



Review

Understanding Wildlife–Livestock–Human Interface for Prevention and Control of Emerging and Re-Emerging Infectious Diseases

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Simple Summary

Infectious diseases that spread between animals and humans are more prevalent and present a serious challenge to public health, livestock production, and the economy. Anthropogenic activities such as deforestation, changes in land use, rapid urban growth, and increased travel not only disrupt the natural ecosystems but also increase interactions among wildlife, livestock, and people, facilitating cross-species contact and pathogen transmission. This review describes how these environmental changes contribute to the emergence and return of infectious diseases, with examples from India and other parts of the world. It also discusses the importance of addressing human, animal, and environmental health together to better understand disease transmission and reduce future outbreaks. By bringing together current evidence on the environmental drivers of disease emergence and available prevention strategies, this review provides a useful resource for researchers and practitioners working to improve disease surveillance, prevention, and outbreak preparedness.

Abstract

Emerging and re-emerging infectious diseases (EIDs and REIDs) continue to pose a major threat to human and animal health globally. The close interactions among wildlife, livestock, and humans especially in areas where natural habitats are disturbed create ideal conditions for diseases to spill over from animals to humans. Changes in land use, deforestation, climate change, urban expansion, and global travel have contributed both to the rise in new infections and the return of old ones. Outbreaks of Nipah virus in Malaysia, Ebola in West Africa, and COVID-19 highlight the large-scale epidemics caused by human–wildlife contact. Ecological pressure and increasing movement of people and goods have facilitated the cross-species transmission of pathogens. In India, outbreaks of diseases like Lumpy Skin Disease, avian influenza, and Nipah virus have affected both public health and the livestock sector, causing significant economic losses. The One Health approach—linking



Academic Editor: Stephen K. Wikel

Received: 3 August 2026

Revised: 2 October 2026

Accepted: 13 October 2026

Published: 15 October 2026

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human, animal, and environmental health—is now essential for controlling disease risk. Strategies like improved surveillance, better diagnostics, vaccine development, responsible use of antibiotics, and restoration of ecological buffer zones are essential in mitigating the risk of disease. This review emphasizes the need for coordinated action across disciplines to reduce future outbreaks and improve preparedness for zoonotic and environmentally driven infectious diseases.

Keywords: emerging infectious diseases; re-emerging infectious diseases; wildlife-livestock; public health

1. Introduction

Humans, livestock (cattle, buffalo, goat, and sheep) and wildlife at wildlife–livestock–human interface (WLHI) may play an important role in the epidemiology and transmission of emerging and re-emerging infectious diseases (EIDs and REIDs). WLHI are areas where the range and resource use of human, wildlife, and livestock species overlap. Rapid deforestation has led to the shrinking of boundaries between wildlife and livestock wherein the natural habitats are being turned into agricultural land and grazing pastures [1]. These interfaces may act as critical spillover zone for cross-species transmission of pathogens. Indirect contacts between wildlife and livestock that share resources like food and water and exposure to an environment polluted by pathogens (aerosols or excretion from infected animals, feces, saliva, or any natural discharge from an infected animal) can result in disease [1].

Infectious disease has been recorded in humans and animals (domesticated and wild), and they are caused by a variety of pathogens, including viruses, bacteria, parasites, fungi, and others, with many pathogens capable of infecting several species and being zoonotic in nature. With high morbidity, mortality, and healthcare expenditures; infectious illnesses constitute a serious threat to global health security. In the past few decades, many infectious diseases have emerged and reemerged because of dynamic host–pathogen interactions viz. Peste des petits ruminants (PPR) in ruminants, Crimean-Congo Hemorrhagic Fever (CCHF) in red deer, African swine fever (ASF) and foot-and-mouth disease (FMD) in wild boar, West Nile Fever (WNV) in wild birds, etc. These interactions are influenced by anthropogenic selection, niche adaptation, and climate change. Traditional diseases that were “on their way out” (such as malaria and tuberculosis) are resurging and may become more common in the near future, while at least a dozen “new” diseases have been identified, including acquired immunodeficiency syndrome (AIDS), Legionnaires’ disease, hantavirus pulmonary syndrome (HPS), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), monkeypox, and others [2]. While infectious diseases continue to be the most prevalent cause of mortality worldwide, they pose a threat to both humans and animals. Understanding the epidemiology of EIDs and REIDs at WLHI helps in developing practical operative prevention, control, and eradication of shared infectious pathogens where the wildlife host acts as a carrier or natural reservoir [3]. Therefore, regular and thorough surveillance (active and passive) and early detection is required to monitor spillover at WLHI and prevent disease transmission between humans, animals, and wildlife in either direction. The current review will provide an in-depth look at emerging and re-emerging infectious diseases at the WLHI with respect to zoonotic and economically important diseases. It further outlines the current approaches to surveillance, prevention and control of disease emergence and transmission at WLHI, and represents the existing knowledge gaps such as fragmented surveillance, limited understanding of transmission pathways of

the disease and insufficient longitudinal studies that require attention to strengthen One Health-based research, preparedness, and intervention strategies.

2. Literature Search Methodology

This article is structured as a comprehensive narrative review designed to synthesize current epidemiological, ecological, and socioeconomic evidence surrounding pathogen spillover and transmission dynamics at the WLHI.

Databases and Information Sources: A literature search was conducted across electronic databases including PubMed/MEDLINE, Google Scholar, Scopus, and Web of Science. In addition to peer-reviewed academic literature, grey literature, surveillance updates, and epidemiological bulletins were identified through official institutional repositories, including the World Health Organization (WHO), the Centers for Disease Control and Prevention (CDC), the World Organisation for Animal Health (WOAH, formerly OIE), the Indian Council of Medical Research (ICMR), and the Department of Animal Husbandry and Dairying (DAHD), Government of India.

Search Strategy and Keywords: Literature was retrieved using combinations of Medical Subject Headings and free text keywords combined with Boolean operators ('AND', 'OR'). Key search prompts included, ("emerging infectious diseases" OR "re-emerging infectious diseases" OR "zoonoses" OR "zoonotic spillover") AND ("wildlife-livestock-human interface" OR "One Health" OR "buffer zones") AND ("deforestation" OR "land-use change" OR "climate change" OR "antimicrobial resistance") AND ("India" OR "South Asia" OR "global").

Period Covered: The search prioritized peer-reviewed articles, epidemiological reports, and surveillance datasets published between January 1980 and June 2026, capturing major outbreak events, molecular epidemiological findings, and current One Health frameworks. Seminal historical records and foundational outbreak reports prior to 1980 were also identified through cross reference searching to provide critical chronological context.

Study Selection and Eligibility Criteria: Identified records were independently screened by title, abstract, and full text for topical relevance.

Inclusion criteria: The study included reviewed research articles, epidemiological investigations, systematic and scoping reviews, official agency reports, and policy guidelines published in English that specifically addressed (i) cross-species pathogen transmission at the wildlife–livestock–human interface, (ii) underlying anthropogenic, climatic, or ecological drivers of spillover, (iii) public health and economic impacts (with particular attention to low- and middle-income countries and the Indian subcontinent) and, (iv) One Health-oriented surveillance and intervention frameworks.

Exclusion criteria: Studies lacking relevance to wildlife, livestock, or human interface dynamics, non-peer-reviewed commentaries without verifiable data, non-English publications without verified translation and duplicate entries were excluded. Reference lists of selected articles were manually screened to retrieve additional relevant publications.

3. Emerging Infectious Diseases (EIDs)

EIDs are newly identified and previously unknown infectious agents that cause public health problems locally or globally; however, they also include diseases that have occurred throughout history but have only recently been recognized as distinct diseases caused by an infectious agent viz. Ebola, Zika, West Nile Fever, Hantavirus Pulmonary Syndrome, Lassa fever, etc. [4,5].

Emerging Infectious Diseases (EIDs)—A Chronological and Multispecies Perspective

Emerging infectious diseases (EIDs) are infections that have newly appeared in a population or have existed but are rapidly increasing in their incidence or geographic range. They may arise due to newly identified infectious agents, changes in host–pathogen interactions, zoonotic spillovers, ecological disturbances, or global travel and trade [6]. EIDs pose a significant threat to global public health, impacting both human and animal populations and stressing healthcare systems and biosecurity frameworks. The cause of pandemics by viral pathogens is escalated due to the close proximity of humans with animals. The population growth and expansion into wildlife have increased the risk of encountering new viruses from animals to humans. This can eventually lead to the spread of EIDs which can rapidly transmit into naïve populations. Nearly 75% of all EIDs have zoonotic origin and may circulate in animal hosts without causing apparent disease, while being capable of causing infections in humans [6]. This has exacerbated due to anthropogenic ecological disturbances such as climate change and urbanization [7].

A One Health approach is applied in monitoring viruses in aquatic environments [8,9]. The wider availability of molecular detection techniques such as quantitative polymerase chain reaction (qPCR) and digital PCR (dPCR) has eased the assessment of viruses in wastewater. These have been used in wastewater surveillance for targeting enteric pathogens and other zoonotic emerging viruses [10]. The most urgently needed research and development preparedness for seven virus-associated infections proposed by WHO includes Crimean Congo haemorrhagic fever; filovirus diseases (i.e., Ebola virus disease and Marburg virus disease); emerging coronavirus disease (COVID) (i.e., Middle East Respiratory Syndrome (MERS) CoV & Severe Acute Respiratory Syndrome (SARS) CoV); Lassa fever; Nipah virus infection, Rift Valley fever, and “Disease X”, a yet unknown or novel pathogen, most likely of zoonotic origin and capable of infecting the respiratory tract in humans and/or animals [7]. Table 1 chronologically outlines notable EIDs, the causative agent, and details their modes of transmission.

Table 1. Chronological emergence of key infectious diseases in humans.

Year	Disease	Pathogen	Host(s)	First Reported Location	Transmission	References
1931	Rift Valley Fever	Rift Valley Fever Virus	Mosquito (vectors: <i>Aedes</i> , <i>Culex</i>), domestic livestock (amplifying host), humans	Kenya	Direct exposure to blood, organs or secretions of infected animals, bite of infected mosquitoes	[11]
1944	Crimean-Congo hemorrhagic fever	Crimean-Congo hemorrhagic fever virus	Infected Ticks (vector), wild and domestic animals, birds, humans	Crimea, Europe	Direct contact with blood, saliva, organs or body fluids	[12]
1967	Marburg Virus Disease	Marburg Virus	Egyptian fruit bat (<i>Rousettus aegyptiacus</i>), non-human primates, humans	Marburg and Frankfurt, Germany, Belgrade, Serbia	Direct contact with blood and body fluids of infected persons or animals	[13]
1969	Lassa Fever	Lassa virus	Rodents (<i>Mastomys natalensis</i>), humans	Lassa, Borno State of Nigeria	Exposure to excreta, urine, body fluids (saliva, blood), inhalation of rodent excreta	[14]
1976	Ebola Virus Disease	Ebolavirus	Bats (reservoir), non-human primates, humans	Yambuku, Zaire (now DRC)	Direct contact with blood or body fluids	[15]
1981	HIV/AIDS	HIV-1, HIV-2	Humans; zoonotic origin from non-human primates	USA (recognized), Central Africa (origin)	Sexual, blood, vertical	[16]
1993	Hantavirus Pulmonary Syndrome (HPS)	Sin Nombre virus	Deer mouse (<i>Peromyscus maniculatus</i>), humans	Four Corners region, USA	Inhalation of aerosolized rodent excreta	[17]
1997	Avian Influenza (H5N1)	Influenza A H5N1	Birds (primary), humans	Hong Kong	Contact with infected poultry	[18]
1999	Encephalitis	Nipah Virus	Fruit bats (reservoir), pigs, humans	Malaysia, Singapore	Consumption of contaminated fruits, direct contact with infected animals, body fluids, respiratory droplets	[19]
2002	SARS	SARS-CoV	Bats, civets, humans	Guangdong, China	Respiratory droplets	[20]
2009	H1N1 Pandemic (Swine Flu)	Influenza A H1N1pdm09	Pigs, humans	Mexico, USA	Respiratory secretions	[21]
2012	MERS	MERS-CoV	Bats, camels, humans	Saudi Arabia	Respiratory droplets, zoonotic	[22]
2014	Ebola Virus (Resurgence)	Zaire ebolavirus	Bats, humans	Guinea, Liberia, Sierra Leone	Direct contact, nosocomial	[23]
2015	Zika Virus Outbreak	Zika virus	Humans, mosquitoes (<i>Aedes</i> spp.)	Brazil	Mosquito-borne, sexual, vertical	[24]
2019	COVID-19	SARS-CoV-2	Bats, humans (possible pangolin link)	Wuhan, China	Respiratory droplets, aerosols	[25]

4. Re-Emerging Infectious Diseases (REIDs)

REIDs are diseases that have been known for some time, had dropped to such low levels that they were no longer considered public health problems, and are now showing upward trends in incidence or prevalence worldwide, or have appeared in areas where they were previously unknown [26]. Many infectious disease specialists classify re-emerging diseases as a subcategory of emerging diseases. For example, tuberculosis has resurfaced as a result of bacterial evolution. The pathogen *Mycobacterium tuberculosis* has developed resistance to antibiotics such as isoniazid, rifampicin, as well as fluoroquinolones (either through single nucleotide polymorphisms or insertions and deletions), and long-term antibiotic use (both within an individual and across the population) has selected for the resistant pathogen's proliferation [27]. Additional factors contributing to the resurgence of tuberculosis include human immunodeficiency virus (HIV) epidemic as well as increased migration from tuberculosis-endemic countries [27]. Malaria has also developed resistance to antimalarial drugs such as chloroquine, piperazine artemisinin, and the vector mosquito has developed resistance to pesticides [28]. The re-emergence of diseases such as diphtheria and whooping cough (pertussis) is linked to insufficient population vaccination. When the proportion of immune individuals in a population falls below a certain threshold, the pathogen introduced into the population causes an outbreak of the disease. Table 2 highlights notable emerging and re-emerging infectious diseases of public health significance.

Table 2. Example of few emerging/re-emerging infectious diseases of public importance.

Types of Infectious Disease	Etiology	Emerging/Re-Emerging
Lyme disease	<i>Borrelia</i> spp.	Emerging
Cholera	<i>Vibrio cholerae</i>	Re-emerging
Plague	<i>Yersinia pestis</i>	Re-emerging
Vancomycin-resistant <i>Staphylococcus aureus</i> infections	<i>Staphylococcus aureus</i>	Re-emerging
Pathogenic <i>Escherichia coli</i> infections (food poisoning)	Pathogenic <i>E. coli</i> strains (O157:H7 & O104:H4)	Emerging
Multidrug-resistant tuberculosis infections	<i>Mycobacterium tuberculosis</i>	Re-emerging
<i>Cryptococcus gattii</i> infections	<i>Cryptococcus gattii</i>	Emerging
Cyclosporiasis infections	<i>Cyclospora cayentanensis</i>	Emerging
Drug-resistant malaria	<i>Plasmodium</i> spp.	Re-emerging
Variant Creutzfeldt–Jakob disease	Prion	Emerging
West Nile fever	West Nile virus	Re-emerging
Hantavirus pulmonary syndrome	Hantavirus	Emerging
Dengue fever	Dengue virus	Re-emerging
Japanese encephalitis	Japanese encephalitis virus	Re-emerging
Ebola hemorrhagic fever	Ebola virus	Re-emerging
Hendra virus infection	Hendra virus	Emerging
Nipah virus infection	Nipah virus	Emerging
Highly pathogenic avian influenza	H5N1, H7N9 influenza virus	Emerging
Severe acute respiratory syndrome	SARS-CoV-1	Emerging
2009 Pandemic influenza	Swine-origin H1N1 influenza	Emerging
COVID-19	SARS-CoV-2	Emerging

5. Zoonotic Emerging and Re-Emerging Infectious Diseases

Disease which is transmitted from animals to human is referred to as zoonotic disease and wildlife play an important role in zoonosis [29] Figure 1. In One Health, zoonotic disease provides strong bonds between human, animal, and environment health. Therefore, zoonotic EIDs (Ebola, West Nile Fever, Hantavirus infection, etc.) and REIDs (Rabies, Dengue, Malaria, Japanese Encephalitis, Brucellosis, etc.) may act as an indicator for ecological and environmental changes, biodiversity loss, intensive deforestation, illegal wildlife transport/trade, etc. [30]. As per the available data, out of 60.3% of new zoonotic diseases, 71.8% originated from wildlife [31].

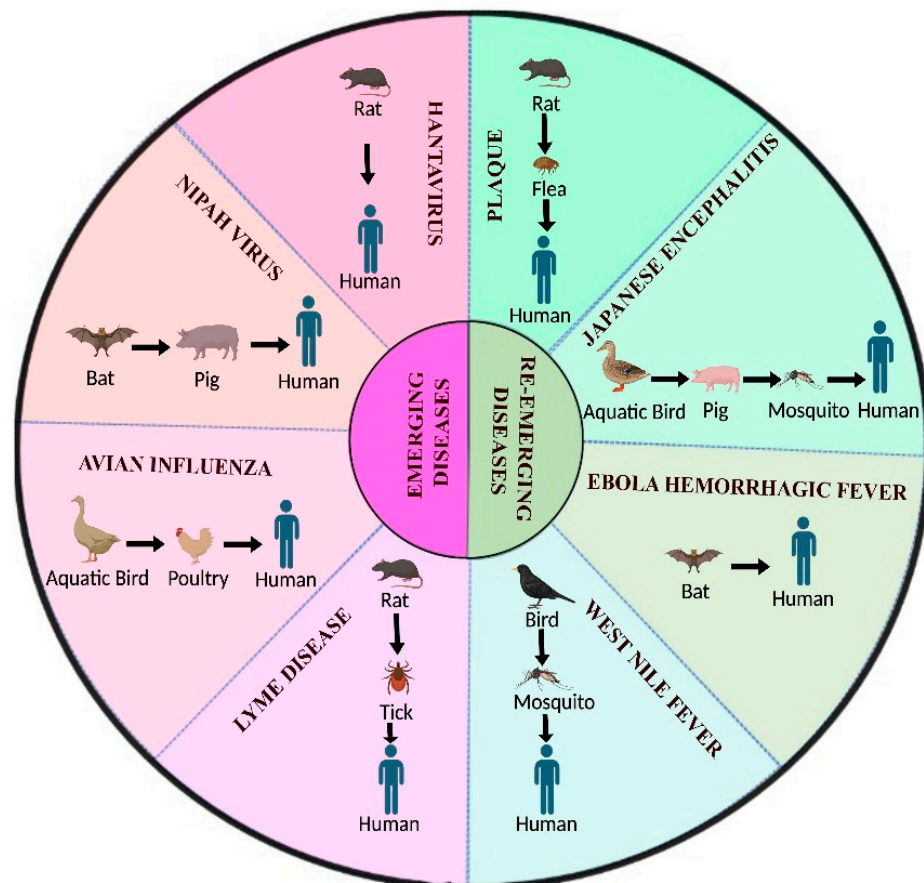


Figure 1. Schematic representation of major emerging and re-emerging zoonotic diseases and their associated transmission routes indicated by arrows.

A classic example of zoonosis is the hemorrhagic fever caused by filoviruses such as Ebola virus and Marburg virus that originate from bats and are transmitted to humans by non-human primates. Outbreaks of Ebola virus disease have most frequently been observed in African countries with a case fatality rate (CFR) ranging from 60 to 90% [32]. Similarly, Marburg virus disease has reported CFR varying from 23% to 88% in African countries and some countries in Europe [13]. Lassa fever is also a deadly viral hemorrhagic disease caused by Lassa virus and spread through infected rodents to humans with a CFR ranging from 15 to 20% in symptomatic patients [14]. CCHF transmitted from infected ticks to humans has a fatality rate of nearly 30% [12]. Effective control of zoonotic disease is challenging since its identification does not occur until a major outbreak. Therefore, there is an urgent need for preparedness for their prevention and control. Important zoonotic diseases associated with wildlife species are depicted in Table 3.

Table 3. List of zoonotic diseases encountered with wildlife species.

Disease	Etiological Agent	Reservoir	Route of Transmission	Occurrence	References
SARS-CoV-2	SARS coronavirus	Bats	Aerosol	Worldwide	[33]
MERS	MERS coronavirus	Camel	Aerosol	Worldwide	[33]
Dengue	Dengue virus	Monkey	Vector (<i>Aedes aegypti</i>)	Africa, Southeast Asia, America, Caribbean, Pacific	[34]
Highly Pathogenic Avian Influenza (H5N1)	Influenza viruses	Birds	Direct contact with feces, saliva, or mucosa of infected bird	China, Hong Kong, Europe, Africa, China, Russia, Kazakhstan	[35]
Ebola Hemorrhagic Fever	Ebola virus	Bats/Apes and Monkey	Direct contact with blood, body fluids, or tissues of infected animals or humans	Democratic Republic of Congo, Sudan, Uganda, Gabon	[33]
Hantavirus p Pulmonary Syndrome	Hanta virus	Rodents	Contact with rodent's feces, urine or saliva	America, Asia, Europe	[33]
Nipah Virus Diseases	Paramyxovirus	Pigs, Bats	Direct contact with infected animals or consuming contaminated food products	Malaysia, Singapore, India, Bangladesh	[33]
Rabies	Lyssa viruses	Raccoons, Skunks, Bat, Foxes	Direct contact (skin, mucous, tissues)/bite of rabid animal	All Continents Except Antarctica	[36]
Rift Valley Fever	Rift Valley Fever Virus	Cattle, Buffalo, Sheep Goat, Camel	Direct contact with infected animals or bite of infected mosquitos	African Madagascar, Saudi Arabia, Yemen	[11]
Septicaemic Plague	<i>Yersinia pestis</i>	Rodents	Flea bites or via skin lesion	Hong Kong, Africa, Asia, South America	[37]
Pneumonic Plague	<i>Yersinia pestis</i>	Rodents, Rabbits, and large animals	Aerosol	Manchuria, Congo, Madagascar, Peru	[37]
Bubonic Plague	<i>Yersinia pestis</i>	Rodents	Flea bites	Europe Africa, Asia, South America	[37]
Anthrax	<i>Bacillus anthracis</i>	Cattle, Sheep, Goats, Horses and Swine.	Inhaling/ingesting food contaminated with spores from infected animals	Asia, Europe, Africa, Australia.	[38]

While zoonotic EIDs and REIDs have emerged across different regions of the world, India, in particular, has experienced multiple waves of emerging and re-emerging infectious diseases affecting both human and animal populations. These include diseases such as *Vibrio cholerae* O139, diphtheria in 1980, plague in 1994, Nipah virus infection in 2001, chikungunya and dengue virus infection, avian influenza (H1N1), CCHF in 2011, acute encephalitis syndrome, SARS-CoV-2, lumpy skin disease (LSD) in cattle in 2019, and monkeypox virus infection. A chronological overview of key disease outbreaks and their emergence in the country is presented in Table 4.

These infectious diseases have significant public health, economic and social impacts. COVID-19, emerging in 2020, caused over 500,000 deaths in India and had a substantial impact on the economy [39]. Similarly, LSD, an emerging transboundary viral disease affecting cattle, was spread across 15 states by 2023, causing large-scale livestock mortality and disrupting milk production [40]. Diseases like monkeypox and CCHF are now part of

India's infectious disease surveillance framework due to repeated importations and local spillovers [41,42].

The wildlife reservoirs can play an important role in pathogen maintenance and spillover to human and animal populations. Environmental disturbances such as deforestation, agricultural encroachment, and livestock grazing in wildlife-dense areas can increase interactions among wildlife, livestock, and humans. Moreover, the degradation of buffer zones especially in states like Kerala, Maharashtra, and Gujarat has heightened the frequency of zoonotic spillovers [43–45]. Ecological transition areas between wildlife habitats and human settlements may therefore serve as important components of disease prevention by controlling cross-species contact.

Table 4. Chronological emergence of key infectious diseases (human and animal) in India.

Disease/Pathogen	First Known Outbreak	Affected Species	Transmission Route	Vaccine/Therapeutics Available	Economic Impact	Reference
<i>Vibrio cholerae</i> O139	1992	Humans	Contaminated water	Yes, Oral Cholera Vaccines (OCVs)	Seasonal burden in East India	[46]
Diphtheria resurgence	1980s	Humans	Respiratory droplets	Yes (DPT)	Rural child mortality	[47]
Plague	1994 (Surat)	Humans	Infected flea bites	Yes (antibiotic treatment available)	Trade panic, emergency measures	[48]
Nipah Virus	2001, 2018, 2023	Humans, bats	Contact with infected bats, animals or humans, consumption of contaminated food	No	Local trade, tourism affected	[49]
Dengue and Chikungunya	Recurrent	Humans	Vector <i>Aedes</i> mosquito	No	Outbreak cycles in metros	[50]
Highly Pathogenic Avian Influenza (H5N1)	2006–ongoing	Poultry, humans	Contact with infected birds	No	Poultry trade loss	[51]
CCHF	2011 onward	Humans, livestock	Ticks, blood contact	No	Occupational risk	[52]
Acute Encephalitis Syndrome (AES)	Seasonal outbreaks	Humans (children)	Viruses, toxins	No	Pediatric deaths in Bihar, Assam	[53]
SARS-CoV-2 (COVID-19)	2020–2022	Humans	Respiratory transmission	Yes (Covaxin, Covishield)	National GDP loss, >500K deaths	[54]
Lumpy Skin Disease (LSD)	2022–ongoing	Cattle	Insects, contact	Yes (Goatpox-based)	Dairy sector losses (INR crores)	[40]

India's One Health strategy aims to create integrated surveillance and response systems at the human–animal–environment interface. Emphasis is now placed on reinstating buffer zones, monitoring wildlife morbidity, and vaccinating livestock to minimize outbreaks, especially in areas near biodiversity hotspots.

6. Public Health and Socioeconomic Considerations of Emerging Diseases

Emerging and re-emerging infectious diseases continue to pose a considerable strain on both healthcare systems and socioeconomic structures. These diseases not only impact the medical services, but also affect the rural livelihood, food systems, and ecological health. The most affected groups are the rural communities near forests, urban slum dwellers, and smallholder livestock keepers. These populations typically lack access to clean water, health services, and education, making them especially susceptible to outbreaks. For instance, vector-borne diseases like Acute Encephalitis Syndrome (AES) disproportionately impact children in low-sanitation regions such as Bihar and Assam [53,55]. These consequences can extend from individual household to national economies.

Globally, both human pandemics and livestock diseases cause economic losses in billions. For example, LSD led to an estimated ₹20,000 crore loss due to cattle mortality and milk production decline [56]. Similarly, the COVID-19 pandemic resulted in GDP contraction, job losses, and increased healthcare costs [57]. In agrarian economies, the loss of even a single productive animal can have severe microeconomic consequences for smallholder families.

Environmental changes can further intensify these public health and socioeconomic impacts by increasing opportunities for contact among wildlife, livestock, and humans. Ecological transition areas between forests and human settlements also known as buffer zones are vital in reducing disease spillover [58]. However, widespread degradation due to deforestation, mining, and unregulated land use has increased contact between humans, livestock, and wildlife. The 2018 Nipah virus outbreak in Kerala, India, is a case in point, occurring in areas where fruit orchards were located near human dwellings and bat roosting sites, highlighting the role of shrinking wildlife habitats in disease emergence [59]. The restoration of these zones is central to One Health preparedness and disease prevention, highlighting the importance of recognizing the interconnected environmental, socioeconomic, and health determinants [58,60].

7. Factors Contributing to Emergence and Re-Emergence of Infectious Diseases

EIDs and REIDs are not random events but rather the direct consequences of intricate interactions between pathogens, hosts, and their shared environment. One of the most profound drivers of EIDs and REIDs emergence is ecological change, encompassing phenomena such as deforestation, climate change, and habitat alteration. These environmental transformations directly impact vector distribution, host populations, and the frequency of human–wildlife interactions, thereby creating novel opportunities for pathogen spillover and amplification [61–63]. The constant need for the development of cost-effective diagnosis, prevention, and therapeutic strategies, as well as the maintenance of real-time epidemiological surveillance, pose significant challenges to the public health and agricultural systems. A comprehensive understanding of these underlying drivers is critical for anticipating future threats and developing effective measures at WLHI for disease prevention and control.

7.1. Pathogen-Related Factors

Pathogenic infectious agent evolution (microbial adaptation and change), mutations, drug resistance development, pesticide resistance of vectors, etc., facilitates the emergence and re-emergence of infectious diseases [64]. Antimicrobial resistance (AMR) is an important example of pathogen adaptation. It is a critical global health threat driven by inappropriate prescribing, patient non-adherence, counterfeit pharmaceuticals, and exten-

sive use of antimicrobials in human, livestock and agriculture [65]. Resistant pathogens often emerge in livestock or wildlife and spill over to humans through direct contact, food, or contaminated environments, especially in buffer zones between human settlements and natural habitats [66]. The emergence of the *mcr-1* gene in China (2015), conferring colistin resistance across pigs, food, and humans, provides a notable example of cross-sector AMR dissemination, underscoring the urgency of integrated surveillance [67]. These interconnected transmission pathways highlight the importance of a One Health approach to AMR surveillance and control [68].

Similarly, pesticide or insecticide resistance in vectors can jeopardize vector-control measures thereby facilitating persistence and transmission of vector-borne pathogens [69]. Moreover, introduction of a pathogen into a new host population can subsequently establish itself in the indigenous wildlife, resulting in major ecological and disease-related consequences. For instance, West Nile virus infection in North-East American birds and plague in wild rodents in North-Western America [69].

The diagnostics tools and techniques also influence identification of EIDs and REIDs. Improved modern diagnostics tools and techniques may disclose the new pathogens or discovery of existing pathogens [70]. Additionally, deliberate release of harmful pathogens represents another pathogen-related threat. Bioterrorism involves the use of biological agents such as anthrax, smallpox, or salmonella to attack people, as seen in the 2001 anthrax attacks in the U.S. [71] and the 1984 *Salmonella* poisoning in Oregon [72]. Other diseases like glanders (used in World War I), plague (used by Japan in China during the 1930s–40s), tularemia (tested during World War II and the Cold War), and melioidosis (studied as a potential weapon) were also used in biological warfare [73–75]. Many of these come from animals and spread to humans, showing the “One Health” link [68]. Such threats further suggest the need for effective surveillance, preparedness and rapid diagnostic capacity in control of EIDs and REIDs.

7.2. Host-Related and Demographic Factors

Human demographic change (moving to new areas) resulting in contact with animals and natural environment; human behavior (sexual and drug use, sharing needles, drug abuse, body piercing); human susceptibility to infection (immunosuppression) due to stress and lifestyle changes; nutritional changes through increased use of pesticides; globalization of travel and trade; agricultural practices such as pig farming (Nipah virus), goose farms (West Nile virus—Israel); and breakdown of public health measures such as breakdown in vector control, etc., may contribute to the emergence and transmission of diseases [76].

Agricultural intensification, particularly the rise of concentrated animal feeding operations (CAFOs) and the continued use of live animal markets (often referred to as wet markets), creates ideal conditions for the EIDs and REIDs of zoonotic pathogens. These environments often house large numbers of genetically similar animals in close confinement, facilitating rapid pathogen transmission [77–79]. In this environment, livestock maneuvers can aid as mixing vessels for disease agents, while agriculture farming can attract disease-carrying wildlife to areas of human activity [80]. Furthermore, outbreaks of Nipah virus in Southeast Asia have been directly linked to the expansion of intensive pig farming into areas adjacent to fruit bat habitats, thereby bridging the transmission pathway from bats to pigs and subsequently to humans [81,82].

7.3. Environmental and Ecological Drivers

Environmental change can affect the distribution, abundance and behavior of hosts, vectors and pathogens. The impact of climate change, particularly rising temperature and altered precipitation pattern, expand the geographical range of arthropod vectors like

mosquitoes. This expansion facilitates the spread of vector-borne diseases such as malaria and dengue fever into previously unaffected regions, while also potentially shortening the extrinsic incubation period of the pathogen within the vector, accelerating the transmission cycles [83,84]. Furthermore, shifts in weather patterns can dramatically influence rodent populations, subsequently elevating human exposure to hantaviruses and precipitating outbreaks of HPS [85,86].

The destruction of natural habitats through deforestation brings human populations into closer proximity with wildlife reservoirs, increasing the likelihood of zoonotic transmission or spillover of other infectious disease having economic importance. This mechanism is clearly observed in the escalating incidence of disease like Lyme disease, where fragmented forest landscapes lead to higher densities of deer and ticks, enhancing the exposure of human populations to *Borrelia burgdorferi* [62,87,88].

Change in biodiversity and predator–prey dynamics may influence disease transmission. High biodiversity is responsible for distribution of effect of pathogens in large number of hosts while biodiversity loss can converse the pathogen distribution in lesser species and can lead to increasing transmission to humans. Moreover, alteration in predator–prey relationships can also modify population sizes and community structure, thereby influencing the disease dynamics [89].

Wildlife farming provides another opportunity for pathogen maintenance and amplification. Mammals like deer, rodents, civets and other fur animals are legally bred for income and protein source worldwide [90–92], but as per the published literature, farming systems are poor which leads to the poor health condition of these captive animals, thus predisposing them to the emergence of many infectious diseases [92,93]. Examples include avian influenza in ostrich farms in South Africa [94], rabies outbreak in Kudu (*Tragelaphus strepsiceros*) population in Namibia [95], and SARS-CoV-2 in mink (*Neogale vison*) farms in the Netherland [96].

7.4. Human and Wildlife Interaction

Wildlife plays an important part in biodiversity and has a vital role in maintaining a healthy environment. Human–wildlife conflicts may occur through crop damage, increased chance of livestock as well as human predation, high probability of disease transmission, illegal wildlife trade, emergence and re-emergence of zoonotic disease, public health issues etc. [97–100]. The wildlife trade, especially illegal trade of exotic animals, the capture, transport, and consumption of wild animals for food, traditional medicine, or the pet trade, may expose humans to these pathogens that would otherwise remain geographically or ecologically isolated [101–103].

Wildlife, livestock, and humans may therefore collectively form interconnected transmission networks at WLHI. Many wildlife act as a carrier or reservoirs for zoonotic pathogens and are responsible for spillover and contamination at WLHI [104,105]. These zones become hotspots for spillover events, especially when intensified by deforestation, agricultural expansion, or climate-driven animal migration, and are responsible for disease transmission from one species to another [105,106]. Frequent spillover of Ebola virus disease from wild animals (natural reservoirs like bats and non-human primates) into human populations have been observed through contact with infected bushmeat or direct interaction [62,107]. The initial SARS outbreak in 2003 was strongly associated with civet cats sold in live animal markets, implicated as an intermediate host in the virus transmission to humans, highlighting the direct link between wildlife commerce and disease emergence [108,109]. Similarly, sporadic outbreaks of monkeypox, though typically less severe, are often traced back to direct contact with infected wild animals, with the global spread occasionally exacerbated by the international trade in exotic pets [110,111]. An-

other good example of spillover of pathogens to humans is HIV, which originated from non-human primates and may have crossed the species barrier due to contact with hunted animals [16,112].

Once a pathogen crosses into rural communities, it can rapidly reach urban populations through livestock trade, human mobility, and weak surveillance systems. A well-documented example is the Nipah virus outbreak in Malaysia (1998–1999), where fruit bats displaced by habitat loss infected pigs, which then transmitted the virus to farmers, eventually leading to cases in urban hospitals [113]. Similarly, the 2014–2016 Ebola outbreak began in the forested region of Guinea and spread to major cities such as Monrovia and Freetown due to high population movement [114]. More recently, COVID-19 (2019-nCoV) has been associated with a possible wildlife origin, with bats considered a potential natural reservoir. The early cases report its spread from live animal markets in Wuhan to the global population via dense urban connectivity; however, the precise wildlife origin and transmission to humans remain uncertain [115]. These cases highlight the need for integrated One Health surveillance across buffer zones and rural interfaces to prevent future pandemics.

7.5. Globalization and Dissemination of Emerging Diseases

Beyond localized ecological shifts, globalization has increased the opportunities for pathogen dissemination by an unprecedented increase in international travel and trade. This increased interconnectedness may allow a novel pathogen to rapidly traverse continents, transforming a localized outbreak into a global pandemic within days or weeks [116]. The SARS epidemic in 2003 and SARS-CoV-2 provided an early and stark illustration of this phenomenon, with the virus swiftly spreading from its origins in Asia to numerous countries via international air travel [117–119]. Similarly, the rapid expansion of Zika virus across America in the mid-2010s was largely attributable to increased human movement and the subsequent introduction of the virus into regions with competent *Aedes aegypti* mosquito populations [120,121].

8. Prevention and Control of EIDs and REIDs: A One Health-Based Strategy

Preventing EIDs and REIDs requires a wide, coordinated effort. The One Health approach, which joins human, animal, and environmental health efforts, plays a key role in controlling these diseases, especially those that pass between animals and people [69]. Sharing health warnings early at all levels, from local to global, could aid in guiding public action [122]. In addition, improving teamwork between countries by sharing outbreak reports, tools, trained manpower, and healthcare training programs is essential for effective disease control and prevention [123]. Offering rapid testing and treatment in rural areas where most diseases spill over from animals to humans is important [113]. Use of antibiotics wisely to avoid creating resistant bacteria could minimize the dissemination of resistant strains [67]. Continued research on vaccines, fast diagnostics, and new treatments for high-risk diseases like Ebola and COVID-19 should be encouraged for preparedness [115]. Furthermore, global health systems with strong political and financial support should be built to respond faster to future outbreaks.

8.1. Surveillance and Response

Quick detection of strange or unexpected disease patterns may aid in early prevention of outbreaks. Additionally, the real-time data sharing between local and global health teams can limit the spread before it becomes serious [115,122]. Monitoring areas where people and animals live closely such as buffer zones or destruction of forest is important in prevention of disease transmission between animals and humans [123,124].

8.2. Applied Research

Scientists and public health teams must work together to study disease patterns and improve ways to diagnose and treat infections. Special focus should be on diseases that come from food or animals, such as *E. coli* and *Campylobacter*, which often spread through meat, milk, or water [125]. Research should also track how antibiotic-resistant infections are rising, such as the spread of *mcr-1*, a gene that makes bacteria resistant to last-line antibiotics like colistin [67].

8.3. Infrastructure and Training

Countries must improve hospitals, labs, and data systems to help detect and manage outbreaks faster. Healthcare workers, vets, and environmental scientists should be trained together under One Health so they can respond better to share health threats [68].

9. Knowledge Gaps and Future Directions

Emerging infections come from complex reasons including changes in the environment, farming, animal health, and human behavior. To manage these risks, we need strategies that connect all areas of health. Despite the importance of WLHI as a central medium for disease emergence, there is fragmented surveillance. Future studies should focus on development of an integrated surveillance system combining epidemiological, veterinary, wildlife and environmental data. In addition, the actual transmission pathways of these diseases are poorly understood. Combining longitudinal surveillance, pathogen genomics and ecological studies may provide a better understanding of the pathways. Moreover, lack of longitudinal studies has limited our prior understanding and effective measures of preventing pathogen spillover. Furthermore, there is a lack of standardized WLHI risk assessment.

Addressing these knowledge gaps should be complemented by strengthening global health systems and improving quick response abilities, watching for new diseases in animals and people before they spread widely, developing and delivering vaccines for diseases like Lassa fever, Ebola, and new coronaviruses, and supporting research on new antibiotics and other medicines, especially for drug-resistant bugs. Avoiding overuse of antibiotics in people, animals, and farming is also essential. Control of disease carriers like mosquitoes, keeping wildlife and domestic animals healthy and education of public to prevent infections, and safe food handling, especially in rural and high-risk zones, should further be incorporated into One Health preparedness strategies.

10. Limitations of the Present Study

The present review has certain limitations. Firstly, since this was a narrative review, the selection and synthesis of literature may be subject to potential selection bias. Additionally, the restriction to English language publications may have resulted in the exclusion of relevant studies published in other languages. The review broadly addressed the drivers of disease emergence at WLHI which limited the understanding of each individual factor in detail. Moreover, since the review was synthesized from previous published studies, certain pathogens and geographical regions may have been extensively studied while certain others remained poorly represented limiting the extent to which region-specific patterns and differences in spillover risk could be assessed.

11. Conclusions

In conclusion, the review represents that the emergence and re-emergence of infectious diseases at WLHI is a multifaceted problem driven by a complex interplay of ecological, environmental and anthropogenic factors including ecological disruption, global connectiv-

ity, intensive agricultural practices, trade and animal consumption, and the insidious rise of antimicrobial resistance. It also highlights that rather than a single factor, convergence of pathogen characteristics, host susceptibility, environmental conditions and interaction patterns among hosts are collectively responsible for pathogen spillover. The complex and interconnected nature of these factors highlights the importance of a One Health approach to improving the effectiveness of public health response and interventions, as well as the recruitment and application of multiple areas of expertise to fight EIDs and REIDs. Thus, strengthening integrated surveillance across these sectors supported by a One Health approach can improve early detection of emerging threats and facilitate timely risk assessment and intervention.

Author Contributions: R.R.: Writing—original draft and review, conceptualization, resource, data curation, visualization, analysis; V.L.: Writing—original draft and review, visualization; P.P.S.: Writing—editing and review, formal analysis, visualization; V.G.: Writing—editing and review; S.D.: Writing—editing and review; S.M.: Writing—editing and review; J.K.B.: Writing—editing and review; P.K.R.: Writing—editing and review; K.K.: Writing—editing and review, visualization. All authors have read and agreed to the published version of the manuscript.

Funding: This research received no external funding.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: All data in this study are used from open source and included in this article.

Acknowledgments: ICAR-National Institute on Foot and Mouth Disease, and authors are grateful to the Indian Council of Agricultural Research (ICAR), Department of Agricultural Research and Education, Government of India for providing the necessary support and facilities to carry out this work. During the preparation of this study, the authors have taken the assistance of AI Academic Writing Tool Paperpal (Cactus Communications) in order to only improve readability and language of the manuscript. After using this tool, the authors have carefully reviewed and edited the content as needed and take full responsibility for the content of the published article.

Conflicts of Interest: Author Vinay Lomash was employed by the company RCC Laboratories India Pvt. Ltd. The remaining authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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