveloped RNA virus with a tripartite genome (L, M, and S), Spherical, 90-120 nm size, single stranded RNA with enveloped lipid membrane.	Aedes mosquitoes and biting flies	High rates of abortion and infant mortality; its clinical manifestations include fever, lymphadenitis, discharges from the nose and eyes, and vomiting. Usually, RVF starts as a dengue-like illness with fever, headache, and frequent bleeding; however, in rare instances, serious complications like retinitis, encephalitis, and hepatitis with deadly hemorrhagic fevers are seen.	(Wilson, Gaudreault, and Hossain, 2005; Kimble et al., 2024)
Crimean Congo Hemorrhagic Fever	Crimean-Congo hemorrhagic fever (CCHFV) Virus, Family: Bunyaviridae, Genus: Nairovirus	Spherical or pleomorphic, enveloped, 90-120nm wide, single-stranded negative sense RNA with a segmented genome consisting of three RNA segments.	Newborn mice, humans	Sudden onset of fever, muscle aches, dizziness, and severe bleeding.	(Whitehouse, 2004)

Hanta Virus	Hanta Virus, Family: Bunyaviridae Genus: Hantavirus	A tri-segmented, negative-sense, single-strand RNA virus	Bank & Yellow - necked mouse	Moles	Flu-like illness, Gastrointestinal symptoms: nausea, vomiting, and diarrhea; Hantavirus Pulmonary Syndrome; Hemorrhagic Fever with Renal Syndrome	(Schmaljohn et al., 1983; MacNeil, et al., 2011)
Brucellosis	Brucella spp.	Gram-negative, non-motile, facultative intracellular coccobacilli.	Domestic and wild animals		Arthralgia, pyrexia (undulant fever), and weariness, meningitis, meningoencephalitis, brain or epidural abscesses, and/or demyelination issues	(Murray and Holt, 2001; Moreno, 2014; Araj, 2016; Hull and Schumaker, 2018; Khan et al., 2021)
Leptospirosis	Leptospira interrogans	Thin, spiral-shaped bacteria with hooked ends, about 6-20µm in length and 0.1-0.25µm in width, Gram negative, highly motile	Mammals & rodents		Sudden-onset of fever, excruciating headaches, aches in the muscles, nausea, and chills are other symptoms.	(Soo, Khan, and Siddiqui, 2020)
Toxoplasmosis	Toxoplasma gondii	Intracellular parasites; Morphology: parasitic protozoan, specifically an apicomplexan, shape, about 4-8µm in length	Domestic cats		Latent infection with tissue cysts	(Weiss and Dubey, 2009)
Echinococcosis	Echinococcus spp.	Small tapeworms, 1 to 11mm in length. triploblastic (ectoderm, middle mesoderm, and inner endoderm), lack a digestive system and anus,	Echinococcal s tapeworm		Cysts in the lungs cause dyspnea, hepatic insufficiency in Liver, digestive issues, and ascites. Brain cysts cause blindness and paralysis.	(Dakkak, 2010; Ibarra-Velarde et al., 2015)
Histoplasmosis	Fungus Histoplasma capsulatum	Dimorphic fungus found in soil enriched with bird or bat droppings,	Bats and birds		Acute pulmonary histoplasmosis, pericarditis, rheumatologic syndromes, chronic pulmonary histoplasmosis, and disseminated histoplasmosis were among the prevalent symptoms.	(Sarosi and Johnson, 1992; Kurowski and Ostapchuk, 2002)
Cryptococcosis	Cryptococcus spp.	Encapsulated yeasts	Birds (Pigeons)		In humans, CNS involvement manifests itself as meningitis, meningoencephalitis, or tumor-like intraparenchymal lumps harboring yeast organisms and inflammatory cells (cryptococcomas)	(Sykes et al., 2010; de Sousa et al., 2021)
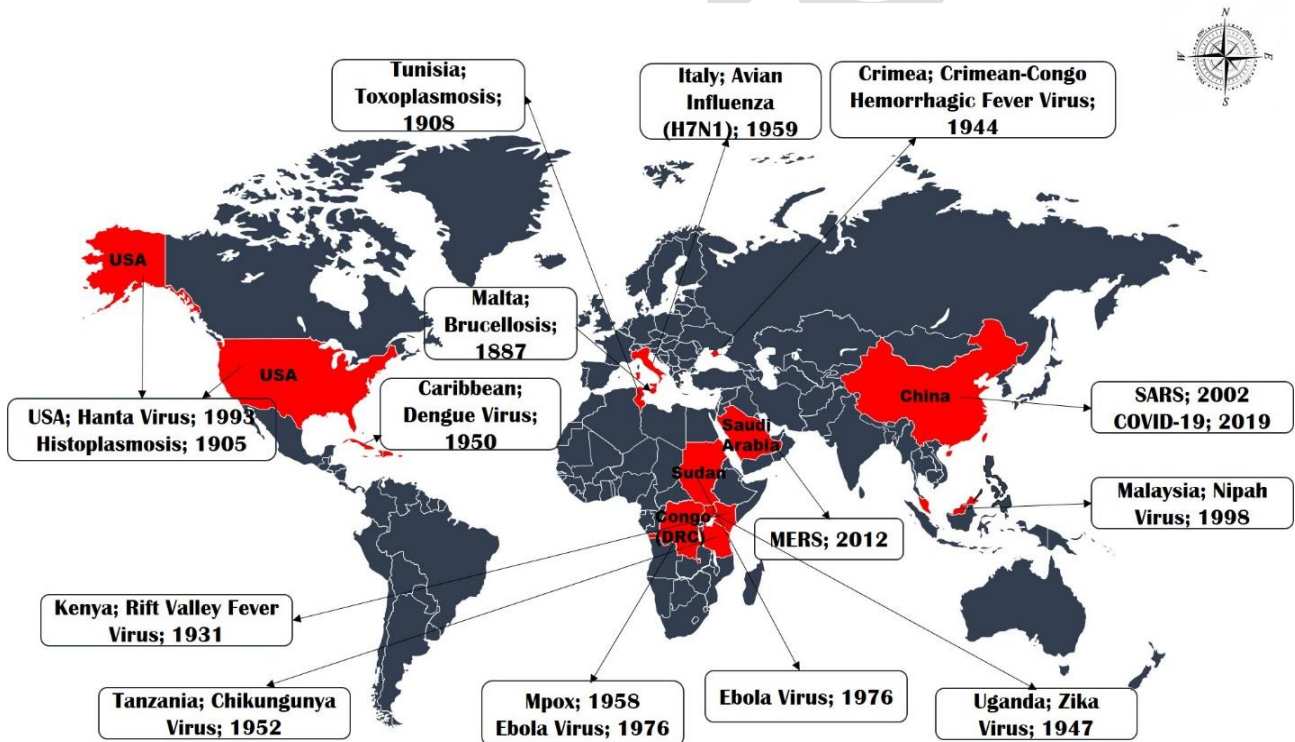
Fig. 2: Geographical distribution of EZDs and their first occurrence year. This map illustrates the first recorded occurrence of various EZDs across different countries. The base map was generated using ArcMap 10.8, with additional labels manually incorporated to indicate the country name, disease, and year of first identification. Countries highlighted in red indicate where specific zoonotic diseases were initially detected.

arboviruses is their life cycle, which involves sequential movement between two hosts: a human (or a reservoir host) and an insect vector (Dobso et al., 2020). Factors such as climate and the need for specific vectors further constrain the geographic spread of these viruses. Moreover, robust human immunity tends to slow transmission, as uninfected vectors face difficulty in locating infectious hosts (Ferguson et al., 2016).
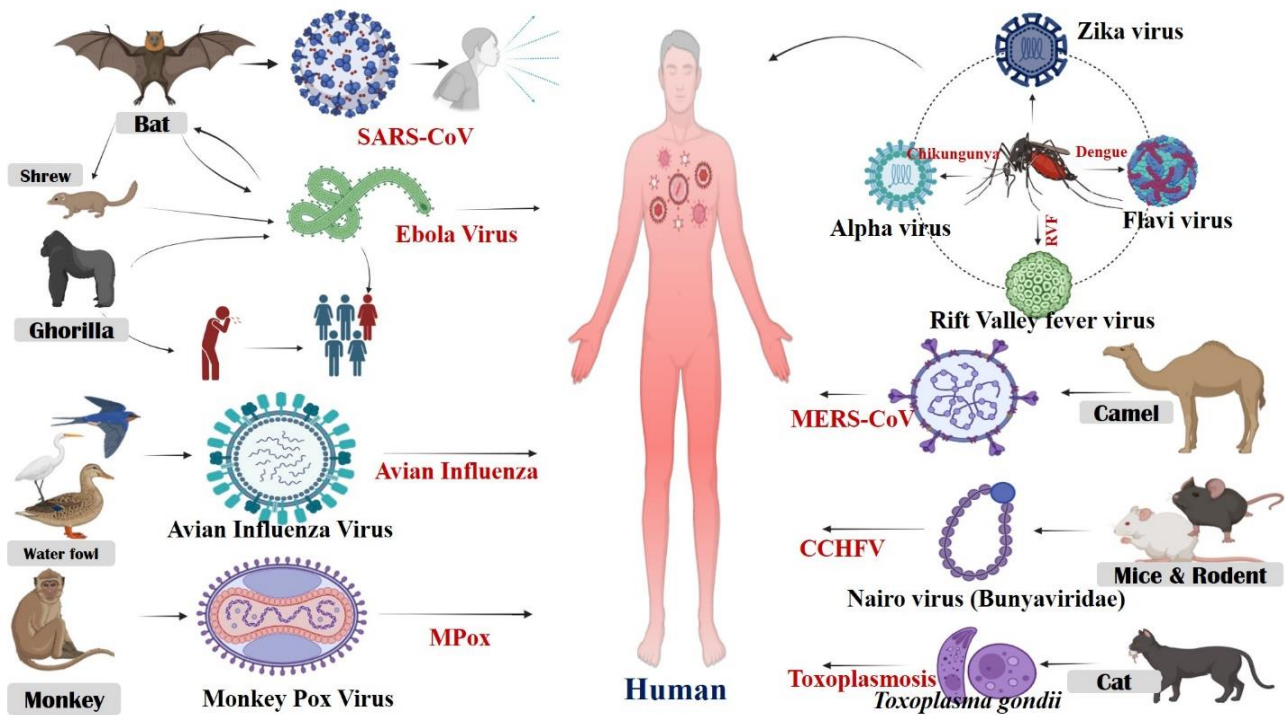
Fig. 3: Pathogen spillover of EZDs. This schematic representation illustrates the transmission pathways of various EZDs, emphasizing their animal reservoirs and vectors. The diagram highlights the role of wildlife, domesticated animals, and arthropod vectors in transmitting zoonotic pathogens to humans.

In most cases, humans infected with zoonotic pathogens are considered terminal hosts, meaning that zoonotic infections such as Lyme disease bacteria, Rift Valley fever virus, and rabies virus typically exhibit little or no transmission between humans. However, around 25% of zoonotic infections, like *Trypanosoma brucei rhodesiense* and *E. coli* O157, can transmit from human to human, though they require continual reintroduction from non-human reservoirs to persist (Woolhouse and Gowtage-Sequeria, 2005). Less than 10% of zoonotic pathogens are capable of sustained human-to-human transmission, such as the measles virus and *Mycobacterium tuberculosis*, or have the potential to do so once introduced from a non-human source, like certain strains of influenza A, *Yersinia pestis*, or SARS coronavirus (Ferreira *et al*., 2021). Because most zoonotic pathogens are not highly transmissible within human populations, they generally do not cause large-scale epidemics, even if they are capable of causing disease. Nevertheless, predicting whether a pathogen will jump to a new species and spread within it remains challenging. These rare events, however, have led to some of the most devastating pandemics in human history, such as COVID-19 and HIV/AIDS (Ferreira *et al*., 2021).

Predictors of Emerging Zoonotic Diseases (EZDs): The emergence of zoonotic diseases is shaped by a variety of interconnected factors (Fig. 4 and 5) that interact in complex and dynamic ways (Walsh *et al*., 2020). Growing human and animal populations are a primary driver, as they increase the likelihood of pathogen transmission through closer interactions between humans and animals (Cutler *et al*., 2010; Wang and Crameri, 2014). This is particularly evident in areas where agricultural practices intensify, leading to changes in farming and trade methods that create hotspots for disease transmission, such as localized food markets, slaughterhouses, and wet markets (Meurens *et al*., 2021).

Pathogen-host interactions, especially in multi-host systems, are strongly linked with fast-changing environments in which these dynamics take place. Habitat alteration through deforestation and urbanization reduces biodiversity, forcing wildlife and livestock into overlapping ecosystems. This might allow the transfer of novel pathogens to natural and susceptible species (Greger, 2007; Keesing *et al*., 2010). All these factors further complicate the picture caused by climate change and affects the life cycles of vectors and pathogens. Rising temperatures, shifting weather patterns allow vectors-like mosquitoes-to expand their ranges, raising risks in areas which these diseases had previously never shown the presence of, such as West Nile virus (WNV) and Rift Valley fever virus (RVFV). Heavy rainfall and droughts reinforce such patterns, often with newly emerging outbreaks (Zinsstag *et al*., 2018).

Another important factor contributing to the wide spread of such zoonotic diseases is global travel and trade. The fast movement of people and animals across borders has contributed to the wider dissemination of the pathogens, as was observed during the outbreaks caused by SARS-CoV in 2003 and SARS-CoV-2 in 2019 (Morse *et al*., 2012). The encroachment on natural habitats implies increasing exposure via infected wildlife from vectors of viruses and infections. It is due to some of their cultural practices related to the transmission of diseases from animals in general, which might have been considered an important avenue in spreading diseases in a zoonotic way. This is related to growing trading and transportation of wild
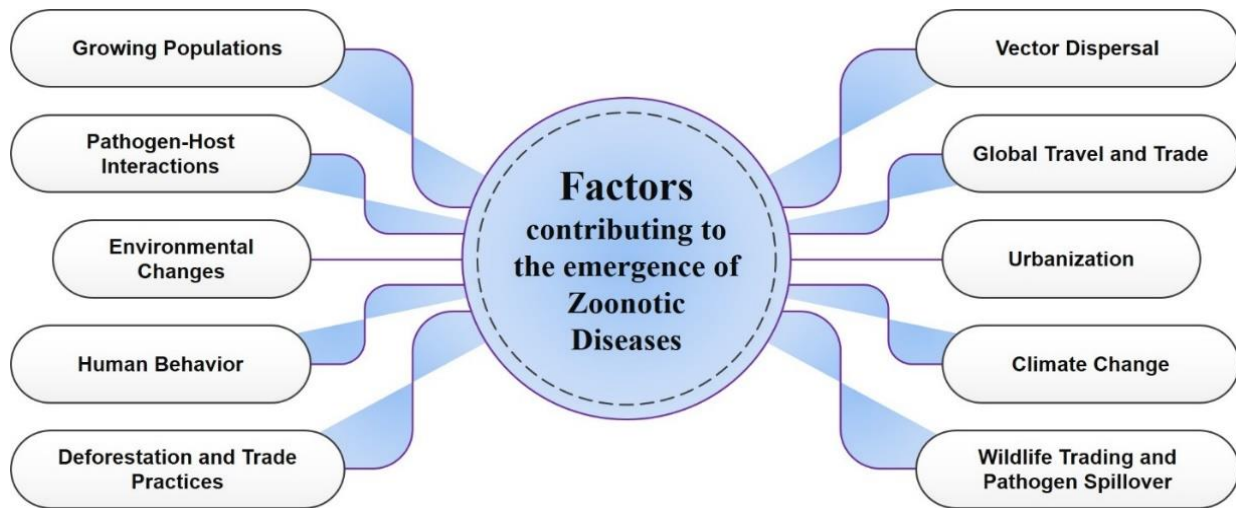
Fig. 4: Factors contributing to the EZDs. This diagram illustrates the key factors that drive the emergence and spread of zoonotic diseases that originate in animals and are transmitted to humans.
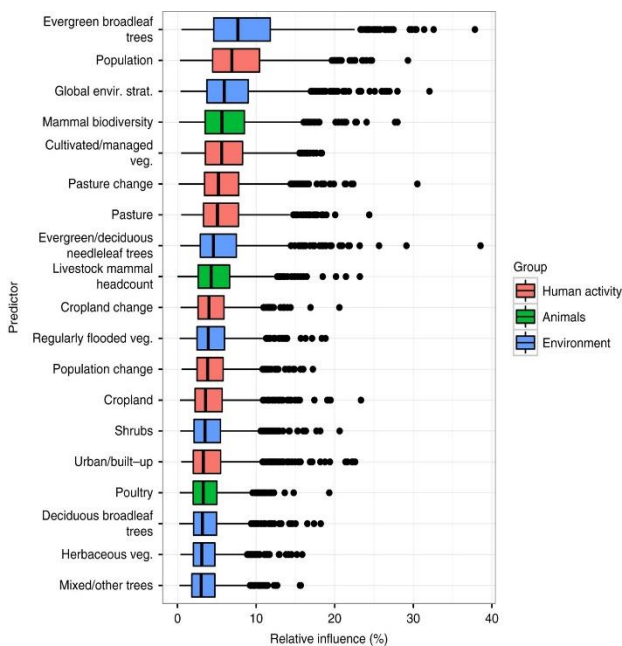
Fig. 5: The analysis of the relative influence of predictors on EZDs event occurrence probability. The figure was directly retrieved from (Allen *et al.*, 2017)

animals to markets where many species exist, allowing viruses to spillover from their reservoirs to humans (Greatorex *et al.*, 2016; Andersen *et al.*, 2020). Yet another layer of risk is added with the fauna of the urban environment: strays and semi-domesticated animals can become reservoirs for zoonotic diseases within the city limits themselves.

The demand for animal products is increasing; this rise, in addition to population growth and urbanization, contributes to greater interaction of humans, livestock, and wildlife (Bengis *et al.*, 2004; Allan *et al.*, 2017). This will require a better understanding of how population growth, the environment, agriculture, human behavior, and climate change contribute to disease spread. Effective interventions must address these factors to prevent outbreaks (Bengis *et al.*, 2004; Greger, 2007; Keesing *et al.*, 2010; Morse *et al.*, 2012; Greatorex *et al.*, 2016; Allan *et al.*, 2017; Zinsstag *et al.*, 2018; Andersen *et al.*, 2020).

Recognizing these many-sided interactions allows the more suitable alignment of public health responses more appropriately to the many complexities found within the dynamics of zoonotic diseases. A boosted regression tree (BRT) model identified key predictor variables contributing to the emergence of zoonotic diseases, along with their relative influences (Fig. 5). The most significant predictors included evergreen trees (7.6%), human population density (6.9%), Global Environmental Stratification (climate) (5.9%), and mammal species richness, representing biodiversity (5.6%) (Allen *et al.*, 2017).

Impact on Public Health: EZDs are naturally transmissible infections between animal populations and humans, hence a big public health concern (Bwaka *et al.*, 1999; Chertow *et al.*, 2014; Edwards *et al.*, 2015; Garbuglia *et al.*, 2023). Such diseases have gained a surge during the past decades due to globalization, environmental changes, and complex interactions between humans and animals. Most EZDs, such as Ebola, Nipah virus, Mpox, Zika, and COVID-19, have caused huge impacts on health, economics, and society at large in the world (Bwaka *et al.*, 1999; Halpin *et al.*, 2000; Breed *et al.*, 2010; Chertow *et al.*, 2014; Garbuglia *et al.*, 2023). This has brought to light the glaring deficiencies in global governance as well as the public health system in responding to the COVID-19 pandemic. A realization has come about that the management of EZDs essentially needs to be ramped up.

COVID-19 has become widespread across the world, causing illness and death, catching health systems off guard, and placing a huge burden on economies. Medical treatment costs, lost production, and mitigation measures have reached unprecedented heights. This incident demonstrates the high public health impact possible resulting from zoonotic spillover (Hunt *et al.*, 2015; Singh *et al.*, 2019). In fact, several other zoonotic diseases, too, have emerged as critical public health emergencies. Among the Ebola outbreaks that swept across Africa, some had devastating mortality rates, a pointer to the importance of adequate surveillance and rapid intervention strategies. The Nipah virus, which is present in bat populations throughout South Asia, has a high case fatality rate and outbreak potential, especially in areas with poor treatment facilities.

Monkeypox, endemic to Central and West Africa, has been at the center of much attention in recent years following the appearance of outbreaks outside known geographic zones, prompting international health responses (Petersen *et al.*, 2019; Bunge *et al.*, 2022; Kaler *et al.*, 2022).

In 2015–2016, the Zika virus massively spread throughout the America via mosquito vectors, causing newborn babies to be born with serious birth defects like microcephaly (Musso and Gubler, 2016). In the same regard, the MERS and SARS outbreaks have brought into focus how respiratory viruses can easily diffuse across borders and cause public health catastrophes. A number of socio-economic factors-especially urbanization, poverty, and poor health systems-influence the epidemiology of Emerging Infectious Diseases (EIDs) to a great degree (Musso and Gubler, 2016; Peiris and Poon, 2021). Indeed, underinvestment in public health infrastructure, especially in less developed and developing countries, has created a fairly huge gap in the prevention and control measures of infectious diseases. Rapid urbanization and the destruction of natural habitats have increased human-wildlife interaction, hence exposing humans to the vectors of zoonotic diseases.

Moreover, the improper and indiscriminate application of antibiotics has brought about the resurgence of formerly controlled diseases but has also exacerbated an already grave concern: antibiotic resistance, making therapeutic courses more unmanageable and elongating the course of those diseases (Amonsin *et al.*, 2006; Wong and Yuen, 2006). These diseases have extensive impacts, including high morbidity and mortality, long-term disability, and economic losses due to healthcare costs and productivity reductions. EZDs increase health inequities since the vulnerable populations, because of lack of access to health care, bear a disproportionate burden of many outbreaks. Control of such diseases calls for continuing vigilance, education, research, improved diagnostics, and sound public health systems that will reduce future pandemic risks.

Morbidity and Mortality of EZDs: The EZDs has generated significant public health challenges characterized by variability in morbidity and mortality within and among pathogens. Many of these infections have had a high toll on human lives, as shown in Table 2, which gives a summary of some key data on morbidity and case fatality rates for selected emerging zoonotic diseases.

Innovative Approaches to Surveillance and Detection of EZDs: Global surveillance and detection of emerging diseases rely on advanced technologies to provide early warnings and facilitate timely interventions. Event-based systems like Global Public Health Intelligence Network (GPHIN), ProMED-mail, and HealthMap monitor and detect outbreaks such as SARS, while web-based tools like Google Flu Trends track real-time disease activity (Sharan *et al.*, 2023). Networks such as Global Outbreak Alert and Response Network (GOARN) enhance global communication and implement preventive measures in response to health threats. Infectious disease modeling, using tools like Global Livestock Environmental Assessment Mode

(GLEAM) and Framework for Reconstructing Epidemic Dynamics (FRED), simulates epidemics to assess disease spread and design containment strategies. Social media platforms, such as Flu Near You, contribute through participatory epidemiology by gathering public data on illnesses (Childs and Gordon, 2009). Additionally, new technologies like genome-wide sequencing and bioinformatics aid in pathogen discovery, wildlife sampling, and predictive modeling, which are vital for understanding host susceptibility and preventing future outbreaks (Halliday *et al.*, 2012; Koopmans, 2013). Together, these methods form a comprehensive global surveillance system essential for detecting and controlling emerging diseases (Table 3). The surveillance and detection strategies are depicted in Fig. 6.

Strategies for Prevention and Control: Zoonotic diseases present significant global challenges, necessitating comprehensive prevention and control strategies. Vaccination against them is important in animals and human beings to curb the transmission between the species. Collaboration in co-development of vaccines targeting wildlife reservoirs, domestic animals, and people is needed to break the cycle of transmission (Wang *et al.*, 2023). For example, JYNNEOS vaccine for Mpox requires two doses four weeks apart for best protection, but persons at risk should keep away from close contact and maintain hygiene (Hossain *et al.*, 2008; Sharma *et al.*, 2019; Skowron *et al.*, 2022). In case of COVID-19, getting updated information on vaccines, good hygiene, and better indoor air quality will serve to limit its transmission. The ERVEBO® vaccine is recommended for Ebola, to which hygiene with post-exposure monitoring must be observed strictly (Monath, 2013; Chu *et al.*, 2020).

Nipah virus control involves reducing contact between humans and animals and implementing biosecurity measures on farms, while among the public health measures, quarantine plays an important role in outbreak control (Halpin *et al.*, 2000; Breed *et al.*, 2010; Sharma *et al.*, 2019; Singh *et al.*, 2019). Prevention for MERS-CoV focuses on avoiding camels and practicing infection control. Though there is no licensed SARS vaccine, works on vaccine development continue with emphases on early detection and control from the public health perspective. Biosecurity, culling of infected animals, and vaccination are the ways for avian influenza prevention, though the continuous surveillance is necessary due to mutation of viruses continuously (De Wit *et al.*, 2016; Modjarrad, 2016; Chu *et al.*, 2020).

Management of Zika virus focuses on the prevention of mosquito bites and eradication of breeding sites. A promising vaccine is also in development (Modjarrad *et al.*, 2018). Prevention of Rift Valley Fever involves vaccinations in livestock and control of vectors; however, due to the absence of a licensed vaccine, human safety precautions are necessary. The main ways of prevention include: prevention of tick bites through the use of appropriate clothes and adequate management of animals; no highly available vaccine has yet been discovered for Crimean-Congo Hemorrhagic Fever (Musso and Gubler, 2016; Dai *et al.*, 2021; Kimble *et al.*, 2024).
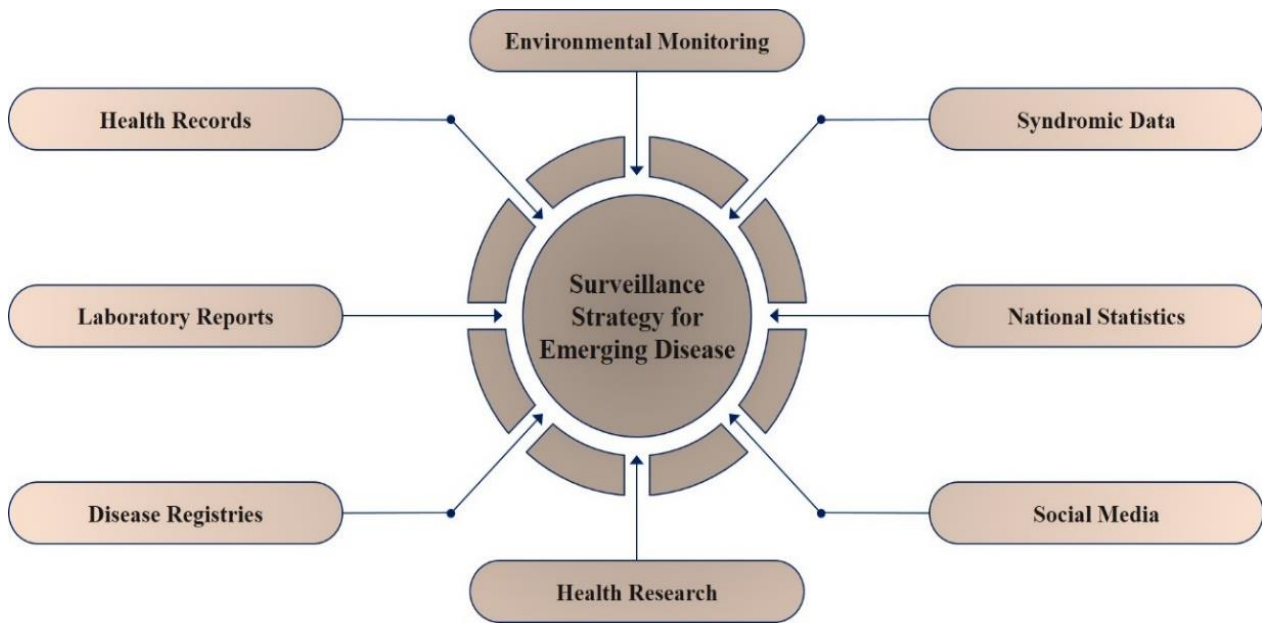
Fig. 6: Surveillance and Detection Strategy of EZDs. This diagram presents a comprehensive framework for the surveillance of emerging diseases, incorporating multiple data sources to enhance early detection, monitoring, and response.

Table 2: Morbidity and Mortality of global EZDs

Disease	Morbidity	Mortality/Case fatality	References
Ebola Virus	Several outbreaks, primarily in Africa; largest outbreak affected 28,000+ people	Average case fatality rate around 50%, varying from 25 to 90%	(Bwaka et al., 1999; Chertow et al., 2014)
Nipah Virus	Reported in Southeast Asia, with outbreaks in Bangladesh and India	Case fatality rate ranges from 40 to 75%	(Halpin et al., 2000; Breed et al., 2010; Sharma et al., 2019; Singh et al., 2019)
Dengue	Estimated annual infections: Approximately 390 million; Clinically manifesting cases: Around 96 million.	Up to 20% without proper medical care.	(Chagas et al., 2022)
Chikungunya	Estimated global cases: Over 1 million reported annually.	Chikungunya is rarely fatal, (mortality less than 0.1%) the debilitating nature of the joint pain can severely impact the quality of life, resulting in considerable socioeconomic burdens.	(Rama et al., 2024)
Monkeypox	Cases reported in Central and West Africa, recent outbreaks in non-endemic countries	Case fatality rate around 1 to 10%	(Petersen et al., 2019; Thakur and Bailey, 2019; Bunge et al., 2022; Kaler et al., 2022)
SARS & MERS	SARS affected over 8,000 people globally in 2003; MERS has sporadic cases mainly in the Middle East	SARS mortality rate about 10%; MERS mortality rate around 35%	(Peiris and Poon, 2021)
Zika Virus	Outbreaks in Africa, the Americas, Asia, and the Pacific	Generally, not fatal, but can cause severe birth defects	(GW et al., 1952; Faye et al., 2014; Musso and Gubler, 2016)
Avian Influenza	Sporadic human infections, primarily in Asia	Case fatality rate for H5N1 around 60%	(Taylor and Turner, 1977; Wong and Yuen, 2006; Webster, Borlase, and Rudge, 2017)
Rift Valley Fever	Outbreaks in Africa and the Arabian Peninsula	Generally low case fatality rate, but severe cases can have higher mortality	(Wilson et al., 2005; Kimble et al., 2024;)
Crimean-Congo Hemorrhagic Fever	Found in Africa, the Balkans, the Middle East, and Asia	Case fatality rate ranges from 10 to 40%	(Whitehouse, 2004)
Hantavirus	Infections occur worldwide, with different strains causing varying symptoms	Case fatality rate for Hantavirus Pulmonary Syndrome (HPS) around 38%	(Schmaljohn et al., 1983; MacNeil et al., 2011)
Brucellosis	Found globally, particularly in the Mediterranean, the Middle East, and Latin America	Low mortality rate, but can cause chronic illness	(Murray and Holt, 2001; Moreno, 2014)
Leptospirosis	Widespread, especially in tropical and subtropical regions	Generally low case fatality rate, but higher in severe cases	(Soo et al., 2020)
Toxoplasmosis	Common worldwide, many people infected but asymptomatic	Rarely fatal except in immunocompromised individuals	(Weiss and Dubey, 2009)
Echinococcosis	Found in regions where livestock farming is common	Low mortality rate with treatment, higher without it	(Dakkak, 2010; Ibarra-Velarde et al., 2015)
Histoplasmosis	Prevalent in the Americas, particularly in areas with bird or bat droppings	Low mortality rate with treatment, significant in immunocompromised individuals	(Sarosi and Johnson, 1992; Kurowski and Ostapchuk, 2002)
Cryptococcosis	Found worldwide, particularly affecting immunocompromised individuals	High mortality rate without treatment, especially in HIV/AIDS patients	(Sykes et al., 2010; de Sousa et al., 2021)

Lastly, prevention from Hantavirus Pulmonary Syndrome is rodent control and proper sanitation, and research in its vaccines is still ongoing (Schmaljohn et al., 1983). All these diseases are zoonotic and take their toll on health and agriculture; public health education and proactive measures will reduce the impact.

Table 3: Global surveillance and detection system of EZDs

Technologies/Resources	Example	Application	References
Event-Driven Monitoring	Global Public Health Intelligence Network (GPHIN), ProMED-mail, HealthMap, EpiSPIDER, BioCaster	Detects outbreaks and public health emergencies (e.g., COVID-19)	
Real-Time Web-Based Monitoring	Google Trends, Google Flu Trends	Surveillance of disease activity in real time (e.g., influenza)	
Systems for Early Detection and Response	Global Outbreak Alert and Response Network	Detects potential health threats, facilitates communication among health organizations, and coordinates timely response efforts (e.g., WHO alerts)	
Modeling Infectious Diseases	Simulation Models (Agent-based, Metapopulation, GLEAM, FRED)	Simulates epidemics and assesses containment strategies	
Monitoring Through Social Media Platform	Community Engagement Platforms (Foodborne Chicago, Flu NearYou)	Engages the public for tracking health trends (e.g., foodborne illnesses)	(Childs and Gordon, 2009; Halliday *et al.*, 2012; Koopmans, 2013; Sharan *et al.*, 2023)
Advanced Pathogen Discovery	Next-Generation Sequencing, Microarray Technology, Bioinformatics	Identifies pathogens/viruses and assesses host susceptibility	

Challenges and Future Directions: EZDs prevention and control face significant challenges, particularly in antimicrobial resistance (AMR), policy, governance, and research and development (R&D) (Naser *et al.*, 2024). Resistance of the zoonotic pathogens to antimicrobials driven by overuse in agriculture and health is a serious threat, while the pathogens like *Salmonella* and *E. coli* have already developed increased resistance (Asha *et al.*, 2024; Emon *et al.*, 2024; Rahman *et al.*, 2024). Accordingly, the One Health approach now emphasizes an integrated approach in linking human, animal, and environmental health in an attempt to control AMR through better regulation of antibiotics and biosecurity. Policy and governance challenges include a lack of global coordination, a multitude of inconsistent biosecurity measures, and limited surveillance across sectors. Improvement in international collaboration will involve strengthening the regulatory framework through a One Health approach. These include: limitation in funding for R&D; poor translation of research into policy and fast tracking of diagnostic and zoonotic vaccines. The future direction is in continuing genomic surveillance, development of next-generation vaccines, and public-private partnership across the world.

Despite providing a comprehensive review of EZDs, this study has some limitations. The review is based on existing literature, which may introduce selection bias and limit the scope of discussion to available data. The review does not provide primary data or empirical analysis, relying instead on secondary sources, which may limit the ability to draw definitive conclusions about the effectiveness of proposed interventions.

Conclusion: The EZDs are becoming a growing threat to global public health due to environmental, social, and anthropogenic factors. The complicated interaction between humans, animals, and ecosystems has accelerated the spillover of pathogens, leading to widespread outbreaks with severe consequences. Effective prevention and control require a coordinated "One Health" approach, integrating human, animal, and environmental health. Although molecular diagnostics, predictive tools, and improved global surveillance systems are in place and offer promise for early detection and response, many challenges still persist. Preventing future zoonotic outbreaks will largely depend on tackling antimicrobial resistance, enhancing

global collaboration, and vaccine development with rapid diagnostics. A unified global strategy in surveillance will be essential for public education and strict biosecurity measures to protect public health and prevent zoonotic spillovers.

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