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Review

Climate crossroads: How global warming drives coronavirus emergence, the long COVID crisis of tomorrow, and AI's role in navigating our future

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ABSTRACT

This narrative review examines the critical nexus between climate change, coronavirus emergence, and Long COVID—a triad that may shape public health outcomes for generations. Climate change disrupts ecological balances that have historically limited viral spillover events, creating novel interfaces between wildlife reservoirs and human populations. The coronavirus family presents particular concern due to its diversity, adaptability, and demonstrated capacity for cross-species transmission. With over 200 coronaviruses identified in bat populations alone, this vast reservoir of genetic diversity, combined with the family's propensity for recombination, creates substantial pandemic potential that climate disruption may further amplify. Long COVID has revealed another dimension of the coronavirus threat: the potential for significant chronic disease burden following acute infection. This complex multisystem condition affects a substantial portion of SARS-CoV-2 infected individuals, with mechanisms including viral persistence, autoimmunity, microclot formation, and mitochondrial dysfunction. Future projections suggest that climate change could increase global viral spillover risk by 30–45% by 2070, particularly in Southeast Asia, Central Africa, and parts of South America. Artificial intelligence offers promising tools for addressing these interconnected challenges through enhanced surveillance, accelerated therapeutic development, and optimized healthcare delivery. Understanding the climate-coronavirus-chronic illness nexus has become essential to the development of resilient health systems and effective planetary health policies face to an uncertain future.

1. Introduction

Climate change and emerging infectious diseases form a complex web of cause and effect calling for integrated scientific understanding [1,2]. The present review examines the nexus between climate change, coronavirus emergence, and Long COVID [3]. Climate change disrupts ecological balances that have historically limited viral spillover events [2,4,5]. Recent modeling suggests climate change could drive over 15,000 new cross-species viral transmission events by 2070, with coronaviruses among the most likely candidates [2].

The coronavirus family warrants specific attention for several reasons. Unlike influenza viruses, which have established seasonal patterns and surveillance systems, coronaviruses have demonstrated increasingly frequent novel spillover events with high pandemic potential [6]. While influenza primarily undergoes antigenic drift and occasional reassortment between known strains, coronaviruses possess tan extremely large RNA viral genome (26–32 kb), extraordinary recombination capacity, and remarkable receptor plasticity facilitating rapid adaptation to new hosts [7,8]. Though numerous, enteroviruses typically cause self-limiting infections without the respiratory transmission efficiency or mortality rates seen in novel coronaviruses. Additionally, the vast reservoir of coronaviruses (over 200 identified in bat populations alone) remains largely uncharacterized, especially in comparison to the more thoroughly documented influenza ecology [9,10]. A combination of genetic adaptability, zoonotic potential, and limited predictability renders coronaviruses particularly susceptible to climate-driven emergence.

Long COVID has revealed another dimension of the coronavirus threat: significant chronic disease burden following acute infection [11,12]. Approximately 10–30 % of SARS-CoV-2 infections result in symptoms persisting beyond 12 weeks [13].

This narrative review explores evidence linking these phenomena and considers how artificial intelligence may help to navigate this intersection of threats.

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2. Climate change as a driver of viral emergence

2.1. Habitat disruption and Biodiversity Loss

Climate change creates new interfaces between humans and viral reservoirs through habitat transformation. Rising temperatures shift habitat ranges for numerous species, including viral reservoirs [13]. A *meta*-analysis found that tropical deforestation combined with climate change has increased human-wildlife contact rates by approximately 4.0 % annually since 2000 [5].

For coronaviruses specifically, bat populations harboring an estimated 3200 coronavirus strains globally are particularly susceptible to climate-driven habitat changes [9]. Climate change has driven an estimated increase of 40 bat species in Yunnan province (China) alone, bringing approximately 100 additional coronavirus species into potential contact with humans [3].

2.2. Changing Animal Migration patterns

Climate change is altering wildlife movement patterns, creating novel ecological interfaces in which previously isolated species intermingle. In response to warming trends, mammals have shown average poleward range shifts of 17 km per decade [14,15].

Carlson et al. [2] employed a model integrating host movement, viral sharing networks, and climate trajectories to predict over 15,000 novel viral sharing events among mammalian species by 2070. The model predicted a 3.8-fold increase in cross-species viral sharing events among bat species and a 2.4-fold increase in bat-to-human spillover opportunities by mid-century.

2.3. Temperature Effects on viral Survival

Climate parameters directly influence viral persistence. While higher temperatures generally reduce coronavirus persistence on surfaces, some strains demonstrate adaptive mutations enhancing thermostability [16,17]. Low relative humidity impairs respiratory epithelium defenses, potentially enhancing susceptibility to coronavirus infection [18].

2.4. Specific risks for coronavirus reservoirs

Bats, which host the greatest diversity of coronaviruses, are highly susceptible to climate-related stressors [10,15]. Research has documented mass mortality events in bat populations during extreme heat events [19]. Climate-displaced colonies establish new roosts in agricultural and urban areas [20], while environmental stressors can suppress immune function in reservoir hosts, potentially increasing viral shedding [21].

3. Coronavirus Family: Diversity and spillover potential

3.1. Overview of coronavirus Taxonomy

Coronaviruses belong to the order Nidovirales, family Coronaviridae. The Orthocoronavirinae subfamily contains all currently known human coronaviruses, classified into four genera [6,22]. To facilitate comparison of the known human coronaviruses and their key characteristics, Table 1 provides a comprehensive overview of these viruses. The table summarizes taxonomic classification, discovery timeline, reservoir hosts, pathogenicity, and distinguishing features of each coronavirus.

Coronaviruses possess the largest genome among RNA viruses (26–32 kilobases). A defining feature is their high recombination rate, enabling rapid adaptation to shifting ecological conditions [7].

Table 1
Key characteristics of human coronaviruses.

Virus	Genus	Year Identified	Primary Reservoir	Intermediate Host(s)	Case Fatality Rate	Key Clinical Features	Notable Genomic Features
HCoV-229E	Alphacoronavirus	1966	Bats	Possibly camelids	<1%	Common cold symptoms	Uses aminopeptidase N as receptor
HCoV-NL63	Alphacoronavirus	2004	Bats	Unknown	<1%	Upper respiratory tract infections, croup in children	Uses ACE2 receptor (like SARS-CoV-2)
HCoV-OC43	Betacoronavirus	1967	Possibly rodents	Cattle	<1%	Common cold symptoms	Likely spilled over from cattle in late 19th century
HCoV-HKU1	Betacoronavirus	2005	Rodents	Unknown	<1%	Common cold, pneumonia in immunocompromised	Difficult to culture in laboratory
SARS-CoV	Betacoronavirus (lineage B)	2003	Horseshoe bats	Palm civets	9.6 %	Severe pneumonia, rapid respiratory deterioration	First coronavirus to cause global outbreak
MERS-CoV	Betacoronavirus (lineage C)	2012	Bats	Dromedary camels	34.4 %	Severe pneumonia, renal failure	Highest case fatality rate among coronaviruses
SARS-CoV-2	Betacoronavirus (lineage B)	2019	Horseshoe bats	Under investigation	~1–3 %	Diverse presentations from asymptomatic to severe pneumonia; vascular complications	Large spike protein with high ACE2 affinity; multiple immune evasion mechanisms

3.2. History of previous coronavirus spillovers

Seven coronaviruses are known to infect humans. Four of these cause common colds globally [23]. Three spillover events in the 21st century have demonstrated the family's potential to cause severe disease: SARS-CoV (2002–2003), MERS-CoV (2012), and SARS-CoV-2 (2019). The increasing frequency of detected spillovers—from approximately one per century to three major events in two decades—suggests either enhanced surveillance or increasing spillover pressure [24].

3.3. Ecological niches

The ecological distribution of coronaviruses spans diverse mammalian and avian taxa, with particularly high diversity in tropical and subtropical regions [9,25]. This distribution correlates with areas of high bat species richness.

Climate change is altering these ecological niches. Modeling suggests that shifts in vegetation types driven by climate change have increased bat species richness in Central China, Myanmar, and Laos by approximately 40 %, bringing multiple coronavirus lineages into newly overlapping ranges [3].

3.4. Genetic factors enabling adaptability

The spike glycoprotein demonstrates remarkable structural plasticity across the coronavirus family [8]. This conformational flexibility enables coronaviruses to explore new receptor interactions without sacrificing binding efficiency to ancestral receptors.

Most pandemic-potential coronaviruses utilize angiotensin-converting enzyme 2 (ACE2) as their primary receptor. SARS-CoV-2 can bind ACE2 orthologs from humans, cats, ferrets, monkeys, and other mammals with varying effectiveness [26].

As few as five mutations in the spike protein can enable effective use of human receptors by bat coronaviruses [27], suggesting that the "species barrier" for coronaviruses may be more porous than previously recognized.

4. Long COVID as a model for Post-Viral conditions

4.1. Definition and prevalence

Long COVID is characterized by persistent symptoms extending beyond the acute phase of SARS-CoV-2 infection. The World Health Organization defines it as occurring "in individuals with a history of probable or confirmed SARS-CoV-2 infection, usually three months from the onset of COVID-19 with symptoms that last for at least two months and cannot be explained by an alternative diagnosis" [28].

Common symptoms include fatigue, dyspnea, cognitive dysfunction ("brain fog"), post-exertional malaise, cardiovascular abnormalities, sleep disturbances, and autonomic dysfunction [11,12]. Recent large-scale cohort studies have provided more refined prevalence estimates. A 2024 nationwide cohort study by Archambault et al. [29] examining emergency department patients found that 38.9 % of SARS-CoV-2 test-positive individuals reported Long COVID symptoms at three months post-infection, compared to 20.7 % of test-negative individuals. A Scottish population cohort study of nearly 200,000 adults demonstrated that after adjusting for confounders, the prevalence of symptoms attributable to SARS-CoV-2 infection was 6.6 %, 6.5 %, and 10.4 % at 6, 12, and 18 months respectively [30].

Risk factors include female sex, pre-existing conditions (asthma, diabetes, obesity), older age, and psychological conditions [31,32]. Of note, while higher rates of Long COVID (50–70 %) have been observed among hospitalized patients, most Long COVID cases occur in individuals having experienced mild acute COVID-19 [33]. This apparent paradox reflects the fact that mild cases represent the vast majority of overall infections, and research shows Long COVID can develop regardless of initial disease severity [34]. Long COVID bears similarities to other post-viral syndromes, most notably myalgic encephalomyelitis/chronic fatigue syndrome (ME/CFS) [35].

4.2. Socioeconomic burden

Long COVID has reduced workforce participation and productivity. Approximately 1.6 million full-time equivalent workers in the United States alone remain out of the workforce due to Long COVID, representing approximately $170 billion in lost wages annually [36].

Cumulative healthcare costs globally are estimated to exceed $3.7 trillion when accounting for direct medical expenses and reduced economic output [37]. Studies have demonstrated significant reductions in health-related quality of life among Long COVID patients.

4.3. Healthcare System preparedness

Integrated, multidisciplinary care models have emerged as essential to effective Long COVID management. Specialized clinics employing collaborative approaches across multiple specialties have been established in many countries [38]. Rehabilitation service capacity has emerged as a critical bottleneck in many healthcare systems [39].

5. Future projections and AI applications

5.1. Climate-Driven viral emergence scenarios

Models project over 15,000 new viral sharing events among mammalian species by 2070, with a 3.8-fold increase in cross-species coronavirus transmission among bat populations [2]. Under moderate mitigation scenarios, global spillover risk is projected to increase by 4.5 % annually by 2050, rising to 7.2 % under more severe warming [3].

Without significant mitigation efforts, climate change could increase global viral spillover risk by 30–45 % by 2070, with coronaviruses among the most affected viral families [40].

5.2. Geographical Hotspot analysis

Regions at elevated risk for future coronavirus emergence include:

Southern China and Northern Southeast Asia: Projected to experience significant climate-driven increases in bat species richness, with a 3.2-fold increase in coronavirus spillover risk by 2050 [2].
Central Africa's Congo Basin: Projected to experience a 2.7-fold increase in spillover risk by 2050 [41].
Western South America: Projected to experience a 2.1-fold increase in coronavirus spillover risk by 2050 [42].

Under moderate climate change scenarios, approximately 1.5 billion people may live in high-risk hotspots by 2050.

5.3. Timeline projections

Temporal projections of coronavirus spillover risk provide insights critical to long-term preparedness planning. The comprehensive assessment from the Lancet Countdown on Health and Climate Change indicates that under current policies (projected to result in approximately 2.7 °C warming by 2100), the average interval between major coronavirus spillover events could decrease from approximately 10 years (the historical average since 2000) to 4–6 years by the 2050 s, and potentially to 2–3 years by the 2080 s. Alternative scenarios demonstrate different trajectories, with a high-emissions scenario (4 °C + by 2100) potentially reducing intervals between major spillover events to as few as 1–2 years by the end of the century [43].

Fig. 1 illustrates the projected changes in coronavirus spillover risk over time under three climate scenarios. The green line represents the

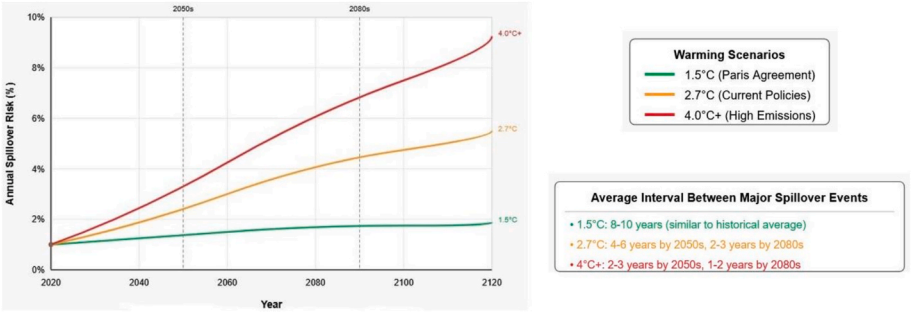

Fig. 1. Projected Coronavirus Spillover Risk Timeline. Annual probability of major spillover events under different warming scenarios. Data sources: [], Carlson et al. [].
Adapted from Romanello et al. 432

Paris Agreement target of limiting warming to 1.5 °C, showing only a slight increase in annual spillover probability. The orange line depicts the trajectory under current policies (2.7 °C warming), with a substantial acceleration of risk by mid-century. The red line shows the high emissions scenario (4 °C + warming), with a dramatic increase in spillover probability that could fundamentally alter global pandemic preparedness requirements.

Carlson et al. [2] conclude that the ecological transition driving increased viral sharing "may already be underway, and holding warming under 2 °C within the century will not reduce future viral sharing.".

5.4. *AI applications for pandemic preparedness and response*

AI offers transformative capabilities across multiple dimensions of pandemic preparedness and response. These applications form an integrated framework addressing the interconnected challenges of climate-driven viral emergence.

AI-Powered Surveillance Systems for Early Detection now integrate diverse data streams for early outbreak detection. Advanced genomic surveillance platforms can identify novel coronavirus strains with zoonotic potential [44]. Environmental surveillance tools detect viral signatures in wastewater and environmental samples weeks before clinical cases appear [45], while digital epidemiology platforms employ natural language processing to analyze social media and search patterns, detecting outbreaks 7–14 days before official reporting.

Fig. 2 presents a proposed conceptual framework illustrating how various AI applications could be integrated across the pandemic response spectrum, from prevention and preparedness to Long COVID management. This proposed framework envisions each stage building upon insights from the previous phase, while a continuous learning loop would enable ongoing refinement of these technologies based on real-world outcomes. This integrated approach demonstrates how AI could create a comprehensive framework for addressing viral threats at every phase of emergence and response.

Machine Learning for Viral Evolution and Zoonotic Potential Prediction has advanced significantly, with models correctly forecasting 74 % of major mutations in SARS-CoV-2 variants before their detection [46]. Advanced computational approaches for protein structure prediction have significantly improved our understanding of coronavirus biology, enabling more accurate assessment of variant transmissibility and immune evasion potential.

AI Tools for Accelerating Therapeutic and Vaccine Development have dramatically reduced development timelines. Drug repurposing systems screen existing pharmaceuticals against novel coronavirus proteins within hours of receiving genomic sequences, while generative AI platforms for de novo drug design have reduced early-stage

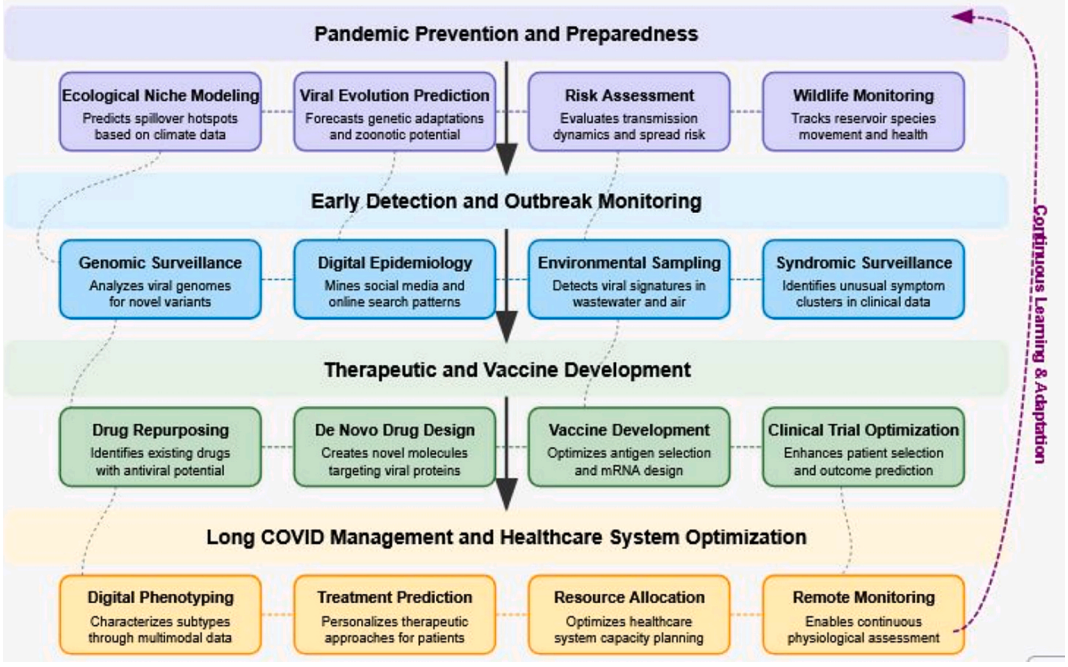

Fig. 2. AI applications across the pandemic response spectrum.

development from years to weeks [47]. Machine learning algorithms have enhanced vaccine design by optimizing antigen selection, while clinical trial processes have been streamlined through AI-powered patient selection and monitoring, reducing development timelines significantly.

Digital Health Infrastructure for Long COVID Management utilizes AI to identify disease subtypes through multimodal data integration, with current systems identifying seven distinct phenotypes with different underlying mechanisms and treatment responses [48]. Remote monitoring technologies paired with machine learning algorithms enable personalized care plans that adapt to patient symptoms and recovery trajectories, improving quality of life outcomes and reducing healthcare utilization.

Predictive Modeling for Healthcare Resources enables planning during overlapping climate and viral crises. Computational modeling systems can now simulate the complex interactions between environmental changes, population dynamics, and viral spread to forecast healthcare needs. Supply chain resilience analysis has correctly identified 83 % of critical shortages during compound disasters [49].

While many of these individual AI capabilities exist today, their full integration as proposed in Fig. 2 represents an aspirational framework that could address viral emergence risks associated with climate change. Implementing this comprehensive approach would enable earlier detection leading to containment before widespread transmission, rapid countermeasure development to reduce outbreak impacts, and advanced resource modeling to optimize responses during compound crises involving both climate impacts and viral emergences.

6. Conclusion

Climate change represents a pervasive alteration of the earth's systems, disrupting ecological balances that have historically limited viral spillover events. The coronavirus family stands as particularly significant due to its diversity, adaptability, and demonstrated capacity for cross-species transmission. Long COVID has shown a potential for significant chronic disease burden following acute infection.

Future projections suggest that climate change could significantly increase global viral spillover risk, particularly in regions of Southeast Asia, Central Africa, and parts of South America. AI offers promising tool addressing these interconnected challenges through enhanced surveillance, accelerated therapeutic development, and optimized healthcare delivery.

Understanding this climate-coronavirus-chronic illness nexus is essential not only for scientific advancement but also for developing resilient health systems and effective planetary health policies.

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Thorsten Rudroff: Writing – review & editing, Writing – original draft, Methodology, Investigation, Conceptualization.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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