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Emerging Viral Threats in the Post-Pandemic Era: Surveillance, Climate Dynamics, and Global Health Preparedness

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Abstract

The COVID-19 pandemic underscored global vulnerabilities to emerging viruses. In the post-pandemic era, other pathogens such as dengue, mpox (monkeypox), avian influenza (H5N1), and Oropouche virus pose significant threats. This paper reviews recent outbreaks, the role of climate change in expanding viral ranges, and the importance of integrated surveillance and preparedness. We analyze publicly available outbreak data and modeling studies to illustrate trends. For example, global WHO data (1996-2023) document 3,013 outbreak events, with countries like the DRC and China reporting hundreds. Climate warming is facilitating vector expansion: one model projects ~60% of the world's population will be at dengue risk by 2080. Key emerging viruses are examined as case studies: dengue's record 2023 epidemic (~5.0 million cases), the 2022 mpox multi-country outbreak, recent H5N1 clusters in Asia, and a surge of Oropouche in South America (Clarke et al., 2024). We emphasize the need for One Health approaches and global coordination. Enhanced genomic, epidemiological, and environmental surveillance-coupled with climate-informed risk assessments-are crucial to prepare for future viral threats.

Keywords: emerging infectious disease, climate change, surveillance, dengue, monkeypox, avian influenza, Oropouche, One Health, outbreak data.

Introduction

The end of the COVID-19 pandemic has not meant the end of infectious threats. New and re-emerging viruses continue to surface, driven by ecological change, travel, and globalization (Hiscox et al., 2025). Pathogens such as dengue virus, mpox (formerly monkeypox), H5N1 avian influenza, and Oropouche virus exemplify these threats. Dengue causes an estimated 100 million symptomatic infections per year and has seen record epidemics in 2022-23. Monkeypox, once confined to Africa, jumped to global spread in 2022 (over 90,000 cases globally) (World Health Organization., 2022). Avian influenza H5N1 sporadically infects humans with high mortality (903 cases, 464 deaths reported globally by 2024). Oropouche virus, a lesser-known orthobunyavirus, caused thousands of cases in South America by 2024. Simultaneously, climate change alters the habitats of vectors and hosts, expanding viral ranges (Hiscox et al., 2025). To confront these challenges, robust surveillance and preparedness are essential. This review synthesizes recent data and studies on emerging viral threats, emphasizing the interplay of climate dynamics and global health strategies. The goal is a comprehensive understanding of post-pandemic viral risks and recommendations for future readiness.

Global Outbreak Trends

Recent analyses reveal an alarming rise in outbreak frequency and diversity. A global WHO data analysis (1996-2023) identified 3,013 outbreak events affecting more than 4 billion people worldwide (Liu et al., 2025). Influenza outbreaks were most common (771 events), followed by Ebola (342) and MERS (305). Figure 1 maps the geographic distribution of reported events; the Democratic Republic of the Congo led with 272 outbreaks, followed by China (254) and Saudi Arabia (202) (Liu et al., 2025). These data underscore that emerging viruses are not limited to one region. In 2023 alone, a global dengue epidemic caused ~5.0 million cases and 5,000 deaths, the largest dengue outbreak on record (Liu et al., 2025). Table 1 summarizes key features of prominent viruses, illustrating their transmission, regions, and recent impact. The breadth of outbreaks highlights that pathogens will continue to emerge or re-emerge in various hotspots, requiring ongoing vigilance.

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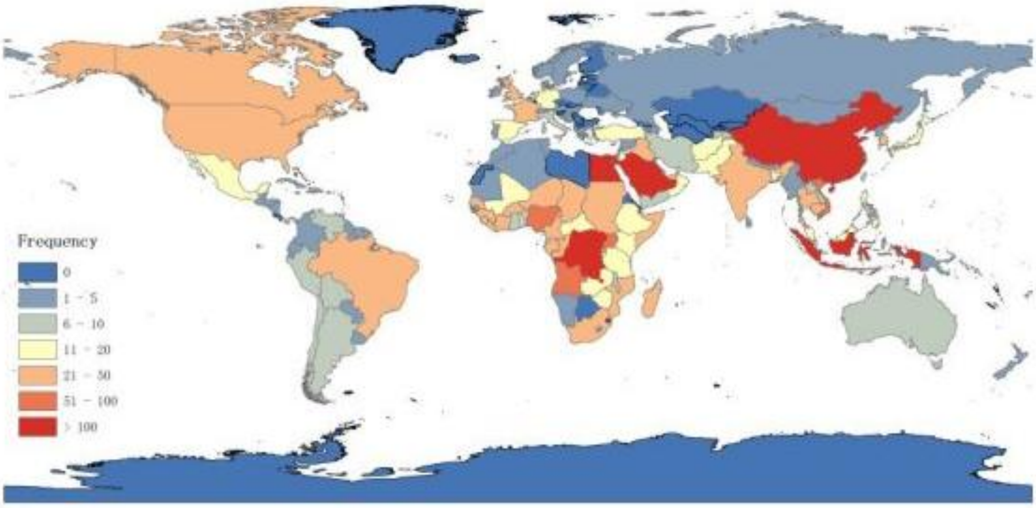

Figure 1 Geographic distribution of reported outbreak events by country (1996-2023). Global WHO emergency data show hotspots in parts of Africa, Asia, and the Middle East (e.g. DRC, China, Saudi Arabia).

Surveillance and Early Detection

Post-pandemic, surveillance systems have expanded, incorporating genomic sequencing, digital epidemiology, and One Health networks. Enhanced sequencing of viral genomes during COVID has accelerated pathogen identification. Platforms like GISAID facilitate real-time data sharing. Sentinel clinics, community testing, and wastewater surveillance have proven valuable. For example, unusual fever clusters trigger investigation for novel viruses. Environmental monitoring (e.g. detecting viral RNA in sewage) offers early warning of community spread. However, surveillance gaps remain, especially in low-resource areas where many zoonoses arise. The WHO's International Health Regulations (IHR) and Joint External Evaluations aim to assess and strengthen country capacities. Collaborative networks (e.g. GOARN, Global Outbreak Alert & Response Network) pool resources for outbreak response.

Despite progress, new technologies must be integrated wisely. The rise of digital disease detection (using social media, search trends) complements traditional reporting. Machine learning models predict hotspots by combining climate, travel, and animal reservoir data. The expansion of this "digital surveillance" offers promise, but requires validation. Overall, a multi-layered surveillance strategy-linking human, veterinary, and environmental data-is critical. Strengthening early detection hinges on timely data sharing between countries and sectors.

Climate Dynamics and Viral Spread

Climate change is reshaping infectious disease patterns. Figure below illustrates global warming trends. Average global surface temperatures increased by ~0.48°C (1999-2008 vs. 1940-1980). Even small temperature rises can enable vectors and pathogens to thrive in new regions. Warmer, wetter conditions accelerate mosquito breeding and viral replication. For example, climate-driven models predict that half the global population could be exposed to Aedes aegypti by 2050, and by 2080 about 60% of the world could be at dengue risk (Hiscox et al., 2025). Similarly, warming allows mosquito and midges to survive winters farther from the tropics. These changes amplify outbreaks: we have already seen dengue, chikungunya, and Zika emerge in higher latitudes as temperatures climbed.

Vector-borne disease maps highlight climate sensitivity. Figure 3 shows the current global distribution of *Aedes aegypti*, the mosquito that transmits dengue, yellow fever, and chikungunya. This tropical mosquito thrives in warm urban areas. With climate warming and urbanization, its habitat is expanding beyond historic boundaries (Hiscox et al., 2025). Regions once too cool or dry for *Aedes* may become suitable. The figure illustrates that large parts of Africa, Asia, and Latin America already harbor this vector.

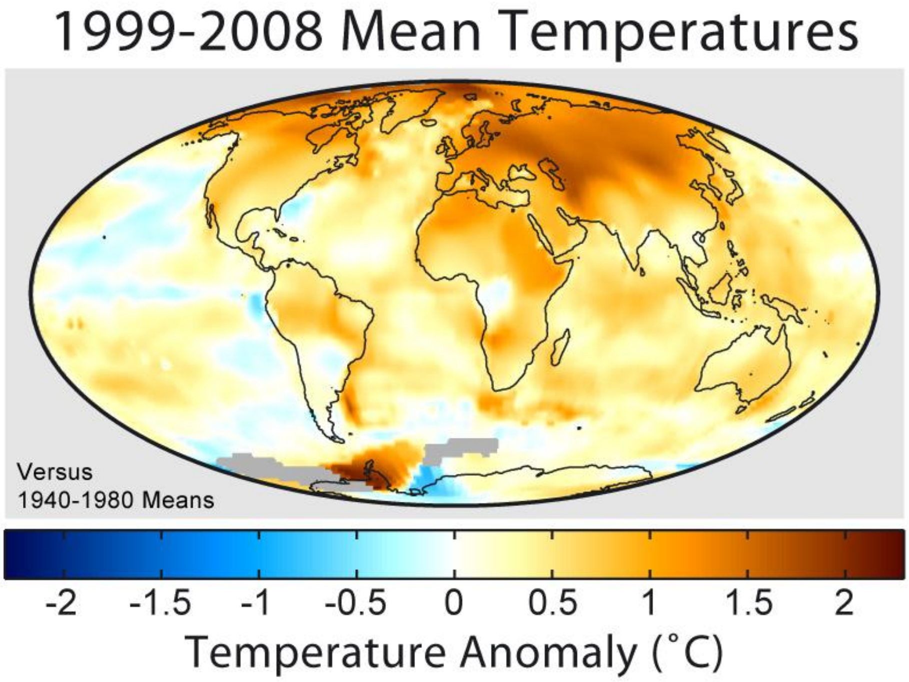

Figure 2 Global temperature anomaly (1999-2008 vs. 1940-1980). Data show widespread warming (~0.48°C increase). Rising temperatures expand habitats for vectors (e.g. mosquitoes) and alter virus survival, increasing outbreak risks.

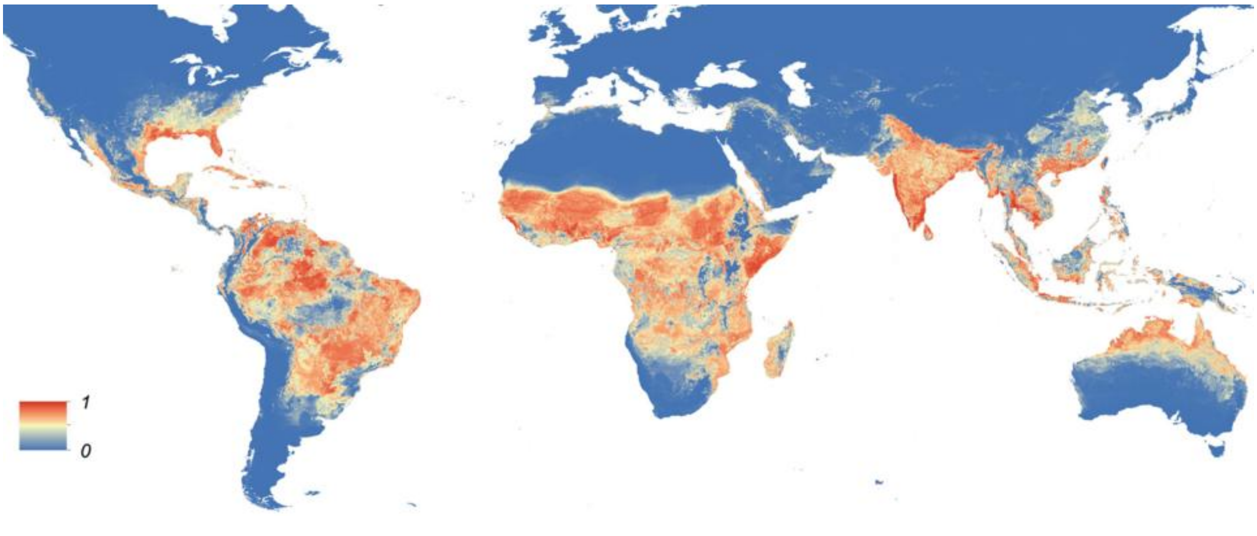

Figure 3 Predicted global distribution of Aedes aegypti (2015). Red areas indicate high probability of mosquito presence. This vector, which transmits dengue and other arboviruses, is projected to expand with ongoing climate change.

Likewise, *Aedes albopictus* (the Asian tiger mosquito) is a competent vector for dengue, chikungunya, and Zika. Originally native to Southeast Asia, *albopictus* has invaded Europe, the Americas, and Africa in the past decades. Its presence in temperate zones is partly due to milder winters. This mosquito's adaptability means that climate shifts could further spread it. Models show that *albopictus* could become established in new regions under future climate scenarios (Hiscox et al., 2025).

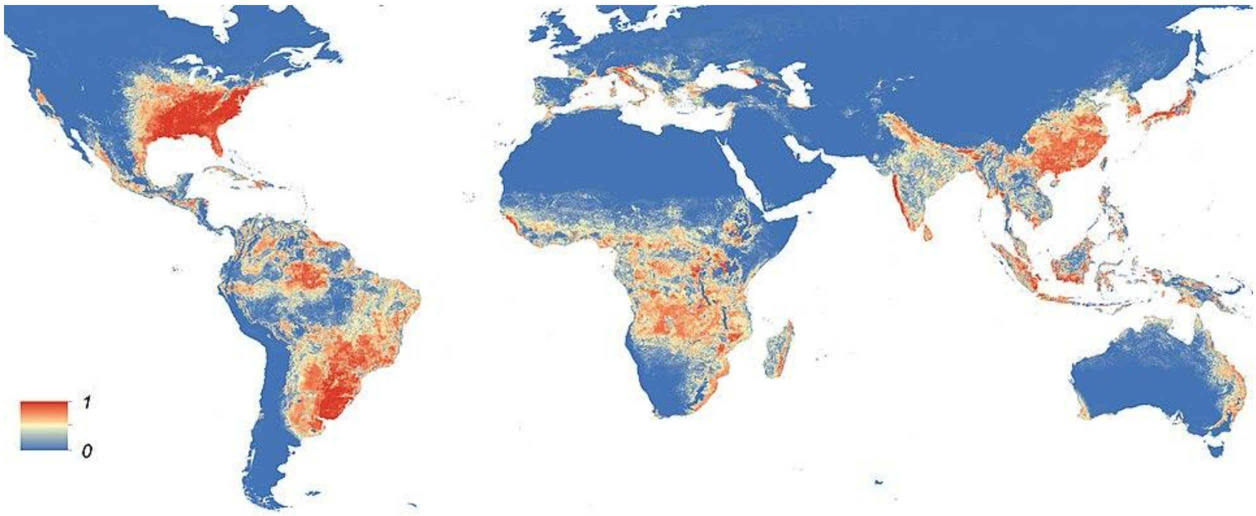

Figure 4 Predicted global distribution of Aedes albopictus (2015). The Asian tiger mosquito's range has grown beyond its native Asia due to warming and globalization. It demonstrates how climate change can enable vectors to invade new areas.

Beyond vectors, climate affects pathogens directly. Temperature and humidity influence viral stability and transmission cycles. For example, increased rainfall can create breeding sites for mosquitoes, while drought may concentrate hosts and vectors around scarce water sources, facilitating spillover. Extreme weather events (floods, storms) can disrupt public health infrastructure and displace populations, compounding epidemic risks. As one review notes, temperature, precipitation, and humidity all significantly affect infectious disease transmission patterns. Overall, the evidence supports that climate dynamics are central to understanding and forecasting emerging viral threats.

Case Study: Dengue Virus

Dengue virus (DENV) exemplifies how climate and globalization intersect. DENV is a flavivirus transmitted by *Aedes* mosquitoes. It causes dengue fever, which can lead to severe disease and death. Pre-pandemic, about 100 million symptomatic dengue infections occurred annually worldwide. Factors such as warmer temperatures, urban crowding, and travel have fueled a dramatic rise. In 2022-2023, many tropical countries experienced record outbreaks. For instance, Central and South America and parts of Asia reported their worst epidemics on record. WHO data indicate ~5.0 million dengue cases and 5,000 deaths in 2023 (Liu et al., 2025). This surge correlates with above-average temperatures and rainfall patterns that year.

Dengue's expansion is partly climate-driven: rising global temperatures are increasing the geographic range of *Aedes* vectors (Hiscox et al., 2025). Urbanization also supports vector proliferation by creating breeding habitats. The combination of climate and socioeconomic change is putting more people at risk: projections suggest 2.25 billion additional people may be at dengue risk by 2080. Control efforts (e.g. vector control, vaccine development) are improving, but challenges remain. Robust dengue surveillance now relies on clinical reporting and vector monitoring. Ongoing genomic studies track viral evolution. As dengue spreads, health systems in subtropical regions must prepare for periodic surges, drawing lessons from the 2023 epidemic.

Case Study: Mpox (Monkeypox)

Monkeypox virus, now re-termed mpox, is an orthopoxvirus similar to smallpox. It is zoonotic, historically circulating in central and west Africa via rodents and primates, with occasional human cases (Van de Vuurst, L., & Escobar, L. E., 2023). In 2022, mpox breached international borders. A widespread outbreak began in non-endemic countries, fueled by travel and social networks. By May 2022, WHO reported 92 confirmed cases and 28 suspected cases in 12 countries outside Africa. Notably, no deaths were reported in these early clusters (World Health Organization., 2022). Within months, cases surged globally. By late 2022, tens of thousands of cases were reported, predominantly affecting networks of close contacts.

The 2022-2023 mpox outbreak taught several lessons. First, even a virus not airborne can cause international epidemics if the right conditions align. Second, waning smallpox immunity (routine smallpox vaccination ended decades ago) may have left populations vulnerable. Third, stigma and delayed recognition hampered early control. Fortunately, the case fatality rate remained very low outside endemic areas. Public health response included raising clinical awareness, testing, contact tracing, and use of smallpox vaccines for high-risk contacts. Mpox highlights the need for surveillance of direct-contact zoonoses and rapid global information-sharing.

Case Study: Avian Influenza H5N1

Highly pathogenic avian influenza A(H5N1) remains a persistent threat. It primarily infects birds, but sporadic human cases with high mortality occur. For example, in 2023-2024 Cambodia saw a cluster of 14 human cases (8 fatal) of H5N1 (World Health Organization., 2024). These infections came from poultry exposures. Globally, WHO reports indicate 903 human H5N1 cases (464 deaths) from 24 countries since 2003, a case fatality ratio of ~51%. The high fatality rate (much higher than COVID-19) is concerning. However, these viruses have not achieved sustained human-to-human transmission; risk is mainly through close poultry contact (World Health Organization., 2024).

The H5N1 pattern illustrates constant surveillance needs: each human case is a potential outbreak seed. Recent years have seen H5N1 re-emerge after quiet periods. Public health response includes intensive tracing of poultry and human contacts, rapid diagnostics, antiviral stockpiling (e.g. oseltamivir), and culling measures in farms. Notably, genetic analyses show reassortment events, meaning new H5N1 strains continually evolve (World Health Organization., 2024). This virus underscores the "global preparedness triad": animal surveillance, human case detection, and vaccine/antiviral readiness. WHO continues to emphasize H5N1 as a top priority pathogen.

Case Study: Oropouche Virus

Oropouche virus (OROV) is an emerging Orthobunyavirus endemic to the Amazon basin. It is transmitted by biting midges (*Culicoides paraensis*) and some mosquitoes. Historically, OROV caused only small outbreaks. However, recent years saw alarming spread. In 2023-2024, OROV cases appeared in new countries in Latin America. As of July 2024, WHO reported 8,078 confirmed cases (2 deaths) in five countries. Previously, only Brazil had reported cases; now Bolivia and even Cuba have reported OROV infections.

This expansion is attributed to environmental and climatic changes. Deforestation and urbanization may have brought humans closer to sylvatic transmission cycles. Increasing temperatures and altered rainfall may improve habitats for vector midges. WHO notes that climate change, deforestation, and unplanned urban growth have facilitated OROV's spread beyond its historical range. Clinically, Oropouche fever resembles dengue (fever, headache, rash) but can progress to neurological symptoms in severe cases. The growing footprint of OROV shows how an obscure virus can rapidly become an emerging threat. It stresses the need for surveillance even of lesser-known arboviruses.

Table 1 Characteristics of selected emerging viruses. Recent outbreak figures are from WHO and published reports (Liu et al., 2025).

Virus	Family (Genome)	Transmission	Regions	Recent Impact / Data
Dengue	Flaviviridae ($ssRNA^{+}$)	Aedes mosquitoes (vector)	Tropics (Asia, Americas)	~5.0 million cases, 5,000 deaths (2023 outbreak)
Mpox	Poxviridae (dsDNA)	Zoonotic, then human-to-human via contact	Africa; 2022-23 global spread	≈90,000 cases globally (2022-23); 0 deaths in initial outbreak
H5N1 Flu	Orthomyxoviridae ($ssRNA^{-}$)	Avian to human (poultry contact)	Asia, Africa (poultry)	903 human cases, 464 deaths (2003-2024)
Oropouche	Peribunyaviridae ($ssRNA^{-}$)	Midges (Culicoides), mosquitoes	Amazonia (Brazil); spreading	8,078 cases, 2 deaths (Jan-Jul 2024)

Global Health Preparedness

In response to these threats, global health initiatives emphasize preparedness via a One Health approach. Figure 5 illustrates this framework, linking human, animal, and environmental health. The WHO, FAO, WOAH and UNEP Joint Plan (2022-2026) calls for collaboration across sectors (World Health Organization., 2024). Key actions include strengthening laboratory networks, training multi-disciplinary teams, and building field surveillance. For instance, animal health workers now often collect samples from livestock and wildlife to test for zoonoses. Integration of climate data (e.g. weather patterns, vector indices) into surveillance is increasingly common.

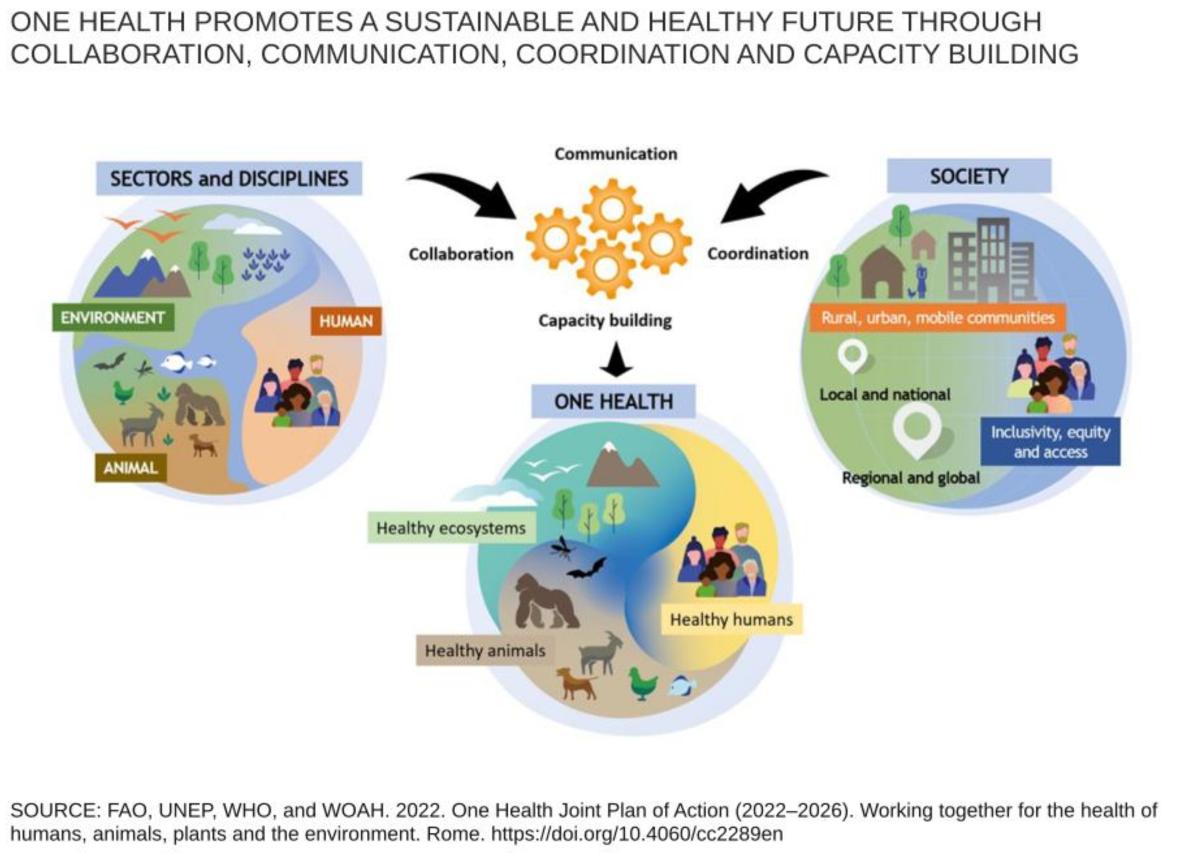

Figure 5 One Health concept integrating human, animal, and environmental health (FAO/UNEP/WHO/WOAH Joint Plan of Action, 2022). Preparedness requires cross-sector coordination and capacity building (Destoumieux-Garzón et al 2018).

Vaccine and drug development is another preparedness pillar. The rapid development of COVID-19 mRNA vaccines showcases new possibilities. Efforts are underway for vaccines against dengue (several licensed in recent years) and emerging threats (prototype vaccines for mpox, influenza). Antiviral stockpiles and treatment protocols are being updated. However, equitable access remains a challenge. Strengthening healthcare systems, especially in rural areas where outbreaks often start, is vital. Training healthcare workers to recognize unusual illness syndromes (e.g. viral hemorrhagic fevers, arboviruses) helps catch outbreaks early.

Global agreements also play a role. The 2005 IHR legally bind countries to report outbreaks and develop core capacities. The World Bank and other partners are exploring financial tools (pandemic bonds, insurance) to rapidly fund outbreak responses. Community engagement and risk communication are necessary for acceptance of control measures. The COVID-19 experience shows that distrust and misinformation can hamper response. Thus, preparedness plans now include social science strategies to combat misinformation and ensure public cooperation.

Ultimately, preparedness is about resilience. Countries are assessed by indices (e.g. Global Health Security Index) on their readiness, but real-world responses to recent outbreaks show gaps remain. Continued investment is needed in public health infrastructure, research, and international cooperation. No country is isolated from these threats, so global solidarity and data sharing are imperative.

Conclusion

The post-pandemic world still faces serious viral threats. Dengue, mpox, H5N1 and Oropouche exemplify how pathogens can emerge or re-emerge under changing ecological and social conditions. Climate change, urbanization, and global travel are key drivers. This review highlights that robust surveillance (spanning clinical, genomic and ecological data) and One Health preparedness are critical. Figures and outbreak data underscore the challenges: large-scale dengue epidemics, intercontinental mpox spread, persistent H5N1 cases, and new Oropouche outbreaks. Addressing these requires sustained effort. Governments and international agencies must heed the lessons of COVID-19 and these recent epidemics. Strengthening health systems, fostering research on climate-disease links, and maintaining rapid response capabilities will be essential. With foresight and collaboration, the world can mitigate the impact of these emerging viral threats.

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