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From Animal Origins to Global Outbreaks: Rethinking Pandemic Preparedness in a Post-COVID World

By

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Abstract

The COVID-19 pandemic revealed significant shortcomings in worldwide pandemic preparedness, highlighting systems that were mostly reactive, disjointed, and insufficiently focused on the ecological sources of infections. To deal with the persistent threat of zoonotic diseases, which make up most of the emerging infectious diseases, there is need to make a significant change to our current approach. This review analyses materials from epidemiology, environmental science, and global health policy, showing evidence regarding the animal origins of these viruses, their transmission dynamics, and the significant deficiencies in pandemic preparedness that the outbreaks have shown. It also submits that effective preparedness in a post-COVID world needs to be completely reoriented towards a proactive and integrated One Health framework. This framework emphasizes that human, animal, and environmental health are all linked and focuses on the factors that lead to viral spillover, such as the trade in animals, changes in land use, and the intensification of agriculture. At the same time, it requires a comprehensive approach that tackles the underlying reasons of emergence and creates structures that are strong, cooperative, and fair to deal with outbreaks when they happen. To lower the likelihood of future pandemics, we need to completely rethink how we prepare for them. This new way of thinking is necessary to lessen the effects of future pandemics in a world that is becoming more connected and less stable environmentally. This means putting prevention at the source through strong, collaborative surveillance and tackling the ecological factors that cause zoonotic spillover.

Keywords*: zoonotic coronaviruses, pandemic preparedness, spillover, One Health, surveillance, COVID-19*

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Introduction

The COVID-19 pandemic, caused by the SARS-CoV-2, showed the catastrophic nature of pandemics as a fundamental and enduring threat to world health, security, and economic stability. Its emergence from a likely animal reservoir highlighted a significant and persistent epidemiological fact: most emerging infectious diseases (EIDs) are zoonotic in origin, with pathogens transferring from wildlife or domestic animals to human populations (Jones et al., 2008; Plowright et al., 2021). The immediate crisis has lessened, but the post-COVID age is not defined by resolution; rather, it necessitates a critical assessment of the shortcomings of pre-2020 disease emergency preparedness frameworks. These mechanisms, frequently based on reactive containment and isolated national reactions, were insufficient against a virus that capitalized on the interconnection of the contemporary globe (Gostin et al., 2020). As a result, public health researchers are coming to the same conclusion: pandemic preparedness needs to be completely rethought (Sharfstein & Lurie, 2023; El-Jardali et al., 2025). This paper contends that a transformational strategy necessitates the incorporation of a proactive One Health paradigm, which acknowledges the inseparable connections among human, animal, and environmental health, alongside enhanced global governance and equal access to medical countermeasures. A resilient strategy must go beyond just looking at human healthcare systems. It must also look at the upstream causes of spillover, like changes in land use, the trade of wildlife, and the intensification of agriculture. At the same time, it must strengthen the downstream abilities in surveillance, prompt diagnostics, and fair vaccine distribution. Such a comprehensive framework is crucial not just for mitigating the next pandemic but also for establishing enduring health security in a time of unparalleled ecological and social transformation.

Emergence of Zoonotic Viruses

Zoonotic viruses such as Lassa, influenza, and coronaviruses have caused numerous significant outbreaks in the 21st century, underscoring their potential for epidemics and pandemics. There have been cases in the past that show how coronaviruses can spread from one species to another, often because of changes in the environment, more interactions between humans and animals, and the virus's ability to change and adapt (Plowright et al., 2017). Coronaviruses are especially interesting because they mutate quickly, have large genomes, and can infect many species, making them perfect for zoonotic spillover (Cui et al., 2019). In late 2002, the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) first appeared in southern China. It is thought to have come from horseshoe bats (Rhinolophus spp.) and gotten to people through other animals, likely civet cats. Before it was confined in 2003 (Zhong et al., 2003), SARS-CoV infected more than 8,000 people over the world, killing around 9.6% of them. Saudi Arabia was the first place to find the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) in 2012. It is thought that MERS-CoV came from bats and that dromedary camels are the main animal reservoir for the virus. MERS still causes random outbreaks that kill a lot of people (around 34% of the time) and do not spread easily from person to person (Zaki et al., 2012). The virus that causes COVID-19, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), was initially found in Wuhan, China, in December 2019. While the precise origins are still being debated, it is closely linked to bat coronaviruses and may have included an intermediary host (Zhou et al., 2020). SARS-CoV-2 caused the biggest pandemic in over a century. As at September 2025, there were more than 770 million confirmed cases of COVID-19 and more than 7 million deaths around the world (WHO, 2025).

Understanding Zoonotic Spillover

Throughout history, outbreaks and epidemics have happened a lot, and sometimes they have grown into pandemics that affect people on many continents. It is believed that over 60% of all novel human infectious diseases come from zoonotic sources, which means they come from pathogens that are usually present in animals (Woolhouse & Gowtage-Sequeria, 2005; Jones et al., 2008). Some studies, including more recent ones, say that this number could go as high as 75% (Taylor et al., 2001; CDC, 2025). It is evident that a substantial proportion of human infectious diseases stem from zoonotic spillover, involving the transmission of pathogens from non-human animals to humans, irrespective of the precise percentage. For example, the Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) first showed up in people in 2002/2003, and the Middle East Respiratory Syndrome Coronavirus (MERS-CoV) followed in 2012. It is likely that both coronaviruses came from bat viruses. Palm civets and dromedary camels may have acted as intermediary hosts for SARS-CoV and MERS-CoV, respectively (de Wit et al., 2016). Human behaviors that increase contact with different animal species and the infections they carry, like handling, hunting, and eating wild animal products, greatly increase the chances of spillover events (Kurpiers et al., 2016; Ellwanger et al., 2020). In addition, several countries have live animal markets, sometimes known as "wet markets," where people can buy wild animals and their products for food, medicine, cultural rituals, souvenirs, or as pets. These markets are important for bringing people and animals together, which makes it easier for pathogens to spread through contact with meat, blood, and other bodily fluids, as well as through aerosols and dirty surfaces (Brown, 2004; Lo et al., 2019; Aguirre et al., 2020; Wassenaar & Zou, 2020). Spillover particularly refers to the “cross-species transmission of a pathogen into a host population not previously infected” (Wells & Clark, 2019), mostly from wildlife to people (Plowright et al., 2017; Wells & Clark, 2019).

***Table 1**: Definitions of Related Terms*

Term	Description	References
Pathogen spillover	This is transmission of a pathogen from a reservoir host to a recipient host species. It occurs when epidemics in a host population are driven not by transmission within that population but by transmission from a reservoir population	Power & Mitchell, 2004; Becker et al., 2019
Zoonotic spillover	The transmission of pathogens from wild animals to humans	Ellwanger & Chies, 2021
Spillback	The transmission of pathogens from humans to wildlife, termed reverse zoonosis, may occur through direct contact or via vectors	Weaver, 2013; Hendy et al., 2020; Olival et al., 2020
Horizontal virus transfer	The transmission of viruses between different species across biological kingdoms, regardless of direction	Dolja and Koonin, 2018
Spillover	It is a multifaceted phenomenon influenced by a range of factors, including features of the hosts, microorganisms, and	Plowright et al., 2017

	their environment. It can also be referred to as host jump	

The probability of a spillover event is chiefly influenced by the incidence and severity of infection in reservoir hosts, typically non-human animals residing in wild environments or agricultural settings. The distribution and density of these infected hosts are important factors to think about when figuring out how likely it is that the disease will spread (Plowright et al., 2017). The pathogen load is affected by the intensity of infection and prevalence among reservoir hosts. This, in turn, affects how pathogens are shed. The hosts' immunological status, interspecies interactions (such as predator-prey dynamics and habitat sharing), and environmental variables (including ecosystem traits and environmental degradation) all have an effect on the ease of transmission of the pathogen. The properties of pathogens also influence spillover risk, as they dictate their environmental resilience and ability to spread among other hosts or vectors (Plowright et al., 2017; Becker et al., 2019; Borremans et al., 2019). Ecological and intrinsic characteristics associated with pathogens can influence spillover risk prior to human involvement, as other animals and pathogens may potentially participate in the process. The frequency of human-animal interactions, coupled with the exposure dose and transmission route of pathogens, ultimately determines spillover risk.

Definition and stages of zoonotic transmission

Coronaviruses are enveloped, non-segmented, positive-sense single-stranded RNA viruses that belong to the family Coronaviridae and the order Nidovirales. The viral genome, which is between 26 and 32 kilobases long, is one of the largest for RNA viruses. It contains structural proteins like the spike (S), envelope (E), membrane (M), and nucleocapsid (N) proteins, as well as several non-structural and accessory proteins that are important for replication and evading the immune system (Fehr & Perlman, 2015). There are four genera of coronaviruses based on their evolutionary relationships: Alphacoronavirus and Betacoronavirus, which mostly infect mammals like humans, bats, pigs, and cats; and Gammacoronavirus and Deltacoronavirus, which mostly infect birds and some marine mammals (Woo et al., 2012). There are seven coronaviruses that can infect people. Four of these (HCoV-229E, HCoV-NL63, HCoV-OC43, and HCoV-HKU1) usually cause minor respiratory diseases. The other three, SARS-CoV, MERS-CoV, and SARS-CoV-2 cause serious respiratory syndromes and global health emergencies (Cui et al., 2019).

Changes in genotypes and phenotypes due to evolution happen when regulation of cellular processes, organism characteristics, environmental influences, and geographical settings all work together in complicated ways. Coronaviruses and other zoonotic viruses have considerable genetic variation in their non-human hosts, such as bats, yet frequently encounter difficulties in efficiently spreading from their primary reservoirs. This challenge arises from physiological disparities among host species, requiring significant evolutionary adaptations, frequently via a co-evolutionary process. Viruses adapt to new hosts in large part through mutations, recombination, genetic drift, and pleiotropy. These evolutionary changes not only help keep viruses in host populations, but they also change how harmful they are. This was shown by the adaptive evolution of the S glycoprotein in bovine coronavirus and human coronavirus (HCoV) OC43, which was studied using phylogenetic and phylodynamic methods. Here are the stages of zoonotic transmission that have been recorded.

Stage 1 (pre-emergence): For zoonotic spillover to happen, a virus must be consistently maintained in a natural reservoir host for a long time, usually without causing significant illness, so it may survive and spread. Bats, especially those in the Rhinolophus group, are very important as reservoir hosts for coronaviruses because they can carry a lot of SARS-related coronaviruses without displaying any signs of illness. For instance, horseshoe bats in Yunnan Province have been recognized as vectors of SARS-like coronaviruses that are closely associated with SARS-CoV-2 (Zhou et al., 2020). Scientists have also found bat coronaviruses that are genetically similar to MERS-CoV in many nations on different continents (Anthony et al., 2017). This shows how pervasive and persistently silent these viruses are in bat populations.

Stage 2: Spillover chances happen often when people or intermediate hosts come into direct or indirect contact with infected reservoir species through different paths. These include the wildlife trade, which involves animals like civets, raccoon dogs, and pangolins; close contact with livestock, like when dromedary camels spread MERS-CoV; and contamination of the environment in high-risk sites like wet markets or places that have bat guano. A significant example is the detection of SARS-CoV-2 RNA in environmental samples collected from wildlife stalls at the Huanan Seafood Market in Wuhan, which clearly suggests a possible initial point of human exposure (Gao et al., 2023).

Stage 3: For a zoonotic spillover to be successful, the virus needs to infect human cells, which it usually does by attaching to specific host receptors. For SARS-CoV-1 and SARS-CoV-2, this means that the viral spike protein binds to the human ACE2 receptor. Genetic modifications in the spike protein, such as mutations or recombination events, can make it easier for viruses to move between species by increasing their affinity and compatibility with hosts cell receptors (Menachery et al., 2015). SARS-CoV-2 exhibits a significant binding affinity for human ACE2, presumably due to adaptive modifications in an intermediate host preceding human infection (Zhou et al., 2020).

Stage 4: The most important part of zoonotic emergence is this stage that required by a virus to easily spread from person to person. This can cause outbreaks in certain areas or pandemics all over the world. Many viruses that affect animals can also infect humans, but they usually have a hard time spreading to other people because of biological or behavioral barriers. Coronaviruses like other zoonotic viruses, on the other hand, have been able to overcome these problems and spread quickly through human populations. For example, coronaviruses spreads easily through aerosols and droplets, and it's even harder to stop the virus from spreading because infected people can spread it before they show symptoms and there are infected people who show no symptoms (WHO, 2021). Moreover, global travel networks expedite the swift spread of emerging coronaviruses, converting local spillover incidents into pandemics.

Factors influencing spillover

The rise in population and movement, as well as the growing cultural demand for food and animals in wildlife trade, are the main causes of new viral infections (Liu et al., 2014). Human activities are increasingly acknowledged as principal catalysts of ecological transformation, resulting in intricate spillover consequences across diverse environmental sectors (Tadda et al., 2021). These spillovers, which can either make the effects of some actions stronger or weaker, are especially clear when it comes to deforestation, climate change, the trade in wildlife, and urbanization (Pfaff & Robalino, 2017). It is important to understand the complicated ways that these elements affect spillover occurrences in order to come up with good ways to lessen their negative consequences and encourage sustainable practices (Pfaff & Robalino, 2017).

Deforestation and Habitat Fragmentation

When trees are cut down, people are more likely to come in contact with animals that carry coronaviruses, like bats, which are the natural hosts for many SARS-related coronaviruses. Forest fragmentation in Southeast Asia and certain regions of Africa results in heightened interactions between bats and domestic animals or humans (Allen et al., 2017). In Yunnan Province of China, where there are many coronaviruses associated to SARS, deforestation and human encroachment have brought horseshoe bats (Rhinolophus spp) and people closer together, making it easier for viruses to spread (Zhou et al., 2020; Gibb et al., 2020).

Socioeconomic Factors

Socioeconomic factors significantly impact the epidemiology of coronaviruses and other zoonotic viruses. Overcrowded housing, limited access to healthcare, and significant social inequalities heighten transmission risks. For instance, people who are poor in cities often live in crowded areas where it is hard to observe a social distance, which makes it easier for SARS-CoV-2 to spread (Patel et al., 2020). Global gaps in vaccine access and healthcare infrastructure exacerbated unequal disease burden, resulting in disproportionately high morbidity and mortality rates in low- and middle-income countries (LMICs). Migrant laborers, low-wage service workers, and informal sector employees frequently lacked social protection and job security in their employment despite infection risks, facilitating community spread (Bambra et al., 2020).

Environmental Factors

Environmental factors are also very important in how spillover and transmission happen. Changes in land use, such as deforestation, agricultural development, and urbanization, make it more likely that animal reservoirs (especially bats) will come into contact with people, which increases the risk of spillover (Ruiz-Aravena et al., 2022). Climate change and changes in the environment could modify where hosts live and how viruses spread, making it even harder to predict risks. Bats have changed their travel patterns because of climate changes including droughts and temperature changes. This has pushed them into places where people live. This is thought to have played a role in the Hendra virus outbreaks in Australia, and it probably also applies to coronaviruses (Plowright et al., 2015). Warming climates affect the number and distribution of bat species. A modeling study from 2021 predicts that climate change could boost the spread of coronaviruses by changing the ranges of bats, especially in Southeast Asia (Carlson et al., 2021). Urban settings, marked by congestion, extensive public transit, and pollution, foster conditions favorable for prolonged human-to-human transmission, exemplified by SARS-CoV-2 (da Silva et al., 2020).

Wildlife Trade and Live-Animal Markets

Live-animal markets were directly responsible for the introduction of SARS-CoV-1 (2002) and SARS-CoV-2 (2019). In most parts of China, wet markets are close to homes and have many different kinds of animals in cages next to each other. This makes it easy for people to come into contact with these animals, which may be carrying new viral diseases. This is a perfect situation for new viruses to emerge that can cross species barriers (Chan et al., 2013; Liu et al., 2014; Woo et al., 2006). In Guangdong, civets and raccoon dogs sold in wet markets were discovered to be infected with SARS-CoV-1, with evidence indicating bat-to-intermediate-host-to-human transmission (Guan et al., 2003). Environmental swabs from Wuhan's Huanan Seafood Market also showed SARS-CoV-2 RNA, especially in stalls selling raccoon dogs. Although still being debated, this suggests that the virus came from an animal (Gao et al., 2023; Worobey et al., 2022). Stress, inadequate sanitation, and interspecies interactions in these marketplaces substantially increase the likelihood of coronavirus recombination and zoonotic transmission (Karesh et al., 2012).

Occupational Factors

Occupational exposure is a significant factor influencing infection risk. Individuals employed in live-animal marketplaces, wildlife trafficking, and slaughterhouses face heightened exposure because of direct interaction with potential intermediate hosts and contaminated surroundings. The introduction of SARS-CoV in 2002–2003 was associated with animal sellers and market workers in Guangdong, China, where civets and raccoon dogs served as amplifying hosts (Cui et al., 2019). Likewise, MERS-CoV has been linked to camel herders, abattoir workers, and healthcare professionals caring for infected patients, underscoring both zoonotic and nosocomial occupational hazards (Letko et al., 2020; Azhar et al., 2014). During the COVID-19 pandemic, healthcare workers continued to be a high-risk group on the front lines since they were constantly exposed to the virus in hospitals, especially in the early phases when there were not many protective measures in place (Nguyen et al., 2020).

Natural Reservoirs and Intermediate Hosts

Natural reservoirs are very important for the persistence and spread of coronaviruses. They serve as ecological sources where these viruses can circulate, evolve, and sometimes spill over infecting new hosts, like humans. Bats are the most important coronavirus reservoirs, especially for alpha- and beta-coronaviruses. Certain bat species, notably Rhinolophus (horseshoe bats), have been thoroughly documented to carry a diverse array of SARS-related coronaviruses without any discernible clinical signs, establishing them as the principal natural reservoirs for SARS-CoV and SARS-CoV-2 (Zhou et al., 2020; Anthony et al., 2017). These viruses can recombine and mutate while silently circulating in bat populations, sometimes gaining features that allow them to spread between different species. The natural reservoir for Middle East Respiratory Syndrome Coronavirus (MERS-CoV) is not definitively identified; however, bat coronaviruses genetically akin to MERS-CoV have been identified in several countries, indicating that bats may represent the primary natural source (Corman et al., 2014). Nonetheless, dromedary camels are regarded as the principal animal reservoir for persistent human illnesses, facilitating viral multiplication and shedding through nasal secretions (Azhar et al., 2014). Conversely, human coronaviruses responsible for common colds, such as HCoV-229E and HCoV-NL63, are thought to have emerged from bat reservoirs, with putative intermediate hosts like alpacas for 229E (Corman et al., 2015). HCoV-OC43 and HCoV-HKU1, both beta coronaviruses, are believed to have originated from rodents, specifically mice or rats; nevertheless, the exact reservoir and transmission history remain inadequately defined (Vijgen et al., 2005; Woo et al., 2005). These reservoirs are important because they sustain coronaviruses in the wild, sometimes in isolated ecological niches. When the correct conditions are present, including habitat destruction, wildlife trade, or habitat encroachment, the viruses can move to intermediate hosts or humans. Identifying and monitoring these natural reservoirs is therefore crucial for comprehending viral ecology, predicting future pandemics, and developing early warning systems for new zoonoses.

Transmission Dynamics

Respiratory viruses, including influenza, SARS, MERS, and COVID-19, mostly spread through close person-to-person contact via respiratory droplets, direct contact, and airborne particles (Peeri NC et al., 2020). Aerosol transmission has been identified as a significant factor in the dissemination of SARS-CoV, MERS-CoV, SARS-CoV-2, and influenza viruses (Nardell et al., 2020). Aerosols are droplets smaller than 5 µm that can stay in the air for a long time (Tellier et al., 2009). Under experimental conditions, the dynamic aerosol efficiency of SARS-CoV-2 exceeded that of SARS-CoV and MERS-CoV, with respirable-sized aerosols of SARS-CoV-2 maintaining infectivity and virion integrity for up to 16 hours (van Doremalen et al., 2020). While coughing and sneezing generate a greater quantity of aerosols per respiratory action compared to regular breathing, the latter can nevertheless produce aerosols (Fabian P et al., 2008), indicating the transmission potential of pre-symptomatic, asymptomatic, and mild illnesses. The main way that SARS-CoV-2 spreads is by respiratory droplets and aerosols. Wu et al. (2021) observed the growing evidence that aerosols, especially in indoor and inadequately ventilated settings, significantly facilitate transmission. Although fomite transmission is biologically feasible, its contribution is regarded as little in comparison to respiratory channels. These results underscore the significance of masking and ventilation as preventive strategies. SARS-CoV-2 has different patterns of viral shedding than SARS-CoV and MERS-CoV. In contrast to preceding coronaviruses, which exhibit peak viral shedding subsequent to symptom onset, SARS-CoV-2 viral loads generally reach their peak at or prior to symptom onset (Chen PZ et al., 2021). This early shedding in the upper respiratory tract makes it possible for people to spread the virus before they show symptoms (Wu et al., 2021). The conclusion is that individuals can disseminate the virus before being recognized through symptom-based screening (Wu et al., 2021).

Current Monitoring Strategies for Emerging Zoonotic Viruses

In response to COVID-19, many coronavirus-focused surveillance systems have been built. Genomic surveillance has become the cornerstone of coronavirus monitoring. High-throughput sequencing and real-time phylogenetic analysis enable quick identification of novel viral variations, follow viral evolution, and find genetic markers connected to host adaptation and transmissibility. There is a One Health approach that involves several professionals, collaborating nationally and internationally to improve the ecosystem between humans and animals. Platforms like GISAID (Global Initiative on Sharing All Influenza Data) (Shu & McCauley, 2017), Nextstrain (Hadfield et al., 2018), and PANGOLIN (Rambaut et al., 2020) now allow for near-real-time global genomic tracking of SARS-CoV-2 variants. This makes it easier to respond to outbreaks and design vaccines (Hadfield et al., 2018; Shu & McCauley, 2017). It gives a lot of detail about viral genomes, which helps in finding mutations that could change how easily they spread, how deadly they are, or how well they can evade the immune system. There have been prompt large-scale sequencing initiatives which enabled the early detection of variations of concern (VOCs), such as Alpha, Delta, and Omicron, and informed vaccine updates and public health actions (Harvey et al., 2021). These tools also allow policymakers to rapidly assess viral introductions, geographic spread, and the emergence of adaptive mutations. Importantly, sequencing has been crucial in discriminating between reinfection and persistent infection, and in identifying super-spreader events. The WHO Global Coronavirus Laboratory Network and the CDC's National SARS-CoV-2 Strain Surveillance (NS3) have also worked together in laboratories to find and describe variations. In

Africa, the Africa CDC's Pathogen Genomics Initiative (PGI) has strengthened regional coronavirus surveillance capacity, enabling the continent to monitor viral evolution and emergence more effectively (CDC, 2021). Some digital monitoring methods developed due to COVID-19 pandemic include the use of platforms like SORMAS for surveillance of population movements under lockdown, as well as closed-circuit television (CCTV), drones, mobile phone usage data, and biometric tracker bracelets. The most notable type of surveillance has been the implementation of mobile applications for COVID-19 tracking (Obi-Ani et al., 2021).

Phylogenetic analysis has also made it possible to put together the history of viral evolution and transmission networks. Phylogenetics can show whether outbreaks are caused through one spillover event or many introductions by comparing virus genomes from different patients and places. Phylogenetic studies have demonstrated that SARS-CoV originated from civets after several bat-to-civet transmission events (Cui et al., 2019), and that MERS-CoV outbreaks were often propelled by recurrent zoonotic introductions from camels instead of prolonged human-to-human transmission (Dudas et al., 2018). Phylogenetic reconstructions of SARS-CoV-2 elucidated that its global dissemination entailed many introductions across nations rather than a singular point-source expansion (Lemey et al., 2021).

Wildlife and livestock monitoring is still very important since coronaviruses come from animals. Keeping an eye on bat populations, camel reservoirs, and live-animal markets is very important for finding any spillover pathways (Ruiz-Aravena et al., 2022). Serological testing and viral metagenomics in high-risk animal populations facilitate the assessment of viral diversity and the possibility for cross-species transmission (Sánchez et al., 2022). Another important strategy is human sentinel surveillance and syndromic monitoring. Early warning systems that keep an eye on groups of people with respiratory illnesses, especially those who work with animals (such healthcare workers, animal traders, and farmers), can help find new infections early on.

Environmental surveillance, especially monitoring of wastewater, has become a strong additional instrument. During the COVID-19 pandemic, wastewater surveillance offered early signs of community transmission patterns, even before clinical cases were recognized, giving a scalable and cost-effective technique of monitoring viral circulation (Medema et al., 2020). Global health networks and collaborative platforms, such as the WHO Global Influenza Surveillance and Response System (GISRS) and the Global Early Warning System (GLEWS+), have grown to encompass coronaviruses and other zoonotic hazards. These platforms coordinate data-sharing, standardize diagnostic techniques, and permit rapid response to outbreaks.

Current Challenges in Detecting Early Spillover Events

Limited monitoring at the human-animal interaction makes it hard to find problems early on. The risk of spillover is greatest in areas where people come into contact with wildlife or farm animals, yet there is still not enough surveillance in these areas. Numerous low- and middle-income countries (LMICs), characterized by heightened zoonotic risk, are deficient in the infrastructure necessary for continuous genomic and serological surveillance in both humans and animals (Grange et al., 2021). Consequently, cross-species transmission events may go unnoticed until human-to-human transmission has already commenced. The limitations in laboratory and diagnostic capacity cause further delay in detection. At the beginning of an outbreak, there may not be any diagnostic tests available, or they may not be very good at finding new viruses. During the first SARS outbreak in 2002–2003, there were no effective genetic assays, therefore cases were identified retrospectively (Cui et al., 2019). The absence of broadly reactive coronavirus assays impedes the identification of novel strains that markedly differ from confirmed viruses (Sánchez et al., 2022).

Delays are sometimes caused by sociopolitical and reporting problems. In other circumstances, poor transparency, political sensitivities, or weak public health reporting systems make it hard to provide information about outbreaks quickly. For instance, both SARS and COVID-19 were initially marked by delayed reporting and ambiguity concerning the degree of human-to-human transmission (Heymann & Shindo, 2020). Ecological intricacy and viral heterogeneity present scientific obstacles. Bats, camels, and other hosts harbor a variety of coronaviruses, many of which have yet to be characterized. It is challenging to identify viruses with authentic spillover potential without extensive ecological research and experimental evaluations of receptor binding and host range (Ruiz-Aravena et al., 2022).

Also, differences in infrastructure and political will continue to make it hard for people in different locations to participate fairly. Low incidence and nonspecific symptoms are a primary obstacle. Initial spillover cases are frequently limited, dispersed, and clinically indistinguishable from prevalent respiratory illnesses, complicating their differentiation from seasonal viral infections. For instance, retrospective studies indicate that SARS-CoV-2 was prevalent in humans weeks prior to official acknowledgment in Wuhan, with initial cases manifesting as "pneumonia of unknown etiology" (Wu et al., 2020). Likewise, initial MERS-CoV cases in the Arabian Peninsula were probably not identified due to their similarity to influenza-like diseases (Zumla et al., 2015).

Lessons Learned and Recommendations for Future Preparedness

The COVID-19 pandemic taught us a lot about how to make international health systems better. To be ready for future health crises, we need to move from reactive to proactive approaches. We need to pay special attention to a few areas:

1. **Early Detection:** Early detection is very important for stopping infection from spreading. Studies show that it costs a lot less to stop contagious diseases before they spread than it does to deal with them once they become a global pandemic (Woolhouse et al., 2012).

2. **Global Coordination and Governance:** The pandemic made working together on a global scale even more important. Countries need to collaborate better in times health crises, confirming the need to establish stronger international health agreements, like the WHO Pandemic Agreement (World Health Organization, 2025). A binding pandemic treaty can help the world work together better in the future (Independent Panel for Pandemic Preparedness and Response, 2021).
3. **Investing in Health Systems:** Most countries, especially the lower income countries, did not have the infrastructure to deal with the pandemic. To be ready for the future, it is important to improve healthcare systems by giving workers better training, building stronger data infrastructure, and making sure there are enough healthcare workers (U.S. Centers for Disease Control and Prevention, 2024). These improvements will help countries to deal with future health crises better.
4. **Leverage technology:** Technology, especially electronic surveillance, was a big help in controlling the pandemic. Digital media and devices, such IoT devices, can be added to global surveillance systems to help find outbreaks early and make responses faster and better (Hossain et al., 2022). The devices are highly useful for keeping track on how diseases spread and making better use of available resources. To improve the accuracy of outbreak predictions and speed up responses, researchers have turned to machine learning and mathematical models. These techniques simulate actual epidemic situations to identify patterns and forecast the appearance or spread of viruses (Murray et al., 2020). The technologies use algorithms that were made using a variety of data sets, such as temperature, humidity, animal movement, and health information for people. LMICs like Nigeria can become more prepared for future outbreaks and respond faster if they put more resources into data science and technology (Tom-Aba et al., 2021).
5. **AI and big data analytics for outbreak prediction:** Incorporating AI and big data analytics tools to outbreak management has improved response to health challenges. These technologies can now be used to look for unusual disease patterns in large amounts of health records, environmental data, population movement patterns, and social media signals (Murray et al., 2020). International platforms like Bluedot and HealthMap employed AI to keep an eye on COVID-19 and find early signs, even before official reports were made (Bogoch et al., 2020). Platforms like SORMAS are starting to use AI-driven technologies in Africa that can warn of a possible outbreak based on real-time data (Tom-Aba et al., 2021).
6. **Public Health Interventions for Zoonotic Control:** The control strategies should be directed at interrupting the ways that diseases spread between animals and humans. One important thing to do would be to monitor high-risk places like abattoirs, live animal markets, and wildlife trading routes where people and animals have a shared environment, which might lead to spillover incidents (FAO, 2020). It is important to focus on vulnerable countries in LMICs that have a lot of livestock production and not very good veterinary services. To do this, there should be awareness campaigns, better biosafety measures, and higher hygiene standards in these states that are at high risk. Nigeria put rules in place for market operations, quarantine and lockdowns, travel restrictions, and contact tracking during the COVID-19 pandemic (NCDC, 2020). These steps were very important in intercepting the virus from spreading to other parts of the country and slowing down its progress.
7. **Cross-sectoral collaboration for pandemic prevention**: In addition to government agencies, successful prevention should engage stakeholders from the academic, local community, and private sectors. Maintaining these partnerships will improve the countries' capacity to prevent, detect, and respond to zoonotic diseases, making the national health security system stronger.
8. **Molecular diagnostics and serological testing in wildlife populations:** Molecular diagnostic techniques have proved essential for monitoring coronaviruses like other zoonotic viruses. It has facilitated early detection prior to transmission to human populations (Plowright et al., 2017). Reverse-transcription polymerase chain reaction (RT-PCR) and real-time quantitative PCR (qPCR) have been employed to identify coronavirus infections (Corman et al., 2020). ELISA has facilitated the identification of both past and recent exposure to coronavirus infections via antibody detection (Perera et al., 2020). Molecular diagnostic tools in wildlife still have some problems, such as not enough educated staff, not enough cold chain capacity, and not enough transportable biosafety laboratories (Nani et al., 2021). Investing in community-driven laboratory structures, training field personnel, and improving the supply of reagents for diagnostics will help close these gaps and make it easier to find diseases early on, before they spread to human populations (WHO, 2020).
9. **Strengthening diagnostic capacity in low- and middle-income countries (LMICs)**: These countries are a global priority since intimate interactions between humans and animals make the risk of spillover the largest worldwide (Grange et al., 2021).
10. **Equity in Preparedness:** Finally, the inequities and unfairness that COVID-19 revealed must be fixed. Vaccines, medical care, and other vital resources

must be available to everyone in the future, no matter their social status, income level or geographical location. The pandemic showed that vulnerable groups are the most at risk and need equal access to care and prevention, thus this should be a top goal (Frisch et al., 2021).

Conclusion

The COVID-19 pandemic revealed significant deficiencies in global health security, including inadequacies in early warning systems, protracted and disorganized international responses, and stark discrepancies in the allocation of medical countermeasures such as vaccines. These flaws show that current preparedness frameworks are not up to the task of dealing with the size and speed of modern pathogen propagation. Future strategies must prioritize strong, flexible health systems, better international governance for sharing data and resources, and plans that make sure that no region is left behind in a crisis by making equity a top priority. Strengthening worldwide surveillance of zoonotic diseases is at the heart of this proactive approach.

In conclusion, the path from animal origins to pandemic is not predetermined. The international community can change how it responds to threats from infectious diseases by financing integrated zoonotic surveillance, dealing with the ecological causes of spillover through environmental conservation and regulated wildlife trade, and building fair and cooperative global health infrastructure. The main goal should be to make the globe not only better able to deal with pandemics, but also to stop them from happening in the first place.

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