

Emerging Infectious Diseases and Their Preventive Measures

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1. Introduction

Infectious diseases are illnesses caused by pathogens such as bacteria, viruses, fungi, or parasites that spread from one person to another. Some examples are the flu (virus), tuberculosis (bacteria), and malaria (parasite) (Verhoef et al., 2019; Zabidi et al., 2023). The landscape of infectious diseases is constantly evolving due to the emergence of new pathogens and the re-emergence of existing controlled infections (Cliff, 2009). From a decade, scientists are trying to monitor these emerging threats, particularly in light of global challenges such as climate change, urbanization, and increased interactions between humans and animals (Myers & Patz, 2009). Recently, the COVID-19 pandemic has demonstrated how quickly infectious diseases can spread worldwide (Baker et al., 2022). Therefore, it is a dire need for rapid surveillance systems and response strategies to combat these threats (Peeri et al., 2020).

It is known that emerging pathogens including novel viruses, bacteria, and parasites, pose significant public health challenges due to their potential for high transmissibility, virulence, and resistance to existing treatments (Levitt et al., 2010). The World Health Organization (WHO) classifies emerging infectious diseases that are newly appeared in a population or already existed in this environment but are rapidly increasing in incidence or geographic range (Dye, 2014). For examples, the emergence of SARS-CoV-2, Zika virus, and antibiotic-resistant strains of bacteria, such as Methicillin-resistant *Staphylococcus aureus* (MRSA) (Janik et al., 2020). Indeed, pathogens are not only threatening individual health but also impose substantial burdens on healthcare systems and economies (Bloom & Cadarette, 2019).

In addition, the zoonotic diseases are major concern and have a significant impact on human health (Rahman et al., 2020). These diseases can transfer from animals to humans, often facilitated by environmental changes and human behaviors (Weiss & McMichael, 2004). It is also important to consider that many risk factors such as deforestation, intensive agriculture, and climate change are involved and may increase the likelihood of zoonotic spillover events (Tazerji et al., 2022). Some researchers have shown that habitat destruction brings wildlife into closer contact with human populations, and may create opportunities for pathogens to transfer (Plowright et al., 2017). Moreover, global travel and trade accelerate the spread of these pathogens, as evidenced by the rapid international dissemination of COVID-19 (Kuo & Chiu, 2021).

Some other researchers have published in openly-access journals that emphasized the importance of the ecological and evolutionary dynamics of emerging pathogens (Salim et al., 2022). The genetic analysis revealed that how pathogens adapt to new hosts, develop resistance to treatments, and change their virulence profiles (Neckers & Tatu, 2008). Therefore, new insights are critical for informing public health strategies and developing effective vaccines and therapeutics (Meganck & Baric, 2021). Additionally, the interdisciplinary approaches that integrate with microbiology, epidemiology, environmental science, and social sciences are crucial for addressing the multifaceted nature of emerging infectious diseases (Janes et al., 2012). In context with the recent studies indicate that marginalized populations often bear a disproportionate burden of infectious diseases

(Quinn & Kumar, 2014). Therefore, effectively managing these diseases requires a swift response through the implementation of health policies and targeted interventions (Haldane et al., 2021).

2.Evolution of Infectious Disease

The evolution of infectious diseases is a complex and multifactorial process that includes different aspects of genetics, epidemiology, and pathogen-host interactions (Forst, 2010). Advances in genetic sequencing and bioinformatics have significantly enhanced our concepts of the genetics and evolution of infectious diseases (Pybus & Rambaut, 2009). Moreover, this includes the study of microbial genetic data and the evolutionary biology of pathogens, such as viruses, bacteria, and fungi (Tibayrenc & Ayala, 2012). In addition, the co-evolution of hosts and pathogens, the evolution of antibiotic resistance, and the role of genetic variation in pathogenesis and epidemiology (Woolhouse et al., 2002). In another study, scientists focus on the evolutionary mechanisms of bacterial pathogens (Martinez, 2009). For example, *Mycobacterium tuberculosis* highlighted its interactions with the lung environment and the evolution of drug-resistant strains (Müller et al., 2013). In some similar studies, they conducted analyses on pathogens like *Burkholderia pseudomallei* and *Klebsiella pneumoniae*, examining their genetic diversity and the evolutionary arms race between these pathogens and their hosts (Chomkatekaew et al., 2021). Additionally, the evolutionary dynamics of antibiotic resistance and the phenotypic changes are associated with resistance acquisition (Hughes & Andersson, 2017).

The field of molecular evolution of infectious agents includes studies on genomic adaptations and the impact of selective pressures such as antibiotics and host immune responses (Sheppard et al., 2018). Some studies emphasize the importance of genetic elements like genomic islands and plasmids in the evolution and epidemic spread of pathogens (Dobrindt et al., 2004). For instance, the emergence and adaptation of SARS-CoV-2 variants during the COVID-19 pandemic serve as an understanding of pathogen evolution and guide public health responses (Telenti et al., 2022).

The evolution of eukaryotic pathogens, such as malaria parasites, *Cryptosporidium*, and *Giardia* were studied (Ortega-Pierres et al., 2009). They explored the interactions between parasites and hosts, the impact of medical interventions on the evolution of drug resistance, and the genetic diversity of these pathogens (Hughes & Andersson, 2015). For instance, *Plasmodium vivax* provides some insights into genetic diversity and resistance patterns, which are crucial for developing effective control strategies (Arnott et al., 2012).

The interplay between host and pathogen is a critical area, as we can examine how genetic changes in pathogens influence their virulence and the host's susceptibility (Casadevall & Pirofski, 1999). In a study, host-pathogen interactions help identify markers for disease severity and inform the development of diagnostic tools and therapeutic interventions (Lydon et al., 2018). This holistic understanding is essential for predicting disease outcomes and managing infectious disease outbreaks effectively (Wearing et al., 2005). These studies collectively highlight the dynamic nature of infectious disease evolution and the continuous need for advanced research to cope emerging challenges in disease control and prevention (Heesterbeek et al., 2015) as shown in Figure 1.

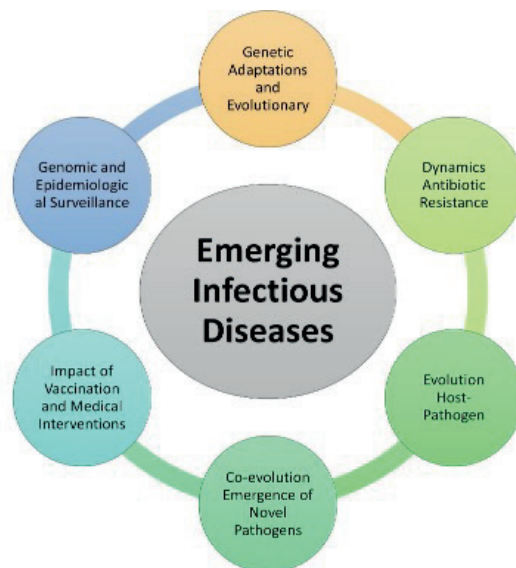


Figure 1. Evevolutionary steps for Emerging Infectious Diseases

3. Global Spread of New Infections

The emergence and re-emergence of infectious diseases are a major public health challenge globally (Church, 2004). New infectious agents are arising from various sources including zoonotic transfers, antibiotic resistance, and changes in human behavior and climate (Vaz□Moreira et al., 2019). The SARS-CoV-2 virus is arised in China and spread worldwide rapidly due to international travel and urban density (Li et al., 2021). Therefore, outbreaks have shown the potential for rapid spread due to human-to-human transmission, particularly in healthcare systems (Herfst et al., 2017). For example, the emergence of Zika virus in the Americas in the 2010s showed changes due to climate and human behavior that affect the distribution of mosquito-borne diseases (Caminade et al., 2019).

It is noted that the spread of new infections is influenced by multiple factors including the increased level of travel and trade that facilitate the rapid movement of people and goods, allowing pathogens to cross borders more easily (Baker et al., 2022). For instance, international air travel played a critical role in the rapid global spread of COVID-19 (Christidis & Christodoulou, 2020). Urban areas play critical role in the outbreaks of these diseases, particularly in low- and middle-income countries because they have higher population densities, poor sanitation, and limited healthcare access (Wilkinson et al., 2020). The WHO has reported that over 55% of the global population now lives in urban areas, a trend projected to rise day by day (Cohen, 2004). In this conditions climate change affect vector populations (e.g., mosquitoes) and lead to the spread of diseases into new geographic areas (Kovats et al., 2001). For example, warmer temperatures have expanded the range of ticks to increase the incidence of Lyme disease in existing unaffected regions (Dantas-Torres, 2015).

The global surveillance systems, such as the Global Outbreak Alert and Response Network (GOARN) is playing a crucial role for early detection and rapid response to outbreaks (Ansell et al., 2012). Vaccines have proven effective in controlling outbreaks. For instance, the rapid development and deployment of COVID-19 vaccines showcased the importance of vaccination in mitigating the impact of new infections (Flanagan et al., 2020). The public education campaigns are critical in promoting preventive measures, such as hygiene practices and vaccination uptake (Weiss et al., 2009). A significant proportion of emerging infections are zoonotic, originating from animals (Bengis et al., 2004). The One Health approach should be emphasized to protect human, animal, and environmental from zoonotic diseases (Erkyihun & Alemayehu, 2022) as shown in Figure 2.



Figure 2. Global Spread of New Infections

4. Ecological Factors in Disease Emergence

Disease emergence is influenced by some complex systems that interplay with different ecological factors such as climate change, deforestation, urbanization, biodiversity loss and global travel and trades between pathogens, hosts, and the environment (McMichael, 2004). These factors are crucial for predicting and management for different infectious diseases (Woolhouse, 2011) as shown in Figure 3. For example, higher biodiversity often leads to a dilution effect, where a greater variety of species reduce the likelihood of transmission of pathogens (Keesing & Ostfeld, 2021). Therefore, diverse ecosystems support a range of hosts, limiting the spread of pathogens that thrive in less diverse system (Dobson, 2004).

Some species act as reservoirs for pathogens that facilitate their transmission to humans such as changes in biodiversity, habitat loss or invasive species alter the dynamics (Crowl et al., 2008). Secondly, the rapid expansion of urban areas that lead to habitat fragmentation and increased contact between wildlife, domestic animals, and humans (Bai et al., 2019). This proximity accelerates the risk of zoonotic diseases. The intensive agriculture disturbs the environments to disease emergence (Mustafa & Makhawi, 2023). For example, monoculture and the use of antibiotics disrupt ecological balance and promote pathogen resistance (Bennett et al., 2012).

There are changes in climate affect the distribution and life cycles of both pathogens and vectors (Gallana et al., 2013). For example, warmer temperatures expand the habitat range for mosquitoes that elevate the risk of diseases like malaria and dengue (Reiter, 2001). Some other factors such as floods and droughts disrupt ecosystems and facilitate disease spread (Semenza et al., 2022). Vectors increase their populations in the grounds, while droughts force wildlife into closer contact with human populations (Sutherst, 2004).

The global wildlife trade introduces pathogens into new environments leading to spillover events (Rush et al., 2021). Therefore, monitoring and regulating this trade are crucial for preventing disease emergence (Tsai et al., 2010). In addition, local cultural practices, such as hunting or consumption of bushmeat increase the risk of zoonotic diseases (Friant et al., 2015). Moreover, public health interventions consider these behaviors to be effective to prevent disease emergence (Raude et al., 2019). Furthermore, surveillance systems that incorporate ecological data can help to predict disease outbreaks (Milinovich et al., 2014).



Figure 3. Ecological Factors in emergence of infectious diseases.

5. Genetic Variations and Disease Evolution

The genetic variations play a vital role in the evolution of diseases i.e influencing susceptibility, progression, and responses to treatments (Rabaneda-Bueno et al., 2021). These variations are linked to genetic diversity that contribute to the emergence and spread of diseases (Davies et al., 2009). Most of genetic variations among individuals influence traits and disease susceptibility. The alterations in the number of copies of a particular gene that affect gene dosage and contribute to complex diseases (Almal & Padh, 2012) as shown in table 1. For example, the larger scale alterations in the genome including inversions and translocations may impact gene function and regulation (Puig et al., 2015). The genetic variations that confer a survival advantage become more prevalent in a population (Perls et al., 2002). Therefore, certain alleles may provide resistance to these infectious diseases, such as the CCR5-Δ32 allele conferring resistance to HIV (de Silva & Stumpf, 2004). Random changes in allele frequencies can lead to the fixation of harmful mutations, particularly in small populations (Whitlock, 2000). Continuous mutations contribute to the genetic diversity of pathogens, especially viruses like influenza and SARS-CoV-2, exploit for rapid evolution (Telenti et al., 2022).

The study of genetic variations has identified many SNPs associated with increased risk for various cancers (Telenti et al., 2022). It is known that variants in the BRCA1 and BRCA2 genes significantly elevate breast and ovarian cancers (Rebbeck et al., 2015). They have shown that variations in genes related to immune functions (Tsuchiya et al., 2002). For instance, in the Human Leukocyte Antigen (HLA) region are linked to different diseases like rheumatoid arthritis and lupus. In another study, viral pathogens such as HIV and SARS-CoV-2, has demonstrated how genetic mutations can lead to increased transmissibility and resistance to treatments and vaccines. The emergence of antibiotic resistance is often driven by genetic variations within bacterial populations that lead to the spread of resistant strains (Normark & Normark, 2002). The recent studies have shown that certain genetic variations are positively selected in human populations in response to environmental pressures such as the ability to metabolize certain foods or resist diseases that are endemic to specific regions (Hancock et al., 2008).

The genetic variations across different populations help to identify at-risk groups and tailor prevention and treatment strategies (Arnett et al., 2007). The integration of genomic data with clinical information is essential to understand the complex relationships between genetic variations and disease outcomes (West et al., 2006). The advancements in genomics are paving the way for personalized medicine, where treatments can be tailored based on an individual's genetic profile (Ginsburg & Willard, 2009). In addition, ethical considerations regarding genetic privacy, discrimination, and the implications of gene editing technologies like CRISPR must be addressed (Brokowski & Adli, 2019). Finally, these variations are fundamental to understand disease evolution and dynamics. Therefore, continue research in this field is crucial for advancing public health, developing effective treatments, and anticipating future disease outbreaks (Brokowski & Adli, 2019).

Table 1: List of Emerging Infectious Diseases (2000-2024), their Genetic Variations, and Evolutionary Changes.

Sr#	Emerging Infectious Disease	Genetic Variations	Disease Evolution	References
1	Severe Acute Respiratory Syndrome (SARS) (2002-2003)	Mutations in SARS-CoV genome, particularly in the spike (S) protein	Rapid spread to multiple countries, high mortality rate, controlled through public health measures	(Chan-Yeung & Xu, 2003)
2	Middle East Respiratory Syndrome (MERS) (2012-present)	Variations in MERS-CoV spike (S) protein, ORF1a	Zoonotic transmission from camels to humans, ongoing sporadic outbreaks	(Chan-Yeung & Xu, 2003)
3	H1N1 Influenza (Swine Flu) (2009)	Reassortment of H1N1 genes from avian, swine, and human influenza viruses	Pandemic spread, high infectivity but lower mortality compared to other pandemics	(Shu et al., 2011)
4	Ebola Virus Disease (2014-2016, 2018, 2021)	Genetic drift and bottleneck events in EBOV genome	Multiple outbreaks with varying mortality rates, zoonotic transmission	(Organization, 2016)
5	Zika Virus (2015-2016)	Mutations in the prM protein, leading to increased neurovirulence	Rapid spread across the Americas, associated with microcephaly and Guillain-Barré syndrome	(Karwowski et al., 2016)
6	Chikungunya Virus (2004-present)	Mutations in the E1 protein, increasing vector competence in Aedes albopictus	Re-emergence in Asia, Africa, and the Americas, causing large outbreaks	(Pialoux et al., 2007)
7	COVID-19 (SARS-CoV-2) (2019-present)	Numerous genetic variations, including Alpha, Delta, Omicron variants	Global pandemic, with significant waves driven by variants of concern	(Ciotti et al., 2020)
8	Nipah Virus (2001-present)	Variability in G and F glycoproteins among different strains	Periodic outbreaks in South and Southeast Asia, high mortality, zoonotic transmission from bats	(Ciotti et al., 2020)
9	H5N1 Avian Influenza (2004-present)	Mutations in the HA and NA proteins, enabling zoonotic transmission	Sporadic human infections, high mortality, ongoing pandemic potential	(Thomas & Noppenberger, 2007)
10	Monkeypox (mpox) (2022-present)	Genetic variations in Clade II associated with human-to-human transmission	Spread beyond endemic regions in Africa to Europe, the Americas; changing transmission dynamics	(Cholli, 2022)

Sr#	Emerging Infectious Disease	Genetic Variations	Disease Evolution	References
11	Crimean-Congo Hemorrhagic Fever (CCHF) (2000-present)	Genetic diversity among strains, particularly in the S segment of the genome	Increasing cases in endemic regions, zoonotic transmission via ticks	(Nasirian, 2020)
12	Marburg Virus Disease (2005-present)	Variations in the GP gene across different outbreaks	Sporadic outbreaks with high mortality rates, zoonotic transmission from bats	(Control & Prevention, 2009)
13	Severe Fever with Thrombocytopenia Syndrome (SFTS) (2011-present)	Genetic reassortment in the SFTSV genome, including NSs protein	Emerging in East Asia, with a high case-fatality rate, tick-borne transmission	(Sharma & Kamthania, 2021)
14	H7N9 Avian Influenza (2013-present)	Mutations in the HA protein, leading to human infections	Sporadic cases, high mortality in infected individuals, potential for reassortment	(Iuliano, 2017)

6. Antimicrobial Resistance and Re-emerging Infections

The World Health Organization (WHO) has recognized antimicrobial resistance (AMR) as one of the top 10 global public health threats (Salam et al., 2023). The AMR has emerged a critical global health issue that threatening the efficacy of antibiotics and other antimicrobial agents. AMR occurs when microorganisms evolve and develop the ability to resist the effects of drugs that once effectively treated them (Ferri et al., 2017). This phenomenon is impaired because of overuse and misuse of antibiotics that leading to rise in infections that are more difficult to treat (Prestinaci et al., 2015). The spontaneous mutations in bacterial DNA may confer resistance. The resistance genes transferred from bacteria to human beings through plasmids, transposons, and bacteriophages (Lerminiaux & Cameron, 2019). Some invitro studies, bacteria exhibit increased resistance due to reduced penetration of antimicrobials and enhanced metabolic state. The inappropriate prescribing practices in both human and veterinary medicine contribute significantly to AMR (Lerminiaux & Cameron, 2019).

The use of antibiotics in livestock for growth promotion and disease prevention is a major contributor to resistance (Singer et al., 2003). Moreover, inadequate sanitation, hygiene practices, and infection prevention measures in healthcare system facilitate the spread of resistant strains (Endale et al., 2023). Re-emerging infections refer to existed controlled or eradicated infectious diseases that have resurfaced due to various factors, including AMR (Hassan et al., 2024). In addition to multi-drug-resistant (MDR), TB and extensively drug-resistant (XDR) TB have emerged as significant public health challenges (Jain & Mondal, 2008). These factors such as incomplete treatment regimens and the global movement of people contribute to the resurgence of diseases (Weiss & McMichael, 2004). MRSA, once confined to healthcare system is now prevalent in community system (David & Daum, 2010). It is resistant to various commonly used antibiotics, complicating treatment options (Bader et al., 2010). Some viral infections, such as influenza and HIV, have also seen the emergence of resistant strains due to mutations, challenging vaccination and antiviral strategies (Boroumand et al., 2021). AMR is associated to increased morbidity and mortality rates, longer hospital stays, and higher healthcare costs (Dadgostar, 2019).

The economic impact of AMR is another major concern (Dadgostar, 2019). They increased healthcare costs as well as low productivity (Gorasso et al., 2022). It is estimated that AMR cost the

global economy up to \$100 trillion by 2050 (Dadgostar, 2019). Therefore, it should be addressed on urgent basis(Kaye et al., 2020) . Some implementing to use effective antibiotic against infectious diseases in healthcare systems to optimize the concentrations of antibiotics to ensure precise prescription and duration (Kaye et al., 2020). The surveillance of antibiotic usage and resistance patterns help to understand the dynamics of AMR and making policy decisions (Tompson et al., 2021). Therefore, it is urgent need for the development of new antibiotics and alternative therapies such as bacteriophages, immunotherapy, and vaccines (Zalewska-Piątek & Piątek, 2021). Secondly, we should educate the healthcare professionals as well as the public about the accurate dose of antibiotics that is essential in curbing AMR (Dhingra et al., 2020). Thirdly, there should be an authority to tackle and quick response to the AMR locally and globally (Baekkeskov et al., 2020).

Table. 2. List of Antimicrobial Resistance Agents, their Associated Genes, Diagnostic Tests, and Re-emerging Infections from 2000-2024.

Sr#	AMR Agent	Associated Genes	Diagnostic Tests	Re-emerging Infections (2000-2024)	References
1	Methicillin-resistant Staphylococcus aureus (MRSA)	mecA, mecC	PCR, culture, PBP2a test	MRSA infections, particularly in community settings	(Lee et al., 2018)
2	Vancomycin-resistant Enterococci (VRE)	vanA, vanB	PCR, culture, E-test	Enterococcal infections	(Tacconelli & Cataldo, 2008)
3	Extended-spectrum β -lactamases (ESBLs) producing Enterobacteriaceae	blaCTX-M, blaSHV, bla-TEM	PCR, culture, ESBL test	ESBL-producing Entero(Organization & Initiative, 2010) bacteriaceae infections	(Lawandi et al., 2022)
4	Carbapenem-resistant Enterobacteriaceae (CRE)	KPC, NDM, OXA-48, VIM, IMP	PCR, culture, Carba NP test, multiplex assays	CRE infections	(Lawandi et al., 2022)
5	Multidrug-resistant Mycobacterium tuberculosis (MDR-TB)	katG, inhA, rpoB	GeneXpert MTB/RIF, Line probe assays, culture	Tuberculosis (MDR-TB and XDR-TB)	(Organization & Initiative, 2010)
6	Neisseria gonorrhoeae (resistant to multiple antibiotics)	penA, mtrR, gyrA, parC	NAAT, culture, E-test	Gonorrhea (drug-resistant strains)	(Hook III et al., 2013)
7	Clostridioides difficile (CDI)	tcdA, tcdB	PCR, enzyme immunoassay (EIA), stool culture	Clostridioides difficile infection	(Feuerstadt et al., 2023)
8	Drug-resistant Plasmodium falciparum	pfprt, pfmdr1, k13	PCR, microscopy, Rapid Diagnostic Tests (RDTs)	Malaria (drug-resistant strains)	(Organization, 2021)
9	Drug-resistant Salmonella typhi (Typhoid fever)	gyrA, parC, blaCTX-M	PCR, culture, Widal test, blood culture	Typhoid fever	(Organization, 2019)

Sr#	AMR Agent	Associated Genes	Diagnostic Tests	Re-emerging Infections (2000-2024)	References
10	Multidrug-resistant <i>Acinetobacter baumannii</i>	OXA-23, OXA-24/40, OXA-58	PCR, culture, MALDI-TOF MS	<i>Acinetobacter</i> infections	(Moss et al., 1988)
11	<i>Candida auris</i> (anti-fungal resistance)	ERG11, FKS1	PCR, culture, MALDI-TOF MS	<i>Candida auris</i> infections	(Prestel, 2021)
12	Multidrug-resistant <i>Pseudomonas aeruginosa</i>	mexA, mexB, mexC, mexE	PCR, culture, E-test, automated systems (e.g., VITEK)	<i>Pseudomonas</i> infections	(Bodey et al., 1983)
13	Colistin-resistant Enterobacteriaceae (mcr-1 positive)	mcr-1	PCR, culture, broth micro-dilution	Colistin-resistant infections	(Shenoy et al., 2019)
14	Influenza A (H5N1, H1N1)	NA, HA	RT-PCR, rapid antigen tests, serology	Avian Influenza (H5N1), H1N1 pandemic (2009)	(Control & Prevention, 2010a)
15	Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)	ORF1ab, S, E, N genes	RT-PCR, rapid antigen tests, serology, whole genome sequencing	COVID-19 pandemic (2019-2024)	(Ciotti et al., 2020)
16	Drug-resistant <i>Klebsiella pneumoniae</i>	blaKPC, blaNDM, blaOXA-48	PCR, culture, automated systems (e.g., VITEK)	<i>Klebsiella</i> infections (hospital-acquired)	(Control & Prevention, 2010b)

7. Public Health Responses to Emerging Diseases

The emerging infectious diseases (EIDs) pose significant challenges to global health systems. Recent outbreaks such as COVID-19, Ebola, and Zika virus have great importance to give rapid public health responses (Guilamo-Ramos et al., 2021). The key strategies have to be employed, lessons should be learnt, and the role of technology and community engagement to address the EIDs. The effective surveillance systems are crucial for early detection of outbreaks (Schierhout et al., 2017). The integration of human, animal, and environmental health data is known as the One Health approach, have to be emphasized (Rock et al., 2009). In addition, the technologies such as the Global Public Health Intelligence Network (GPHIN) facilitate rapid sharing of data that allow for timely responses to the emerging threats (Amir et al., 2021).

The COVID-19 pandemic demonstrated the potential for expedited vaccine development through platforms like mRNA technology (Szabó et al., 2022). Therefore, collaborative efforts such as COVAX have aim to ensure equitable access to vaccines. The rapid development of therapeutics including antiviral treatments and monoclonal antibodies, has been critical in managing outbreaks (Hotez et al., 2021). The strengthening healthcare systems, particularly in low and middle income countries are essential for effective responses. Therefore, this includes training of healthcare workers to enhance laboratory capacity (Almal & Padh, 2012). These regularly updating emergency plans can help to mitigate the impact of outbreaks. These simulations and trainings are essential for testing response capabilities.

To engaging communities through transparent communication has a major role for building trust (Frerichs et al., 2017). The Public health messages must be culturally sensitive and accessible to ensure compliance with health measures (Resnicow et al., 1999). Therefore, community leaders and stakeholders have to be involved in decision-making that increase public engagement and adherence to health guidelines. Moreover, collaborative efforts among countries, NGOs, and international organizations (e.g., WHO) are critical for coordinated responses. These partnerships facilitate resource sharing and technical assistance. The global research initiatives should be promoted to share findings for best practices to enhance the cumulative response to EIDs (Theobald et al., 2018).

The COVID-19 pandemic highlighted the need for countries to invest in public health infrastructure plans. If nations with pre-existing frameworks for managing outbreaks is far better to control the spread of viruses (Williams et al., 2023). The use of digital health tools, including contact tracing apps and telehealth services, became essential during the pandemic. These technologies helped to mitigate the impact of social distancing measus (Alo et al., 2021). The inequitable distribution of vaccines and resources during the COVID-19 pandemic emphasized the importance of addressing health disparities. Therefore, public health responses must prioritize equity to ensure all populations are protecting, so the world continues to face new health threats (Shadmi et al., 2020).

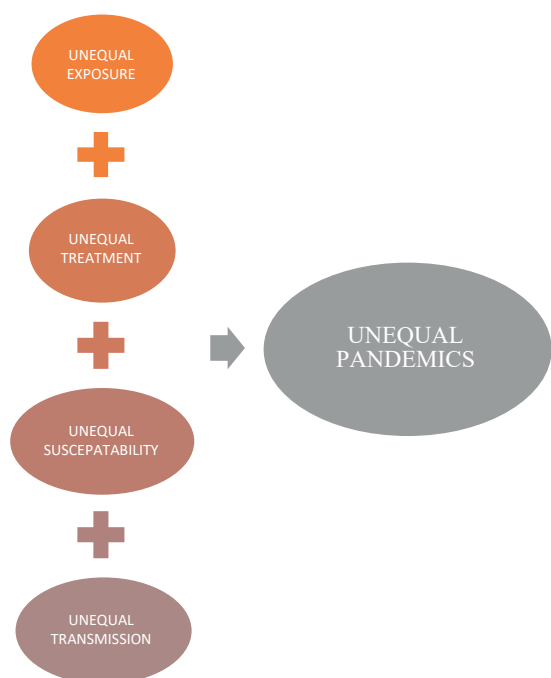


Figure 4. Reasons of Un-equal Pandemics

8. Emerging Diseases Challenges

Emerging infectious diseases (EIDs) pose significant challenges to global health systems due to their complex nature and rapid evolution. Recently some scientists highlighted the importance of timely and accurate diagnosis for effective management and containment of these diseases. One of the primary challenges in diagnosing of EIDs is the vast diversity of pathogens, such as viruses, bacteria, fungi, and parasites (Heesterbeek et al., 2015). Many of these pathogens have unique and often overlapping clinical symptoms that make their differential diagnosis difficult. For instance, the diseases i.e Zika virus and chikungunya can present with similar symptoms that complicate clinical assessment (Álvarez-Argüelles et al., 2019). In some other studies, researchers emphasized the need for advanced diagnostic methods that can quickly identify a range of pathogens like multiplex PCR and multiplex ELISA etc (Panwar et al., 2023).

The rapid mutation rates of different emerging pathogens complicate diagnosis. These pathogens such as influenza and coronaviruses undergo frequent genetic changes that may lead to variations

that evade standard diagnostic tests (Zabidi et al., 2023). The emergence of new variants render existing assays, ineffective, therefore, it is necessary to be updated. Moreover, the rise of AMR among bacterial EIDs poses additional challenges (Pennington, 2023). The AMR mechanisms may not be adequately detected by traditional diagnostic methods that lead to inappropriate treatment choices and worse clinical outcomes. (Okeke et al., 2020). Many regions lack the infrastructure, trained personnel, and resources that are required to implement sophisticated diagnostic techniques. As a result, diseases may go undiagnosed or misdiagnosed, leading to ineffective control measures and increased transmission. Point-of-care (POC) tests have shown promise in improving access to diagnostics in remote areas. However, many POC tests are not sensitive or specific enough, and their performance in real-world systems may vary significantly. Moreover, ensuring the reliability and accessibility of these tests are essential for improving diagnostic capabilities in these populations (Boehme et al., 2011).

The ethical implications of diagnosing EIDs, particularly in relation to testing and treatment, may not be overlooked (Tejiokem et al., 2011). The rapid tests may produce false negative or positive results that lead to mismanagement of cases (Simpson et al., 2020). These collaboration among public health organizations, regulatory agencies, and the diagnostic industry are essential to streamline the approval process for new diagnostic tools, ensuring that they are safe, effective, and accessible in a timely manner. The diagnosis of emerging infectious diseases is fraught with challenges that demand a multifaceted approach. Furthermore, improve diagnostic capabilities that is essential to invest in research and development of novel technologies to increase surveillance systems, and to ensure equitable access to diagnostic resources (Adachi et al., 2023).

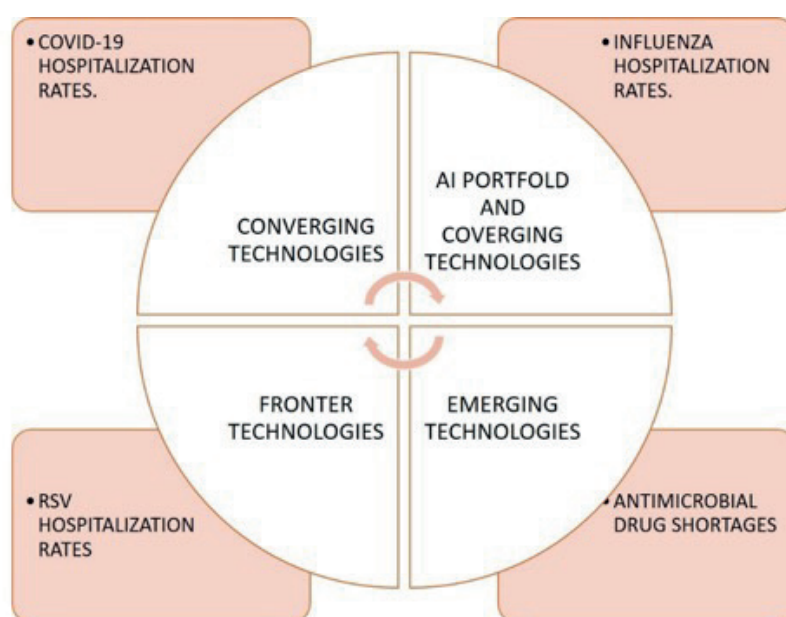


Figure 5. Challenges against Emerging Infectious Diseases

9. Preventative Strategies and Vaccination

Preventative strategies and vaccination efforts play a critical role in public health by reducing the incidence of infectious diseases and controlling outbreaks. For instance, the COVID-19 pandemic has emphasized the importance of these measures, prompting an acceleration in research, development, and implementation of vaccines and public health strategies. The success of mRNA vaccines against COVID-19 has spurred interest in mRNA technology for other diseases. This research leads to develop mRNA vaccines for influenza, Zika virus, and many other diseases. The flexibility of mRNA platforms allows for rapid updates and adaptations in response to emerging variants and pathogens. Moreover, vaccine uncertainty remains a significant barrier to achieving herd immunity. Therefore, recent studies highlighted the need for targeted communication strategies

that address specific concerns among different demographic groups. Therefore, these community leaders and social media effectively can help to build trust in vaccination programs.

Secondly, the global initiatives like COVAX have aim to ensure equitable access to vaccines, particularly in low and middle income countries. Furthermore, recent studies emphasized the importance of collaboration between governments, NGOs, and private sectors to increase distribution networks and address logistical challenges. The achievements of herd immunity through vaccination is essential for controlling outbreaks. The community engagement initiatives, such as educational campaigns and local vaccination drives, have proven effective in increasing vaccination rates. These are involving local healthcare providers may also foster trust and participation. Moreover, increasing surveillance systems are critical for early detection of outbreaks. The use of digital tools and data analytics may help to track disease patterns and vaccination coverage. Therefore, the quick response teams may be mobilized to contain outbreaks that have been seen in recent responses to measles and polio resurgence in certain countries.

Thirdly, some strong public health policies that mandate vaccinations for school entry and certain jobs have demonstrated efficacy in increasing vaccination rates. These policymakers are encouraged to take measures while ensuring exemptions are appropriately managed to protect public health. Furthermore, distribution of vaccines, especially in rural and deprived areas, poses logistical challenges. In addition, cold chain requirements for certain vaccines complicate transportation and storage. In future, efforts must focus to develop some stable formulations and innovative delivery methods, such as microneedle patches. The emergence of new pathogens need a proactive approach to vaccine development. Therefore, research to develop some universal vaccines, such as influenza multi-vaccine, is crucial. Moreover, the collaborations between academic institutions, industry, and governments can expedite the research and development process.

Finally, a multi-faceted approach combining vaccination with other preventative measures (such as hygiene, sanitation, and education) is essential. Those programs that promote comprehensive health education may empower communities to adopt healthier behaviors and improve cumulative public health outcomes. In additionally, recent literature may play a pivotal role to make preventative strategies to protect the public health. While challenges remain, innovative approaches and collaborative efforts offer hope for more effective prevention and control of infectious diseases in the future.

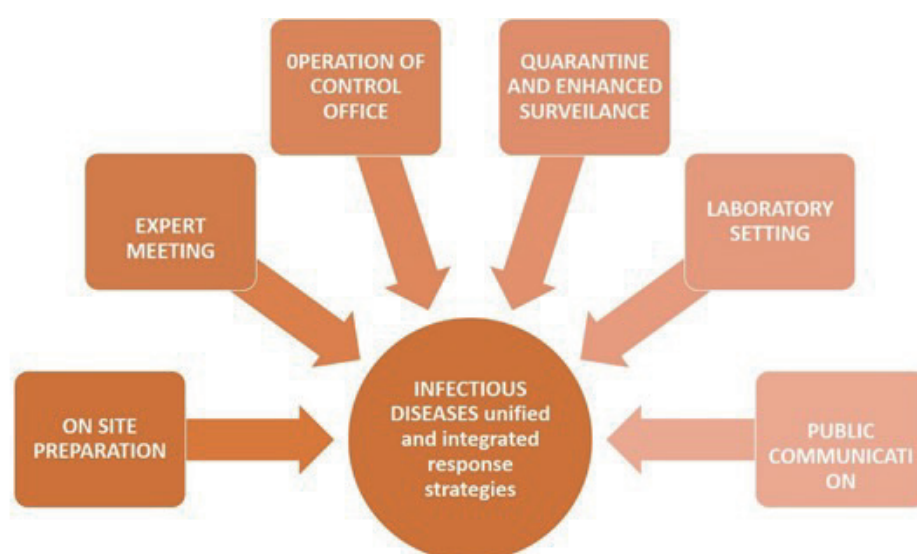


Figure 6. Preventative Strategies and Vaccinations against Infectious Diseases

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