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Emerging and Re-emerging Microbial Pathogens: Global Challenges and Public Health Implications

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Abstract: Emerging and re-emerging microbial pathogens remain a significant global health threat fuelled by rapid urbanization, climate change, population movement, environmental disruption, antimicrobial resistance and weaknesses in health systems. They may be newly introduced by humans or have recently been brought into the human population and include pathogenic bacteria, viruses, fungi and parasites that cause outbreaks resulting in substantial morbidity, mortality and socioeconomic expense. They arise from intricate interplays of human behavior, changes in ecosystems, animal reservoirs and evolutionary jumps of pathogens. The COVID-19 pandemic, again highlights how a new infectious agent can rapidly cross frontiers, overwhelm health services everywhere and expose inequities in the capacity to prepare for and respond to such threats. This article provides a review of the major types of emerging and re-emerging microbial pathogens, their primary drivers and their public health implications. Furthermore, it explores the importance of surveillance systems, laboratory diagnostics, genomic technologies, infection prevention measures, vaccination campaigns to decrease transmission and antimicrobial stewardship and risk communication to contain effects. It also emphasizes ongoing issues in low- and middle-income countries, driven by limited resources and delayed detection as well as difficulty in accessing health care intensifying vulnerability to outbreaks. This perspective emphasizes the One Health approach as a critical framework for understanding pathogen emergence at the human-animal-environment interface. Preparedness is further strengthened through global efforts, investment in public health infrastructure and interdisciplinary collaboration. Future efforts will need to incorporate early warning systems, epidemiological data driven outbreak prediction, and a bias for diagnostic access and countermeasure equity. For this reason, knowledge of the changing epidemiology of threats to human health from microbes will be central to preserving population health and strengthening resilience in times of future epidemics and pandemics.

Keywords: Emerging pathogens, Re-emerging infections, Public health, Antimicrobial resistance, Disease surveillance

Introduction

Emerging and re-emerging microbial pathogens continue to be some of the most persistent and consequential challenges to global public health due to their ability to breach species barriers, transmit

swiftly within populations, and challenge pre-existing prevention and treatment paradigms. Examples of these deadly pathogens include newly emerging or re-emerging bacteria, viruses, fungi and parasites in the human populations with different transmission dynamic features [1] as well as virulence factor patterns or antimicrobial resistance profiles [2], [3].

The rise of these viral diseases is determined by a combination of factors which include ecosystem destruction, human migration, urban expansion, agricultural intensification/land-use change, climate variability and weakening public health infrastructure [1], [4], [5], [6]. The outbreaks of SARS, the Ebola epidemic, Zika virus epidemic, Middle East respiratory syndrome, avian influenza in humans and antimicrobial-resistant bacterial infections have emphasized that emerging infections are a global threat [7], [8], [9], [10]. The experience of the COVID-19 pandemic offered the most straightforward example to date of how the geopolitical context can manifest through saturation of health systems, breakdowns in economies and preceding structural inequities in preparedness and response capacity across countries and internally within them [11], [12], [13].

At the same time, developing and developed countries share another, more unnerving threat: the relentless increase in antimicrobial resistance has turned even previously treatable infections into severe clinical and public health challenges everywhere, but particularly in contexts of poor diagnostic capacity and ineffective antimicrobial stewardship [14], [15], [16]. The emergence of new pathogens is not simply a biological phenomenon but also influenced by environmental and social determinants. Increasing opportunities for zoonotic spillover by deforestation, wildlife disturbance, and livestock expansion and the impact of climate change on host-vector or host-reservoir ranges [6], [17], [18]. Also, rapid dissemination occurs swiftly in an era of international travel, trade and migration combined with dense metropolitan habitation once a pathogen is established in human populations [9], [19], [20].

This is an important recognition because many of these pathogens follow a One Health approach because they impact human, animal and environmental health [21], [22]. Recent technological advancements in genomic sequencing, molecular diagnostics, and digital surveillance have enabled rapid pathogen identification along with tracing transmission pathways during outbreaks [23], [24]. But, technically advancing cannot substitute access, governance and an investment case for ongoing public health systems [13], [25].

Definitions and Conceptual Framework

Emerging and re-emerging microbial pathogens are not just static taxonomic entities; these are dynamic processes at the heart of contemporary research in infectious diseases. According to Woolhousey & Gowtage-Sequeria; Morse et al, emerging infectious diseases are defined as infections whose incidence has increased in the past decades or threatens to increase in near future, while re-emerging infections comprise previously recognized disease which had declined in incidence but have again become major public health problems [3], [19]. This distinction is important because emergence may stem from the introduction of a new agent, the appreciation of an undetected infection (for example, HIV), evolution of antimicrobial resistance or the expansion of a known pathogen into unfamiliar ecological or geographic territory [2], [26].

In microbiological terminology, pathogens that can cause disease in humans are called microbial pathogens or simply pathogens – including a variety of entities such as bacteria, virus, fungi and parasite. However, their significance for public health also relies on the ability to achieve transmission and adapt to hosts, immunity systems, and variations happening in environmental or social context [1], [4] An important conceptual framework for the life history of a pathogen is to begin with introduction and establishment: a pathogen spills over from an external source into a new host population, acquires the ability to sustain transmission in human communities through continuous environmental exposures, food systems, vectors or travel [6], [19].

A One Health approach enhances this framework by locating pathway emergence at the convergence of human, animal and environmental health [21]. Re-emergence deserves distinctive focus as it can be a consequence of inadequate maintenance of control through reduced vaccination, poor infection prevention, antimicrobial resistance, impaired health services or changes in population dynamics favoring transmission [7], [9].

Major Pathogen Groups

Emerging and re-emerging microbial pathogens show diverse transmission pathways, geographic distributions and public health impacts – making them a challenge for epidemiologic study. While viruses may capture the most attention because of pandemic potential, significant threats include bacterial, fungal and parasitic pathogens that are increasing in importance as global forces (antimicrobial resistance, ecological disruption, climate change, urbanization and globalization) shape emerging host-pathogen interactions [1], [2].

However, since such viral outbreaks are common, especially because of the rapid evolution potential and host-switching capacity of RNA viruses, a significant proportion of emerging infectious disease events are associated with them coupled with zoonotic spillover capacities [1], [6]. Antimicrobial resistance still continually transforms bacterial pathogens into urgent threats in communities and healthcare settings, maintaining them as a major focus of the re-emergence landscape line [14], [16]. Natural selection has also resulted in increasing recognition of fungal pathogens, notably those among immunocompromised patients and in hospitals, with organisms such as *Candida auris* now regarded as a high-priority threat because of resistance and delayed diagnosis [27]. Transmission and re-emergence driven by vector ecology, migration, environmental change, and virologic diversity in endemic and low-resource settings continue to matter for parasitic pathogens [2], [19].

Table 1. Major groups of emerging and re-emerging microbial pathogens

Pathogen group	Main epidemiological features	Typical drivers of emergence/re-emergence	Examples
Viruses	Rapid spread, zoonotic spillover, outbreak and pandemic potential	Wildlife-human contact, travel, climate and vector shifts, viral mutation	SARS-CoV-2, avian influenza viruses, Ebola virus, Zika virus
Bacteria	Healthcare-associated spread, drug resistance, recurrent community outbreaks	Antimicrobial misuse, weak infection control, hospital transmission, poor sanitation	MRSA, CRE, MDR <i>Pseudomonas aeruginosa</i> , drug-resistant <i>Mycobacterium tuberculosis</i>
Fungi	Severe disease in immunocompromised hosts, delayed diagnosis, rising resistance	Antifungal resistance, healthcare exposure, climate-linked ecological shifts, weak mycology capacity	<i>Candida auris</i> , <i>Candida albicans</i> , <i>Aspergillus fumigatus</i> , <i>Cryptococcus neoformans</i>
Parasites	Persistent endemicity with periodic resurgence, strong environmental and vector dependence	Vector expansion, disrupted control programs, migration, climate and water-related changes	<i>Plasmodium</i> spp., <i>Leishmania</i> spp., <i>Trypanosoma</i> spp.

Drivers of Emergence and Re-emergence

The emergence and re-emergence of microbial pathogens occurs through the interplay, rather than dependence on a single isolated cause of interacting ecological, biological, behavioral and socio-epidemiological factors along with predisposing health-system determinants [2], [19]. Land-use change [including, but not limited to: deforestation, habitat fragmentation, agricultural expansion, irrigation projects, mining and unplanned urban growth] promotes contacts between humans domestics animals

and wildlife, which creates opportunities for zoonotic spillover Jones et al; Plowright et al. Climate change also changes how temperature, humidity, rainfall, seasonality and extreme weather patterns modify vector distribution as well as pathogen survival and host susceptibility [1], [6], [5], [18].

Urbanization and globalization/octetbn: lie at the heart of this. Local outbreaks can quickly escalate into regional or even global threats due to overcrowding, inadequate sanitation, ineffective infrastructure systems and the relentless nature of migration, travel and international trade (Morens & Fauci 2020; Jones et al. Microbially, mutation, recombination, host switching and resistance evolution [3], [15] allow pathogens to infect novel hosts as well as escape immunity or persist in the face of treatment pressure. Re-emergence is also closely linked to faltering public health measures: decreasing vaccination coverage, or interruption of vector control; feeble infection prevention response to outbreaks or even delayed surveillance or reporting [7].

Table 2. Major drivers of pathogen emergence and re-emergence

Driver	Mechanism of action	Public health consequence	Examples
Land-use change	Increases contact among humans, wildlife, and domestic animals; disrupts habitats	Greater zoonotic spillover risk and novel outbreak potential	Deforestation, agricultural expansion, mining, habitat fragmentation
Climate change	Alters vector ecology, pathogen survival, seasonality, and host distribution	Expanded transmission zones and shifting disease burdens	Mosquito-borne disease spread, waterborne outbreaks after floods
Urbanization	Promotes crowding, poor sanitation, and infrastructure stress	Faster transmission and outbreak amplification	Informal settlements, megacities with weak services
Global travel and trade	Moves pathogens, vectors, and infected hosts rapidly across borders	Rapid international dissemination of local outbreaks	Pandemic spread through air travel and trade routes
Microbial adaptation	Facilitates mutation, host switching, immune escape, and drug resistance	Increased transmissibility, persistence, or treatment failure	RNA virus evolution, multidrug-resistant bacteria
Breakdown of control measures	Weakens vaccination, surveillance, vector control, and infection prevention	Re-emergence of previously controlled diseases	Measles resurgence, drug-resistant healthcare infections
Conflict and displacement	Disrupts health systems, sanitation, and continuity of care	Increased outbreak vulnerability and delayed response	Refugee settings, conflict-affected regions

Public Health Implications and Control Measures

Emerging and re-emerging microbial pathogens exert considerable public health burden by adding to morbidity, mortality, disability, and repeat epidemic danger in many settings [9], [28]. Their effects are not limited to the immediate impact of infection; they also have medium- and longer-term health consequences, including disruption in essential services, amplifying inequities and

overwhelming hospitals [29], laboratories and supply chains, infection prevention programs and the health workforce capacity [25]. Directly, infectious disease crises are sometimes accompanied by economic and social disruption through reducing labour productivity, affecting trade and travel, driving household outlay to increase in prevention and health care [30].

One other important ramification is regarding the rise of drug resistance that decreases the effectiveness of conventional treatments and also increases the probability of long periods of sickness, hospitalization and death [14], [31]. Accordingly, control solutions must integrate surveillance, early warning systems, laboratory and genomic diagnostics, vaccination, infection prevention & control and risk communication in a One Health coordinated response [2].

Table 3. Core control measures and their public health roles

Control measure	Main role	Expected benefit
Surveillance and early warning	Detect unusual events rapidly	Faster containment and reduced spread
Laboratory and genomic diagnostics	Confirm pathogens and track transmission	Better targeting of response measures
Infection prevention and control	Limit transmission in healthcare and community settings	Reduced outbreak amplification
Vaccination and immunization programs	Prevent infection and severe disease	Lower morbidity and mortality
Antimicrobial stewardship	Reduce inappropriate antimicrobial use	Slow resistance emergence and preserve treatment efficacy
Risk communication and community engagement	Improve public adherence and trust	Stronger outbreak response and prevention behavior
One Health coordination	Address human, animal, and environmental drivers	More comprehensive and sustainable control

Conclusion

Asserts that arriving and resurgent microbial pathogens remain key and dynamic future challenges for global public health. They are important not only because of their potential to cause outbreaks, epidemics, and pandemics, but also because they reveal startling gaps in our ability to surveil infections, prepare for future risks, control the spread of pathogens, and provide equitable access to diagnosis and treatment [2]. Such threats stem from a range of related drivers, including land-use change, climate variability, rural to urban migration, globalization of trade and travel networks, antimicrobial resistance (AMR), and failure of sustained public health action against transmissible disease. Thus, a One Health approach is needed to improve early warning, integrated surveillance, outbreak response and long-term prevention.

Preparedness for the future depends on continued investments in resilient health systems, laboratory capacity, workforce training and antimicrobial stewardship, along with coordinated cross-sector governance. Emerging and re-emerging pathogens will continue to take advantage of ecological disruption and institutional incapacity, with likely recurrent public health emergencies without such measures. This culminates in a proactive, interdisciplinary and multisectoral global approach that should be the cornerstone of successfully tackling microbial threats to health in an increasingly interconnected world.

REFERENCES

- [1] K. E. Jones *et al.*, “Global trends in emerging infectious diseases,” *Nature*, vol. 451, no. 7181, pp. 990–993, 2008, doi: 10.1038/nature06536.
- [2] D. M. Morens, G. K. Folkers, and A. S. Fauci, “The challenge of emerging and re-emerging infectious diseases,” *Nature*, vol. 430, no. 6996, pp. 242–249, 2004, doi: 10.1038/nature02759.
- [3] M. E. J. Woolhouse and S. Gowtage-Sequeria, “Host range and emerging and reemerging pathogens,” *Emerg. Infect. Dis.*, vol. 11, no. 12, pp. 1842–1847, 2005, doi: 10.3201/eid1112.050997.
- [4] P. Daszak, A. A. Cunningham, and A. D. Hyatt, “Emerging infectious diseases of wildlife: Threats to biodiversity and human health,” *Science (1979).*, vol. 287, no. 5452, pp. 443–449, 2000, doi: 10.1126/science.287.5452.443.
- [5] C. J. Carlson *et al.*, “Climate change increases cross-species viral transmission risk,” *Nature*, vol. 607, pp. 555–562, 2022, doi: 10.1038/s41586-022-04788-w.
- [6] R. K. Plowright *et al.*, “Pathways to zoonotic spillover,” *Nat. Rev. Microbiol.*, vol. 15, no. 8, pp. 502–510, 2017, doi: 10.1038/nrmicro.2017.45.
- [7] A. S. Fauci and D. M. Morens, “The perpetual challenge of infectious diseases,” *N. Engl. J. Med.*, vol. 366, no. 5, pp. 454–461, 2012, doi: 10.1056/NEJMra1108296.
- [8] E. Petersen *et al.*, “Rapid spread of Zika virus in the Americas—Implications for public health preparedness,” *Lancet Infect. Dis.*, vol. 16, no. 12, pp. 1301–1304, 2016, doi: 10.1016/S1473-3099(16)30173-5.
- [9] D. M. Morens and A. S. Fauci, “Emerging pandemic diseases: How we got to COVID-19,” *Cell*, vol. 182, no. 5, pp. 1077–1092, 2020, doi: 10.1016/j.cell.2020.08.021.
- [10] A. R. Collaborators, “Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis,” *The Lancet*, vol. 399, no. 10325, pp. 629–655, 2022, doi: 10.1016/S0140-6736(21)02724-0.
- [11] P. Venkatesan, “The changing landscape of infectious diseases,” *Lancet Microbe*, vol. 1, no. 1, p. e1, 2020, doi: 10.1016/S2666-5247(20)30021-1.
- [12] C. Wang, P. W. Horby, F. G. Hayden, and G. F. Gao, “A novel coronavirus outbreak of global health concern,” *The Lancet*, vol. 395, no. 10223, pp. 470–473, 2020, doi: 10.1016/S0140-6736(20)30185-9.
- [13] I. Kickbusch, A. M. Gülmezoglu, and H. Gulati, “Leading health in the 21st century,” *The European Journal of Public Health*, vol. 24, no. 1, pp. 3–5, 2013, doi: 10.1093/eurpub/ckt195.
- [14] R. Laxminarayan *et al.*, “Antibiotic resistance—the need for global solutions,” *Lancet Infect. Dis.*, vol. 13, no. 12, pp. 1057–1098, 2013, doi: 10.1016/S1473-3099(13)70318-9.
- [15] E. Tacconelli *et al.*, “Discovery, research, and development of new antibiotics: The WHO priority list of antibiotic-resistant bacteria and tuberculosis,” *Lancet Infect. Dis.*, vol. 18, no. 3, pp. 318–327, 2018, doi: 10.1016/S1473-3099(17)30753-3.
- [16] C. J. L. Murray *et al.*, “Global burden of bacterial antimicrobial resistance in 2019: A systematic analysis,” *The Lancet*, vol. 399, no. 10325, pp. 629–655, 2022, doi: 10.1016/S0140-6736(21)02724-0.
- [17] S. Altizer, R. S. Ostfeld, P. T. J. Johnson, S. Kutz, and C. D. Harvell, “Climate change and infectious diseases: From evidence to a predictive framework,” *Science (1979).*, vol. 341, no. 6145, pp. 514–519, 2013, doi: 10.1126/science.1239401.
- [18] S. J. Ryan, C. J. Carlson, E. A. Mordecai, and L. R. Johnson, “Global expansion and redistribution of Aedes-borne virus transmission risk with climate change,” *PLoS Negl. Trop. Dis.*, vol. 13, no. 3, p. e0007213, 2019, doi: 10.1371/journal.pntd.0007213.
- [19] S. S. Morse *et al.*, “Prediction and prevention of the next pandemic zoonosis,” *The Lancet*, vol. 380, no. 9857, pp. 1956–1965, 2012, doi: 10.1016/S0140-6736(12)61684-5.
- [20] L. Simonsen *et al.*, “Global mortality estimates for the 2009 influenza pandemic from the GLaMOR project,” *PLoS Med.*, vol. 10, no. 11, p. e1001558, 2013, doi: 10.1371/journal.pmed.1001558.
- [21] J. S. Mackenzie and M. Jeggo, “The One Health approach—Why is it so important?,” *Trop. Med. Infect. Dis.*, vol. 4, no. 2, p. 88, 2019, doi: 10.3390/tropicalmed4020088.

- [22] D. Destoumieux-Garzón *et al.*, "The One Health concept: 10 years old and a long road ahead," *Front. Vet. Sci.*, vol. 5, p. 14, 2018, doi: 10.3389/fvets.2018.00014.
- [23] J. L. Gardy and N. J. Loman, "Towards a genomics-informed, real-time, global pathogen surveillance system," *Nat. Rev. Genet.*, vol. 19, no. 1, pp. 9–20, 2018, doi: 10.1038/nrg.2017.88.
- [24] Y.-Z. Zhang and E. C. Holmes, "A genomic perspective on the origins and emergence of SARS-CoV-2," *Cell*, vol. 185, no. 14, pp. 2356–2361, 2022, doi: 10.1016/j.cell.2022.05.003.
- [25] M. P. Kieny, D. B. Evans, and G. Schmets, "Health-system resilience: Reflections on the Ebola crisis in western Africa," *Bull. World Health Organ.*, vol. 92, no. 12, p. 850, 2014, doi: 10.2471/BLT.14.149278.
- [26] Institute of Medicine, *Microbial threats to health: Emergence, detection, and response*. National Academies Press, 2003.
- [27] F. Bongomin, S. Gago, R. O. Oladele, and D. W. Denning, "The World Health Organization fungal priority pathogens list: A call to action," *Lancet Microbe*, vol. 3, no. 12, pp. e889–e890, 2022, doi: 10.1016/S2666-5247(22)00361-8.
- [28] V. Y. Fan, D. T. Jamison, and L. H. Summers, "Pandemic risk: How large are the expected losses?," *Bull. World Health Organ.*, vol. 96, no. 2, pp. 129–134, 2018, doi: 10.2471/BLT.17.199588.
- [29] X. Luo, Q. Yuan, J. Li, and et al., "Alterations in the prevalence and serotypes of *Streptococcus pneumoniae* in elderly patients with community-acquired pneumonia: A meta-analysis and systematic review," *Pneumonia*, vol. 17, p. 5, 2025, doi: <https://doi.org/10.1186/s41479-025-00156-0>.
- [30] National Academies of Sciences Engineering and Medicine, *The economics and modeling of emerging infectious diseases and biological risks*. National Academies Press, 2018.
- [31] S. A. McEwen and P. J. Collignon, "Antimicrobial resistance: A One Health perspective," *Microbiol. Spectr.*, vol. 6, no. 2, 2018, doi: 10.1128/microbiolspec.ARBA-0009-2017.