

Emerging Human Viral Diseases: Drivers, Countermeasures, and Future Challenges

Abstract

Aims: To summarize current evidence on the ecological, environmental, socioeconomic, and health-system drivers of viral emergence and re-emergence; Review advances in preventive and therapeutic countermeasures; Evaluate the contribution of the One Health framework; And identify major global preparedness gaps and potential solutions for future outbreaks.

Information & Methods: Relevant literature and outbreak-related reports on emerging human viruses were retrieved from PubMed and Google Scholar using predefined keywords. This narrative review synthesized evidence regarding drivers of viral emergence, prevention and treatment strategies, One Health implementation, surveillance systems, and global preparedness challenges.

Findings: Emerging viral diseases are driven by viral evolution, environmental change, human activities, and weaknesses in public health systems. Advances in vaccines, antivirals, monoclonal antibodies, and novel therapeutic approaches have improved outbreak preparedness and response. However, major challenges remain, including fragmented surveillance, inequitable access to countermeasures, health-system limitations, and misinformation. The One Health approach provides a framework for strengthening prevention, early detection, and coordinated response.

Conclusion: Mitigating the increasing threat of emerging viral diseases requires a comprehensive and multidisciplinary strategy that combines biomedical innovation, integrated One Health surveillance, resilient health systems, equitable access to diagnostics, vaccines, and therapeutics, and sustained international collaboration. Addressing persistent preparedness gaps through coordinated governance, long-term investment, and cross-sectoral partnerships will be essential for strengthening global health security and improving readiness for future outbreaks.

Keywords

Viruses [<https://www.ncbi.nlm.nih.gov/mesh/68014780>];

One Health [<https://www.ncbi.nlm.nih.gov/mesh/2023382>];

Public Health Surveillance [<https://www.ncbi.nlm.nih.gov/mesh/68062486>]

1. Introduction

Emerging viruses are defined as pathogens that have newly appeared in a population or have existed previously but are rapidly increasing in incidence or geographic distribution, posing substantial threats to global health security ^[1, 2]. The frequency of emerging viral diseases has increased considerably over recent decades, driven by complex interactions among environmental, ecological, and societal factors. Rapid urbanization, population growth, globalization, climate change, land-use modifications, and intensified human-animal interactions have created favorable conditions for zoonotic spillover and the dissemination of novel pathogens across regions and continents ^[1, 3]. These interconnected drivers have reshaped the epidemiological landscape of infectious diseases, increasing the likelihood of both spillover events and widespread transmission once human infection is established.

The Coronavirus disease 2019 (COVID-19) pandemic highlighted the profound health, economic, and social consequences that emerging viruses can impose on a global scale. Beyond COVID-19, recurrent outbreaks caused by pathogens such as the Ebola virus, Zika virus, Nipah virus, avian influenza viruses, and other zoonotic agents have demonstrated the continuing vulnerability of health systems to emerging infectious threats ^[4-8]. These outbreaks have not only resulted in significant morbidity and mortality but have also disrupted healthcare delivery, weakened economies, and exposed structural weaknesses in global health preparedness. Importantly, they have underscored the critical need for early detection systems, rapid diagnostic tools, and coordinated international response mechanisms.

Despite substantial advances in vaccine development, antiviral therapies, and outbreak response mechanisms, significant challenges remain. Weak surveillance infrastructures, insufficient cross-sectoral collaboration, disparities in access to medical countermeasures, and limited long-term investment continue to hinder global preparedness and response efforts. In many regions, delays in reporting and inadequate laboratory capacity further exacerbate the risk of uncontrolled transmission. Increasing recognition of the interconnectedness of human, animal, and environmental health has further reinforced the importance of the One Health approach in addressing emerging viral threats ^[9-11]. Strengthening this integrated framework is essential for improving prevention, detection, and response strategies at the human-animal-environment interface.

Although several reviews have addressed specific emerging viruses or individual determinants such as climate change, zoonotic transmission, or pandemic preparedness, there remains a need for an integrated synthesis that collectively examines the major drivers of viral emergence alongside advances in preventive and therapeutic strategies and persistent global preparedness gaps. This narrative review addresses this gap by providing a comprehensive overview of the multifactorial drivers of viral emergence, evaluating current countermeasures, and highlighting critical weaknesses in global surveillance and response systems within a One Health framework. Given the growing burden of emerging viral diseases and the persistent gaps in preparedness, this narrative review aims to provide a comprehensive overview of the major drivers of viral emergence, advances in preventive and therapeutic countermeasures, the role of public health within the One Health framework, and the critical global challenges that must be addressed to strengthen future outbreak preparedness and response.

2. Drivers of emerging viruses

2.1 Viral evolution

The accelerating emergence of novel viral pathogens is not a random phenomenon but rather the product of complex, interconnected drivers that create favorable conditions for cross-species transmission and global spread. A seminal framework established by the Institute of Medicine (IOM), initially outlining 6 factors in 1992 and expanded to 13 in its 2003 report, provides a systematic structure for understanding these multifactorial threats to global health security ^[12]. These drivers reflect the consensus that viral emergence arises from converging pressures across microbial evolution, host susceptibility, environmental change, and human systems. At the microbial level, viruses adapt with their hosts through mutation, recombination, and reassortment, which enhances transmissibility and immune escape. The particularly high mutation rate of RNA viruses is central to this process ^[13]. For example, the emergence of the Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Omicron variant was associated with an exceptional accumulation of spike mutations that increased transmissibility and reduced susceptibility to immunity induced by vaccination or prior infection ^[14]. Host vulnerability further amplifies this risk, especially when the immune system

is suppressed ^[15]. The rapid global spread of SARS-CoV-2 illustrates this point clearly, as the absence of pre-existing immunity facilitated pandemic expansion in contrast to seasonal coronaviruses ^[3].

2.2 Environmental & climatic drivers

Environmental and climatic changes also shape viral emergence by altering vector distribution and virus survival. Variations in temperature, precipitation, and humidity can expand the geographic range of arthropod vectors and modify the environmental persistence of viruses ^[16]. Accordingly, climate-driven expansion of *Aedes aegypti* and *Aedes albopictus* has increased the risk of dengue, chikungunya, and Zika outbreaks in previously non-endemic areas of Europe and North America ^[17]. Similarly, ecosystem disruptions such as deforestation and habitat fragmentation bring wildlife, livestock, and human populations into closer contact, increasing the likelihood of zoonotic spillover ^[18]. The Nipah virus outbreak in Malaysia is a well-known example in which deforestation displaced fruit bats closer to pig farms, facilitating viral amplification and subsequent transmission to humans ^[7].

2.3 Human behavior & urbanization

Human behavior and patterns of human development further intensify these risks. Rapid population growth, urbanization, and densely populated environments facilitate human-to-human transmission, while activities such as bushmeat hunting increase opportunities for zoonotic spillover ^[9]. Highly populated urban centers such as Wuhan and New York facilitated the rapid amplification and spread of SARS-CoV-2 ^[19]. Simultaneously, environmental changes driven by agriculture, mining, and dam construction can disrupt ecological balance and increase contact between humans and wildlife ^[10]. Similarly, irrigation projects can contribute to Rift Valley fever outbreaks by creating favorable breeding conditions for mosquitoes ^[20]. Increasing global connectivity has facilitated the transition of localized outbreaks into international public health threats. Modern air travel enables infected individuals to travel across continents within hours, accelerating the rapid dissemination of emerging pathogens ^[21]. The 2003 Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) outbreak reached 29 countries within a few months through international travel, a pattern that was later observed on a much larger scale during the COVID-19 pandemic ^[22]. Technological and industrial advancements can inadvertently contribute to viral emergence. While these interventions offer critical diagnostic and therapeutic benefits, practices such as convalescent plasma administration and gain-of-function (GOF) research may inadvertently influence viral evolution ^[23]. GOF refers to experiments in which an organism acquires a new biological property or enhanced function. In influenza research, the term has become associated with potentially risky studies that may increase viral transmissibility, virulence, or the ability to evade host immunity. For example, serial passage of the H5N1 virus in ferrets led to variants capable of mammalian transmission. However, similar experimental approaches have also contributed to important medical advances. Passage of viruses in cells from other species has historically been used to attenuate pathogens and develop vaccines, such as the poliovirus vaccine. Therefore, GOF is a widely used tool in biomedical research. The primary concern is not the concept of GOF itself, but experiments that generate pathogens with increased transmissibility or virulence in mammals, which could pose public health risks if accidentally or deliberately released. While the debate has largely focused on influenza virus research, these concerns also extend to other potential pandemic pathogens, including coronaviruses ^[24]. Furthermore, the widespread use of monoclonal antibody (mAb) therapy has been shown to exert selective pressure, potentially driving the emergence of resistant variants ^[25].

2.4 Health system factors

Weaknesses in public health systems and broader social determinants of health are also critical factors. Inadequate surveillance, poor sanitation, and weak reporting systems can delay outbreak detection and response, allowing epidemics to expand before effective control measures are implemented ^[11]. The 2014-2016 West African Ebola epidemic provides a notable example of how fragile healthcare systems in Guinea, Liberia, and Sierra Leone contributed to delayed containment efforts and sustained transmission ^[26]. Poverty and social inequality further intensify these vulnerabilities by limiting access to healthcare, worsening nutritional status, and forcing many individuals into overcrowded living conditions ^[27]. During the COVID-19 pandemic, mortality rates were disproportionately high among marginalized and low-income populations ^[28].

2.5 Socioeconomic & political factors

Conflict, famine, and population displacement further weaken public health resilience, as illustrated by the cholera crisis in Yemen following the destruction of water, sanitation, and hygiene infrastructure [29, 30]. In addition, insufficient political commitment and chronic underinvestment in preparedness continue to leave health systems vulnerable to emerging outbreaks [31, 32]. Beyond these structural challenges, the deliberate misuse of biological agents remains an important threat to both public health and global security [33, 34].

The conceptual framework presented in Figure 1 illustrates the multifactorial and interconnected drivers of emerging viral diseases. As shown, environmental disruption, climate change, urbanization, wildlife spillover, global travel, poverty, conflict, and weak health systems act as distinct but highly interdependent drivers that collectively shape the risk landscape. Rather than functioning in isolation, these factors reinforce one another; For example, climate change and environmental degradation alter ecosystems and increase human-animal contact, while urbanization and global mobility accelerate transmission once spillover occurs. Socioeconomic instability, including poverty and conflict, further amplifies vulnerability by weakening healthcare infrastructure and limiting access to timely diagnosis and intervention. Weak health systems act as a critical issue, allowing localized zoonotic events to persist and expand. The convergence of these drivers ultimately lowers the threshold for spillover and facilitates the transition from sporadic infections to sustained outbreaks and global dissemination.



Figure 1. Drivers of emerging viral diseases. Schematic representation of eight key interconnected drivers of emerging viral diseases, including environmental disruption, urbanization, climate change, wildlife spillover, global travel, poverty, conflict, and weak health systems. These factors do not operate independently but interact synergistically to shape the risk landscape of viral emergence. Through ecological disruption, increased human-animal contact, population mobility, and weakened healthcare infrastructure, they collectively lower the threshold for zoonotic spillover and facilitate sustained human-to-human transmission, ultimately increasing the likelihood of local outbreaks and global spread

3. Therapeutic and prophylactic strategies

The landscape of therapeutic and prophylactic strategies for emerging human viral infections has evolved substantially over recent decades, shifting from conventional antiviral development toward

integrated, multi-platform approaches that target both viral pathogens and host determinants of disease. This progress reflects advances in molecular biology and immunology, as well as lessons learned from recent outbreaks such as Ebola, Zika, and COVID-19, which underscore the need for rapid, scalable, and equitable implementation of medical countermeasures [35].

Vaccination remains the cornerstone of viral disease prevention and the most cost-effective strategy to achieve population-level immunity. The field has transitioned from classical live-attenuated and inactivated vaccines to recombinant subunit, viral vector, and nucleic acid platforms that enable faster design and adaptive response to emerging pathogens [36]. The unprecedented speed at which mRNA and adenoviral vector vaccines were developed and authorized during the COVID-19 pandemic demonstrated the versatility of these platforms, providing protection exceeding 90% against severe disease. Similarly, the recombinant vesicular stomatitis virus-Zaire Ebola virus vaccine (rVSV-ZEBOV) showed high efficacy and was successfully used in ring vaccination campaigns, ultimately becoming the first licensed Ebola vaccine [37]. While these platforms share the goal of inducing protective immunity, they differ in important practical aspects. mRNA vaccines allow rapid redesign and scalable production but often require cold-chain storage, whereas viral-vector vaccines may induce stronger cellular immunity but can be affected by pre-existing vector immunity [38].

mAbs have reshaped the therapeutic landscape by enabling passive immunization that rapidly neutralizes circulating virus. They are particularly important for protecting high-risk populations and immunocompromised individuals who may not mount adequate adaptive immune responses after vaccination [39]. The antibody cocktail casirivimab/imdevimab (REGEN-COV) significantly reduced hospitalization and mortality in early COVID-19 infection [40], illustrating the clinical potential of targeted immunotherapy.

Similar antibody-based strategies have also demonstrated efficacy against other emerging viruses, including Ebola virus disease, where monoclonal antibody therapies such as REGN-EB3 and mAb114 significantly improved survival in clinical trials [41].

However, their effectiveness can be rapidly undermined by antigenic drift and escape mutations that alter viral epitopes [42], emphasizing the importance of continuous epitope surveillance and cocktail design.

Alongside biologics, direct-acting antivirals (DAAs) that target key viral enzymes or replication pathways remain essential components of antiviral therapy. Advances in structural virology and computational drug discovery accelerated the development of agents such as remdesivir, the first Food and Drug Administration (FDA)-approved antiviral for COVID-19, and nirmatrelvir/ritonavir (Paxlovid), both of which significantly reduced hospitalization when administered early [43, 44]. Antiviral drugs have also long played a role in controlling other viral infections, such as neuraminidase inhibitors (e.g., oseltamivir) for influenza [45].

As emerging pathogens continue to challenge existing prevention and treatment strategies, next-generation approaches are being developed to address the limitations of current technologies. Novel vaccine platforms aim to improve the durability of immune responses, thermostability, and the breadth of protection. Self-amplifying and thermostable mRNA technologies may provide broader protection against divergent viral strains, while universal vaccine strategies targeting conserved epitopes are being explored to strengthen preparedness for future pandemics [46, 47].

In parallel with these innovations, host-directed therapies (HDTs) target cellular and immunological processes exploited by viruses during infection rather than the virus itself. By modulating host pathways involved in endosomal trafficking, protease activation, and inflammatory signaling, these approaches may provide broad-spectrum antiviral activity while reducing immunopathology [48]. For example, baricitinib, a Janus kinase (JAK) inhibitor, showed clinical benefit in severe COVID-19 by attenuating excessive inflammatory responses, supporting the therapeutic potential of HDTs in viral diseases [49]. Broad-spectrum antivirals are also being developed to target conserved viral or host factors shared across multiple viral families and are less prone to mutational escape. Recent studies have identified inhibitors of the coronavirus main protease (Mpro) and flaviviral NS5 polymerase, several of which are progressing toward clinical evaluation [50, 51].

Gene-based therapies represent another promising area of antiviral research. RNA interference (RNAi) and Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)-based gene-editing technologies enable the selective silencing or cleavage of viral genomes within infected cells [52]. Lipid nanoparticle-delivered siRNAs targeting Ebola or Marburg viruses, along with CRISPR-Cas systems designed to degrade viral RNA, are currently under investigation as potential antiviral strategies capable of providing sustained cellular protection [53].

Future antiviral preparedness will likely depend on integrating complementary strategies, including advanced vaccine platforms, direct-acting antivirals, monoclonal antibodies, host-directed therapies, and gene-based interventions. However, translating these innovations into real-world public health impact requires addressing several implementation challenges, including high manufacturing costs, large-scale production capacity, cold chain logistics, and equitable access to vaccines and therapeutics in low and middle-income countries (LMICs) ^[54]. Developing scalable and globally accessible therapeutic infrastructures will be essential for responding not only to current viral epidemics but also to future emerging infectious threats ^[55].

4. Public health and the One Health approach

Emerging viral diseases highlight the close connections among human, animal, and environmental health. In this context, the One Health approach provides an integrated framework that recognizes the interdependence of human populations, domestic and wild animals, and shared ecosystems. This perspective is particularly important for understanding the factors that drive viral emergence, given that nearly 60% of known human infectious diseases and approximately 75% of emerging pathogens are zoonotic in origin ^[56].

The One Health framework provides a structured mechanism to address drivers by integrating environmental monitoring, veterinary surveillance, and human public health systems into coordinated early warning networks ^[57].

For decades, the separation of human, animal, and environmental health sectors has contributed to missed early warning signals, delayed responses, and inefficient use of resources during outbreaks. At its core, the One Health approach aims to address the underlying drivers of spillover rather than focusing solely on outbreak response. This includes reducing deforestation and habitat fragmentation, regulating high-risk wildlife trade, and promoting sustainable agricultural practices that minimize risky interactions between humans and animals ^[58]. Effective outbreak response also requires coordinated collaboration among veterinarians, ecologists, physicians, epidemiologists, and public health authorities. Several outbreaks illustrate the practical value of One Health implementation. The 2014-2016 West African Ebola outbreak demonstrated how human encroachment into forested areas and contact with wildlife reservoirs can precipitate large-scale epidemics, highlighting the importance of integrated ecological and epidemiological surveillance ^[59]. Similarly, highly pathogenic avian influenza outbreaks (such as H5N1 and H7N9) have required coordinated monitoring of poultry, migratory birds, and human infections to reduce cross-species transmission ^[60]. Arthropod-borne viruses such as Zika virus and West Nile virus further illustrate how environmental factors, vector ecology, and human mobility interact to shape outbreak dynamics ^[61, 62]. This multidisciplinary approach proved particularly valuable during Nipah virus outbreaks in Bangladesh, where integrated investigations involving human cases, bat reservoirs, and contaminated date palm sap helped clarify transmission routes and identify sources of infection ^[63]. More recently, the emergence of SARS-CoV-2 reinforced the importance of wildlife surveillance, genomic monitoring, and rapid cross-sector data sharing for early detection and coordinated response ^[56]. Importantly, the One Health framework also supports the implementation of prevention and treatment strategies described in Section 3 by guiding surveillance systems that inform vaccine development, antiviral preparedness, and targeted public health interventions. The COVID-19 pandemic demonstrated that, despite longstanding recognition of its importance, the implementation of One Health remains uneven, underfunded, and insufficiently integrated into public health systems worldwide. Key operational barriers include fragmented governance structures, limited cross-sector data sharing, insufficient laboratory capacity in resource-limited settings, and inadequate long-term financing for integrated surveillance systems ^[56, 64-66].

Advancing One Health from a largely conceptual framework to a more fully operational component of national and global health security remains a critical challenge for future pandemic preparedness ^[67]. Figure 2 shows the One Health concept.

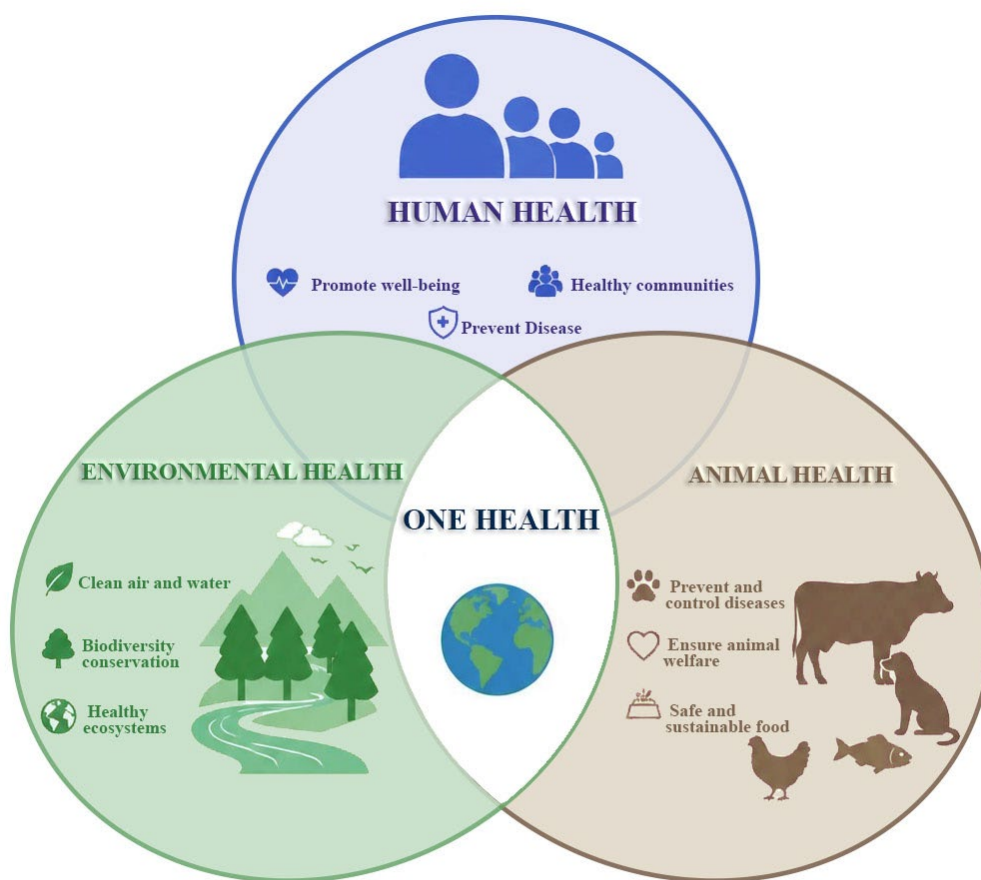


Figure 2. A clear scientific infographic illustration of the One Health concept

5. Major global gaps and evidence-based solutions

A critical assessment of global responses to major pandemics indicates that persistent structural vulnerabilities continue to undermine collective health security. Despite substantial advances in pathogen discovery and the development of medical countermeasures, the systems supporting global preparedness remain uneven, fragmented, and underfunded. These shortcomings reflect a set of recurrent gaps that weaken the capacity of health systems to anticipate and respond to future viral threats. Inequitable access to medical countermeasures remains among the most visible and consequential challenges. During the COVID-19 pandemic, high-income countries secured and administered vaccine doses approximately fifteen times faster than low-income nations, an imbalance widely described as “vaccine apartheid” that prolonged transmission and facilitated the emergence of new variants [68]. Structural disparities in intellectual property, manufacturing capacity, and financing demonstrate that innovation without equitable access can deepen global vulnerability. Short-term measures include strengthening and expanding the WHO mRNA Vaccine Technology Transfer Hub to establish regional production capacity in underserved regions, while longer-term protection will likely require binding international agreements to ensure equitable sharing of pathogens and fair allocation of diagnostics, vaccines, and therapeutics [69]. Equally concerning is the persistent lack of coordination in cross-sectoral surveillance systems. Viral surveillance in wildlife, vectors, and livestock remains limited or absent across more than 60% of global biodiversity hotspots, while human, animal, and environmental data systems often operate independently [70]. This fragmentation weakens early warning capacity and limits effective implementation of the One

Health approach. Strengthening integrated surveillance will require sustained investment in coordinated sentinel programs. Building on recommendations from the One Health and global health security literature, a dedicated Global One Health Surveillance Fund could be considered as a potential financing mechanism to support integrated surveillance activities in low-resource settings. Such a mechanism would complement AI-supported data integration platforms that combine information from veterinary laboratories, meteorological monitoring systems, and human syndromic surveillance to generate real-time spillover risk assessments ^[56, 71]. Health system fragility further amplifies the impact of outbreaks. Many national health systems, particularly in low- and middle-income countries, continue to face limited surge capacity, fragile supply chains, and workforce shortages despite rising disease burdens ^[72]. As a result, response delays and diagnostic bottlenecks can substantially reduce the effectiveness of outbreak control efforts. Immediate measures such as Joint External Evaluations and investment in workforce development may help identify critical gaps. In addition, several studies have emphasized the need for sustainable preparedness financing mechanisms to strengthen public health institutions and laboratory networks. In this context, a Global Health Security Matching Fund could be considered as a potential policy option, whereby international investments are matched with domestic commitments to enhance long-term preparedness capacity; However, such approaches remain largely conceptual and require further evaluation regarding governance and feasibility ^[73, 74].

Another important challenge is the limited integration of climate science into health policy. Although climate models can predict the expansion of vector habitats, including those of *Aedes* and *Culex* mosquitoes, this information is not consistently incorporated into proactive vector control strategies or preparedness planning for arboviral diseases ^[16]. Addressing this gap will require closer collaboration between meteorological and health agencies, including the development of regular climate-health risk assessments and stronger alignment of vector control funding with climate-driven risk models ^[17].

The long-term health consequences of viral infections remain substantial yet frequently underestimated. Post-acute conditions such as Long COVID and persistent neurological sequelae following West Nile virus encephalitis highlight the enduring impact of acute viral illness ^[75]. However, rehabilitation services and long-term longitudinal research in this field remain limited. We propose the development of a Global Neuro-Infectious Disease Registry as a future international initiative to facilitate the standardized collection of longitudinal clinical data across countries. Such a registry does not currently exist as a dedicated global platform but could complement large multinational cohort studies aimed at clarifying the pathophysiology of post-viral syndromes and supporting the development of targeted therapeutic strategies ^[76]. The erosion of public trust through misinformation has become a major challenge in pandemic response. The global “infodemic” during COVID-19, as well as the 2018-2020 Ebola outbreak in the Democratic Republic of the Congo, contributed to vaccine hesitancy, weakened public health communication, and reduced public cooperation with control measures ^[77]. Addressing misinformation will require stronger infodemic management capacity within public health agencies, together with broader investment in digital literacy and evidence-based health education within national educational systems ^[78]. Beyond gap-specific interventions, comparative analyses of solution-oriented studies underscore the multidimensional character of preparedness. Afrough *et al.* ^[79] and Trovato *et al.* ^[80] both emphasize the importance of accelerating the development of biomedical countermeasures, particularly vaccine platforms, although they differ in their operational focus. Afrough *et al.* provide a detailed comparison of established vaccine technologies in terms of immunogenicity and feasibility for outbreak deployment, whereas Trovato *et al.* concentrate on translational and regulatory challenges, highlighting the need for greater harmonization and standardized evaluation frameworks to accelerate vaccine development. Together, these studies suggest that coordinated regulatory and implementation strategies must accompany advances in vaccine platform preparedness. Yu *et al.* ^[81] broaden the discussion by highlighting systemic factors, such as workforce capacity, data interoperability, and cross-sector governance, that shape whether biomedical innovations can be delivered equitably to global populations. Aw *et al.* ^[82] add an evolutionary perspective by documenting the risk of antiviral resistance and recommending adaptive clinical trial designs together with integrated genomic surveillance to reduce the likelihood of resistance-driven treatment failure. Complementing these perspectives, the consensus article by Adisasmito *et al.* ^[56] outlines the operational foundations of the One Health framework, emphasizing cross-sector collaboration, joint surveillance, and equitable governance as core elements of sustainable

preparedness. However, several persistent gaps remain: Limited attention to equitable manufacturing capacity in low-resource settings [79,80], insufficient real-world evaluation of proposed governance reforms [56, 81], and weak integration between antiviral resistance surveillance and vaccine strategy [82].

Alongside these studies, comparative analysis of forecasting studies highlights the potential and limitations of predictive approaches in pandemic preparedness. Alizon [83] and Holmes [84] examine the challenges of forecasting viral virulence and shifts in host range. Alizon suggest that predictive modelling, when supported by robust phylogenetic and ecological data, may help anticipate evolutionary trends, whereas Holmes emphasizes the uncertainty associated with sparse early outbreak data and the inherently stochastic nature of zoonotic spillover events. Hunter [85] and Liao *et al.* [86] use demographic and socioeconomic projections to estimate future disease burden and the climate-driven redistribution of infectious disease risk. He *et al.* [87] extend this work by modelling how climate change may alter the seasonality of respiratory viral infections.

Collectively, these studies demonstrate broad agreement regarding the importance of strengthening surveillance systems, accelerating vaccine development, improving workforce capacity, and promoting cross-sector collaboration through One Health approaches. However, important differences remain regarding implementation priorities. While some authors emphasize biomedical innovation and vaccine platform preparedness, others prioritize governance reforms, financing mechanisms, and health-system resilience. Furthermore, substantial evidence gaps persist regarding the effectiveness of proposed governance structures, sustainable financing models, and the translation of predictive surveillance tools into operational public health decision-making. Addressing these gaps should be a priority for future preparedness research. Table 1 provides a summary of the major global gaps, their consequences, and the corresponding evidence-based solutions discussed in this section.

Table 1. Summary of major global gaps in pandemic preparedness and their proposed evidence-based solutions

Global gap	Consequences	Proposed solutions
Vaccine inequity	Delayed access, variant emergence	Regional manufacturing hubs, pathogen-sharing agreements
Surveillance fragmentation	Delayed outbreak detection	Integrated One Health surveillance
Health-system fragility	Reduced response capacity	Workforce development, preparedness financing
Climate-health disconnect	Increased vector-borne disease risk	Climate-health forecasting integration
Post-viral sequelae	Long-term disability burden	Longitudinal cohorts, neuro-infectious disease registry
Misinformation	Vaccine hesitancy, reduced compliance	Infodemic management, digital literacy

6. Conclusion

Emerging and re-emerging human viral infections represent a persistent and increasingly complex global health threat shaped by ecological disruption, intensified global connectivity, and ongoing viral evolution. Despite substantial advances in diagnostics, vaccines, and antiviral development, preparedness remains constrained by structural weaknesses in surveillance systems, inequitable access to countermeasures, and insufficient integration across human, animal, and environmental health domains. This review highlights that effective mitigation of future viral threats will depend on a fundamental shift from reactive outbreak control to anticipatory, system-level preparedness. Strengthening integrated surveillance, closing gaps in global vaccine and therapeutic equity, and operationalizing One Health approaches across governance structures emerge as central priorities for global health security. Future progress will require the convergence of scientific innovation with sustained political commitment and coordinated international financing mechanisms. In particular, advances in genomic epidemiology, predictive modelling, and climate-informed surveillance must be translated into interoperable, real-time public health systems capable of guiding rapid decision-making.

Ultimately, reducing the burden of emerging viral diseases will depend not only on technological progress but on the ability of global institutions to operationalize equity, coordination, and resilience at scale.