Infectious disease in an era of global change

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Abstract | The twenty-first century has witnessed a wave of severe infectious disease outbreaks, not least the COVID-19 pandemic, which has had a devastating impact on lives and livelihoods around the globe. The 2003 severe acute respiratory syndrome coronavirus outbreak, the 2009 swine flu pandemic, the 2012 Middle East respiratory syndrome coronavirus outbreak, the 2013–2016 Ebola virus disease epidemic in West Africa and the 2015 Zika virus disease epidemic all resulted in substantial morbidity and mortality while spreading across borders to infect people in multiple countries. At the same time, the past few decades have ushered in an unprecedented era of technological, demographic and climatic change: airline flights have doubled since 2000, since 2007 more people live in urban areas than rural areas, population numbers continue to climb and climate change presents an escalating threat to society. In this Review, we consider the extent to which these recent global changes have increased the risk of infectious disease outbreaks, even as improved sanitation and access to health care have resulted in considerable progress worldwide.

In premodern times, colonization, slavery and war led to the global spread of infectious diseases, with devastating consequences (FIG. 1a). Human diseases such as tuberculosis, polio, smallpox and diphtheria circulated widely, and before the advent of vaccines, these diseases caused substantial morbidity and mortality. At the same time, animal diseases such as rinderpest spread along trade routes and with travelling armies, with devastating impacts on livestock and dependent human populations[1]. However, in the past two decades, medical advances, access to health care and improved sanitation have reduced the overall mortality and morbidity linked to infectious diseases, particularly for lower respiratory tract infections and diarrhoeal disease (FIG. 1d). The swift development of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) vaccine speaks to the efficacy of modern science in rapidly countering threats from emerging pathogens. Nevertheless, infectious disease burden remains substantial in countries with low and lower-middle incomes, while mortality and morbidity associated with neglected tropical diseases, HIV infection, tuberculosis and malaria remain high. Moreover, deaths from emerging and re-emerging infections, in comparison with seasonal and endemic infections, have persisted throughout the twenty-first century (FIG. 1c). This points to a possible new era of infectious disease, defined by outbreaks of emerging, re-emerging and endemic pathogens that spread quickly, aided by global connectivity and shifted ranges owing to climate change (FIG. 1d).

Here, we review how recent anthropogenic climatic, demographic and technological changes have altered the landscape of infectious disease risk in the past two decades. In terms of climate change, we consider both the influence of recent warming and projected future changes. For demographic change, we include trends such as urbanization (FIG. 1b), population growth, land-use change, migration, ageing and changing birth rates. For technological changes, we primarily consider advances that enable cheaper, faster global travel and trade (FIG. 1b), as well as improved health care. We do not explicitly address economic change; however, economic changes, including economic development, are crucial drivers of these three factors: climate, demography and technology. We also do not explicitly discuss natural drivers of pathogen evolution or biological processes unless they interact with human-driven global change.

New infections chart a pathway beginning with emergence, followed by local-scale transmission, movement beyond borders and possible global-scale spread. Global changes may differentially affect the risk of emergence, the dynamics of disease within a local population and the global spread of diseases between populations. We provide an overview of each step, first considering features of recent global change that have altered the risks of spillover of viral, fungal, bacterial and apicomplexan

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(malaria) infections into human populations, then detailing how spread within human populations, driven by the seasonal dynamics of transmission, may be impacted by global change, of relevance to both emergent and established pathogens. Finally, we consider changes to the drivers of global spread, focusing in particular on travel, migration and animal and plant trade.

Pathogen emergence into human populations

Recent decades have seen repeated pathogen emergence from wild or domestic animal reservoirs into human populations, from HIV-1 and HIV-2, to the 1918 influenza virus, to Middle East respiratory syndrome coronavirus, to SARS-CoV-2 (REFS[2–4]). For a novel pathogen to become a threat to human populations, first, contact between humans and the animal reservoir must occur; the pathogen must either have or evolve (BOX 1) the capacity for human-to-human transmission[5]; and finally, this human-to-human transmission must enable expansion of the pathogen's geographical range beyond the zone of spillover. Recent global changes have affected each of these steps.

Patterns of contact between human and wildlife reservoirs have increased as human populations move into previously unoccupied regions. Population growth and agricultural expansion, coupled with increasing wealth and larger property sizes, are driving factors for these interactions and the resulting habitat destruction. This may occur alongside behaviours that increase the potential for spillover, such as consumption of wild meat[6], or intensifying contact between wild and domestic animal hosts. For example, Nipah virus has been identified in several bat populations, particularly flying foxes, but in 1999 caused a severe disease outbreak in Malaysia, primarily among pig farmers[7]. It is hypothesized that the spillover of Nipah virus from bats to pigs was driven by three factors related to global change: pig farms expanding into the bat habitat; intensification of pig farming, leading to a high density of hosts; and international trade, leading to the spread of the infection among other pig populations in Malaysia and Singapore[8]. Expanding

Fig. 1 | **Human connectivity and infectious disease outbreaks in premodern and modern times. a** | Examples of epidemic periods associated with different eras of human transportation (land, maritime and air travel) are shown. Overland trade networks and war campaigns are thought to have contributed to multiple epidemics in the Mediterranean in late classical antiquity (green), beginning with the Antonine plague, which reportedly claimed the life of the Roman emperor Lucius Verus[125–128]. Maritime transportation (red and grey) leading to European contact with the Americas and the subsequent Atlantic slave trade resulted in the importation of *Plasmodium falciparum* malaria and novel viral pathogens[129]. In modern times, air travel (purple) resulted in the importation of severe acute respiratory syndrome (SARS) coronavirus to 27 countries before transmission was halted[130]. **b** | In recent years, increases in air travel, trade and urbanization at global (left) and regional (right) scales have accelerated, indicating ever more frequent transport of people and goods between growing urban areas (source World Bank). **c** | Log deaths from major epidemics in the twenty-first century (source World Health Organization). **d** | Disability-adjusted life years lost from infectious diseases (source Our World in Data). MERS, Middle East respiratory syndrome; NTD, neglected tropical disease.

agriculture and its intensification may create conditions that favour pathogen circulation within domestic animal (or plant) reservoirs via high-density farming practices[9]. Beyond creating opportunities for emergence of problematic livestock pathogens, this could also increase opportunities for evolution of novel variants of risk to humans in domestic animal reservoirs. This may occur alongside increasing risk to workers interacting with animal populations[10] as a result of work practices. Global increase in the demand for and resulting intensification of meat production will importantly drive these processes, and associated use of antibiotics in domestic animals has the potential to select for resistant strains of bacteria with potential to affect human health[11].

The nature of human populations that are exposed to potential spillover is also changing. For example, the elimination of smallpox led to the cessation of smallpox vaccination, which may have enabled the expansion of monkeypox[12]. More generally, globally ageing populations may provide an immune landscape that is more at risk of spillover, as ageing immune landscapes are less capable of containing infectious agents[13]. The intersection between declining function of immunity at later ages[14] and globally ageing populations may increase the probability of pathogen emergence, but this remains conjectural and an important area for research. The changing global context may allow existing human pathogens to both evolve novel characteristics and expand in scope. Selection for drug resistance now occurs worldwide, and antibiotic resistance has and will evolve repeatedly[15]. As with antibiotic resistance, rapid global spread is commonplace for antimalarial resistance following evolution[16].

Climate change may play a role in the risk from pathogen spillover. Changing environmental conditions can alter species range and density, leading to novel interactions between species, and increase the risk of zoonotic emergence[17]. A series of compounded environmental

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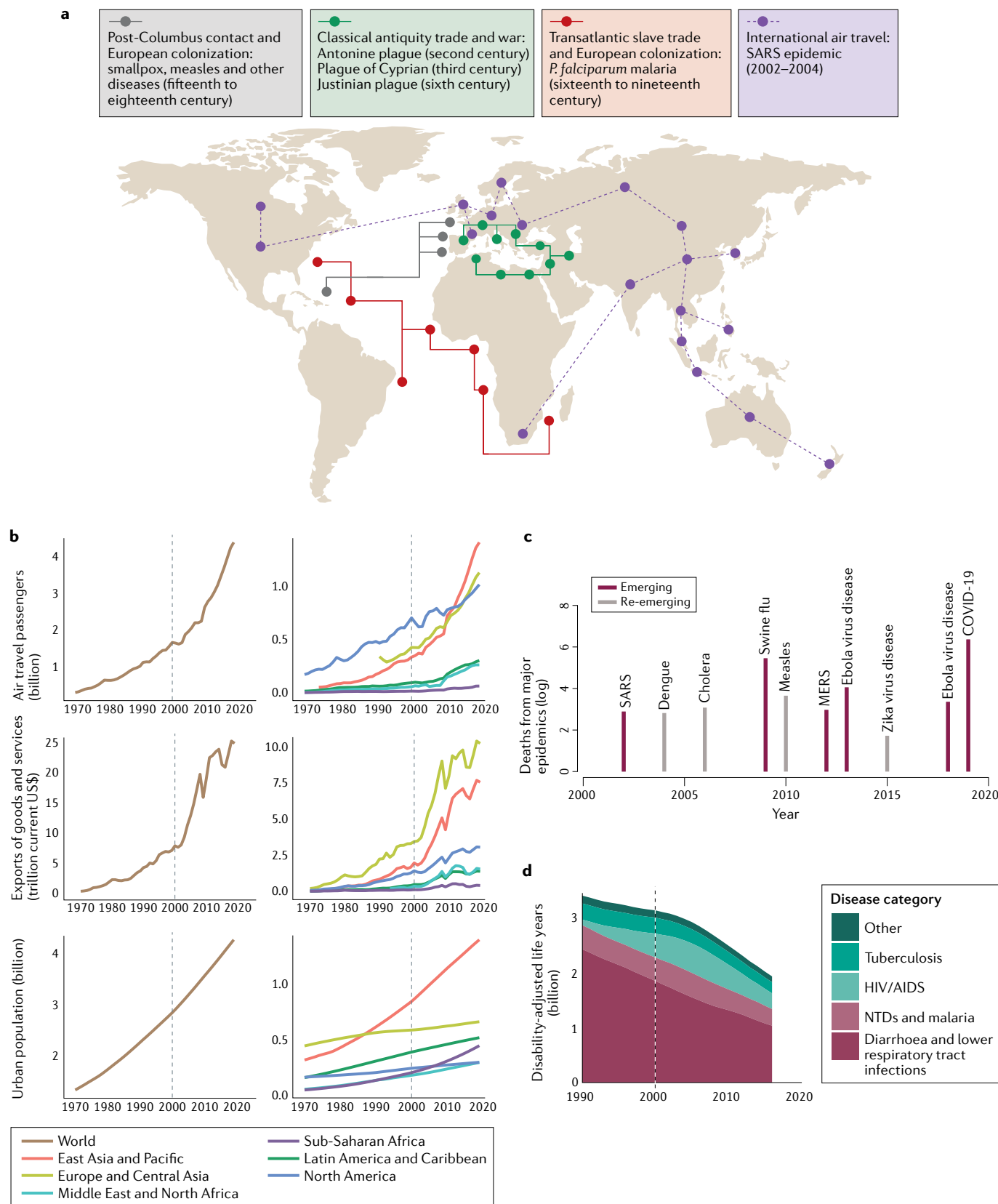
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a

Post-Columbus contact and European colonization: smallpox, measles and other diseases (fifteenth to eighteenth century)

Classical antiquity trade and war: Antonine plague (second century) Plague of Cyprian (third century) Justinian plague (sixth century)

Transatlantic slave trade and European colonization: *P. falciparum* malaria (sixteenth to nineteenth century)

International air travel: SARS epidemic (2002–2004)

b

Air travel passengers (billion)

Exports of goods and services (trillion current US$)

Urban population (billion)

World
East Asia and Pacific
Europe and Central Asia
Middle East and North Africa
Sub-Saharan Africa
Latin America and Caribbean
North America

c

Deaths from major epidemics (log)

Emerging
Re-emerging

SARS · Dengue · Cholera · Swine flu · Measles · MERS · Ebola virus disease · Zika virus disease · Ebola virus disease · COVID-19

Year

d

Disability-adjusted life years (billion)

Disease category
Other
Tuberculosis
HIV/AIDS
NTDs and malaria
Diarrhoea and lower respiratory tract infections

factors, including a long period of drought followed by extreme precipitation, is hypothesized to have driven an upsurge in rodent populations causing the emergence of pulmonary hantavirus in 1993 (REF.[18]). Similarly,

evidence suggests that populations of the black flying fox in Australia, a key reservoir of Hendra virus, have moved 100 km southward in the past 100 years owing to climatic changes. This shifting range likely caused Hendra

virus to spill over into southern horse populations, and these horses subsequently infected humans[19,20]. Patterns of change are likely occurring in other bat populations globally but remain understudied — a clear cause for concern given the crucial role bat populations play as a reservoir host for several high-fatality pathogens[21].

Rapid rates of urbanization in low-income and middle-income countries, and the increase in populations residing in crowded, low-quality dwellings, have created new opportunities for the emergence of infectious diseases (FIG. 2). Urbanization has promoted the emergence and spread of arboviral diseases such as dengue, Zika virus disease and chikungunya, which are transmitted by *Aedes aegypti* and *Aedes albopictus* mosquitoes that are well adapted to urban areas[22–24]. Population density appears correlated with the preference of *Ae. aegypti* for human odour, and hence the evolution of human-biting — the transmission pathway for arboviral disease[24]. However the role of urbanization in vector-borne disease spread is complex: the preference of the *Anopheles* spp. vector for rural environments may have led to a decline in the prevalence of malaria in urbanizing regions[25]. Nevertheless, dense and highly connected urban areas are potential hot spots for the rapid spread of diseases such as COVID-19 and SARS, and cities can serve as a catalyst for rapid local and global transmission.

Local-scale disease dynamics

Emerging, re-emerging and endemic pathogens in human populations may exhibit distinct dynamic patterns of spread at the local scale. These patterns will be governed by demographic factors, including the effects of human behaviour on transmission (for example, school terms drive transmission of many childhood infections[26] and sex-specific travel patterns may result in higher burdens of chikungunya in women in Bangladesh[27]) and immunity (which, for immunizing infections such as measles and rotavirus infection, is, in turn, shaped by replenishment of susceptible individuals via births[28,29] and depletion by vaccination where vaccines are available[30]). Transmission may also be affected by climatic variables acting spatially or over the course of the year in line with seasonal fluctuations[31,32]. Recent global changes have affected each of these drivers of local-scale dynamics (FIG. 3).

As school attendance not only modulates transmission of childhood infections[26] but also shapes human mobility[33], dramatic increases in rates of school attendance globally thus have the potential to substantially alter the dynamics of many infections. That this has yet to be documented is perhaps in part because this change has happened alongside expansion of access to vaccines that protect children against many of the relevant infections, as well as global declines in birth rates, which also facilitate control efforts by diminishing the size of the susceptible pool[34]. If the burden of disease is age specific, the intersection between immunity and shifting demography may be particularly marked: declining birth rates translate into a smaller pool of susceptible individuals and thus infected individuals, reducing the overall rate at which susceptible individuals become infected, and thus increasing the average age of infection or disease, as reported for dengue in Thailand[35] and rubella in Costa Rica[36] as these countries went through the demographic transition. Conversely, ageing populations may increase transmission; for example, longer shedding has been suggested with increasing age for SARS-CoV-2 (REF.[37]).

Demographic changes to population size and density via urbanization may also affect dynamics. Influenza, for example, tends to exhibit more persistent outbreaks in more populous, denser urban regions[38] (FIG. 2). A similar pattern was reported in the early COVID-19 pandemic[39]. If demographic change has importantly altered the context of infectious diseases in recent years, arguably an even larger effect is caused by changes in the occurrence of immunomodulatory infections, which, in turn, may affect other infections. For example, the emergence of HIV has amplified the burden of tuberculosis[40]. Mass drug administration efforts have reduced helminth prevalence, which will have knock-on effects on the burden of other infections, such as malaria, which may be increased in individuals experiencing a heavy worm burden[41]; both will also intersect with the efficacy of vaccination programmes[42].

Box 1 | Global change and evolution of hosts and pathogens

Mutations constantly arise in the genomes of all species, from viruses to elephants. Some genetic changes may have no observable effects on fitness (and thus will be selectively neutral), but can be used to track pathogen spread; for example, to trace the impacts of global connectivity on an outbreak[70]. Some genetic changes will affect disease phenotypes, potentially increasing the transmissibility, virulence or immune escape of a pathogen lineage[133]. The degree to which such mutations increase in frequency or spread geographically will depend on the degree to which they increase fitness, as well as pathogen population dynamics, which may be modulated by the global change context. Increases in the density and geographical distribution of susceptible hosts (whether they be people, crops or livestock) may provide greater opportunity for novel variants to emerge[9] simply by amplifying pathogen populations and thus circulating mutations. While understanding the nuance of cross-scale selection (that is, how the selective context of the individual host translates into the selective context at the scale of populations) remains a challenging frontier[134], it is likely that ageing populations or the presence of immunosuppressive pathogens might further modulate selection pressures. Indeed, it has been suggested that the emergence of more transmissible or less immune-vulnerable variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was enabled in part by selection processes occurring during chronic infections in immunosuppressed individuals[135]. Greater global connectivity leads to more frequent exchange of this genetic material between populations of the same or different species, potentially leading to the erosion of evolved or engineered host resistance and increased rates of pathogen evolution[136]. Associated spillover followed by spillback can create scenarios that facilitate amplification and potentially selection of problematic pathogen variants[137], an issue highlighted by recent documentation of human to mink to human transmission of SARS-CoV-2 (REF.[138]). Likewise, increased rates of pathogen importation provide increased opportunities for pathogen populations to evolve the ability to utilize novel vectors (as has been observed in the Americas for malaria[129]). Increased population connectivity can also enable pathogens and their vectors to shift to novel host species, from infected mosquitoes travelling on boats or in planes to agricultural pathogens being inadvertently relocated. Hosts that have not previously been exposed to such pathogens, and thus have no co-evolved defences, yet are phylogenetically and/or genetically similar to the original host are often most at risk[139,140], a fact that makes homogenization of crops[141] or livestock a concern. Novel pathogen introductions can have large-scale population and ecosystem impacts, of which one famous example is the extirpation of the American chestnut tree by chestnut blight[142]. Changes in selection pressure resulting from changes in health-care strategies (for example, introduction of vaccination) may have the potential to select for different pathogen characteristics, and could potentially drive the evolution of virulence in pathogens[143,144].
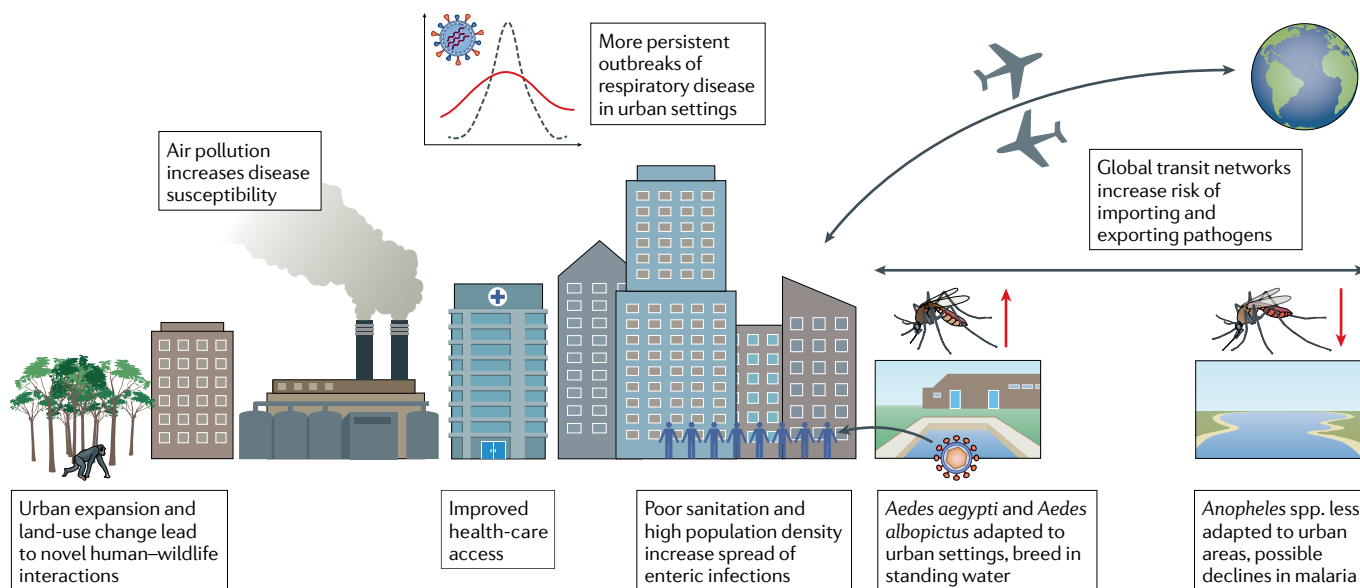

Fig. 2 | **Impacts of urbanization on infectious disease.** Interactions between urbanization and infectious disease are complex, with increased urbanization driving both positive and negative changes to global disease burden.

The climate plays a key role in driving the local-scale seasonal dynamics of many infectious diseases, which may thus be altered by global change in climatic conditions[43,44]. Considering these impacts requires recognizing that interactions with climate differ by pathogen type. For directly transmitted infections, the role of climate is revealed by marked latitudinal gradients in epidemic timing[32,45]. Several respiratory pathogens, including influenza virus, are more highly seasonal in temperate climates and exhibit greater year-round persistence in tropical locations[32,46]. Climate change is expected to lead to an expansion of these tropical patterns, with possible implications for pathogen evolution[43,47]. At the individual level, susceptibility to respiratory viral infections may be impacted by exposure to local air pollution, which is a concern for rapidly urbanizing locations, where urban air pollution may disproportionately affect low-income communities and communities of colour[48,49]. For example, non-Hispanic Black and Hispanic populations in the USA were found to have higher exposure to certain $PM_{2.5}$ components than non-Hispanic white populations[49]. At the same time, globally, a move to an urban location may bring benefits in terms of increased access to health care (FIG. 2).

For some bacterial and fungal diseases, climatic changes may affect the pathogen's environmental reservoir. Incidence of coccidioidomycosis (valley fever), caused by inhalation of fungal spores of *Coccidioides* spp., is expected to increase with climate change as the region with optimal conditions for fungal spore production expands[50]. Climate change may also have played a role in the emergence of the drug-resistant fungal pathogen *Candida auris*. *C. auris* emerged in several continents at the same time and has been shown to have increased thermotolerance compared with other closely related fungal species, which perhaps evolved in response to global warming[51,52]. This increased thermotolerance may have enabled the pathogen to jump from its environmental habitat into an intermediary avian host, given the higher body temperatures of avian fauna, before infecting humans[52].

Demographic change and technological changes may alter a host's interaction with the environmental reservoir. Cholera, caused by the bacterial pathogen *Vibrio cholerae*, persists in the environment, particularly in aquatic settings. Changes to environmental conditions, including elevated sea temperatures, lead to increased reproduction of the pathogen and local epidemics[53], with clear links to longer-term climate phenomena such as El Niño[54]. However, improved sanitation lowers the risk of exposure to *V. cholerae* and has led to a decline of the disease in many locations[53].

For vector-transmitted diseases, biological traits of both the vector and the pathogen may be sensitive to climate. Many transmission-related life cycle traits of the mosquito (biting rate, adult lifespan, population size and distribution) and the pathogen (extrinsic incubation rate) are temperature sensitive, and oviposition patterns depend on water availability[55]. Consequently, the geographical range for dengue, malaria and other vector-borne diseases[56–58] is affected by the local climate, and there is substantial effort to understand how these ranges may change with climate change[59–61]. For certain vector-borne diseases such as Zika virus disease, climate change may lead to an expanded range[62]. However, for other diseases, such as malaria, climate change may shift the spatial range of the infection to higher latitudes[63]. As ever, the footprint of human interventions may loom larger than these changes in local conditions[25].

At the local scale, one of the strongest footprints detectable on the dynamics of many endemic infections in recent years is declines in incidence associated with access to vaccinations[64]. However, the introduction of a vaccine does not imply immediate elimination.

El Niño
A correlated series of climate events associated with the warm phase of the El Niño Southern Oscillation cycle.

As vaccination coverage increases, measles outbreaks, for instance, follow a pathway towards elimination defined by declines in mean incidence but high variability in outbreak size[34]. Imperfect vaccine coverage may allow population susceptibility to increase such that substantial outbreaks can occur if the disease is reintroduced; for example, the 2018 measles outbreak in Madagascar, which led to more than 100,000 cases[65]. Improved surveillance of the landscape of population immunity, via serological surveys, could help determine gaps in vaccination coverage[66].

Global spread

As local conditions alter demographically, or as a result of climate change potentially expanding the range of locations suitable to a particular pathogen or vector, increased global connectivity will enable pathogens to reach these new environments more rapidly (FIGS 3,4). Here, we review the impact of global change on three forms of global connectivity — international travel, human migration and local-scale mobility, and the international trade of animals, animal products and plants — while considering the impact on infectious disease risk. Technological change over the past two decades has dramatically lowered the cost of international travel, while demographic change has led to heightened demand for inexpensive flights (FIG. 1b). Demographic and climatic drivers have altered patterns of local mobility and regional migration, while rising demand and technological change have increased the trade of plants and animals. At the same time, an increasingly urban population is better connected than ever before to global travel networks (FIG. 4). These changes to global connectivity will present unique risk factors for infectious disease spread, enabling pathogens to travel further and faster than ever before.

International travel. The late twentieth century and the early twenty-first century have been marked by technological developments enabling ever swifter movement of people and pathogens over large distances — from trains to planes, and an expanding international airline network (FIG. 4). The total number of airline passengers doubled from just below two billion in 2000 to more than four billion in 2019 (FIG. 1b). This rampant increase in global connectivity brings with it new risks from emerging pathogens (BOX 2). However, many endemic pathogens also circulate via transit routes: seasonal influenza circulation in the USA can be predicted by flight patterns[67,68], with evidence that flight bans following the events of 9/11 caused a delayed outbreak, and a prolonged influenza season within the USA as measured by a 60% increase in the time to transnational spread[68]. Similarly, rapid global air travel is expected to have played a key role in the global spread of SARS-CoV-2. Genetic analyses demonstrate multiple introductions of SARS-CoV-2, driven by air travel, in the Middle East[69], northern California[70] and Brazil[71].

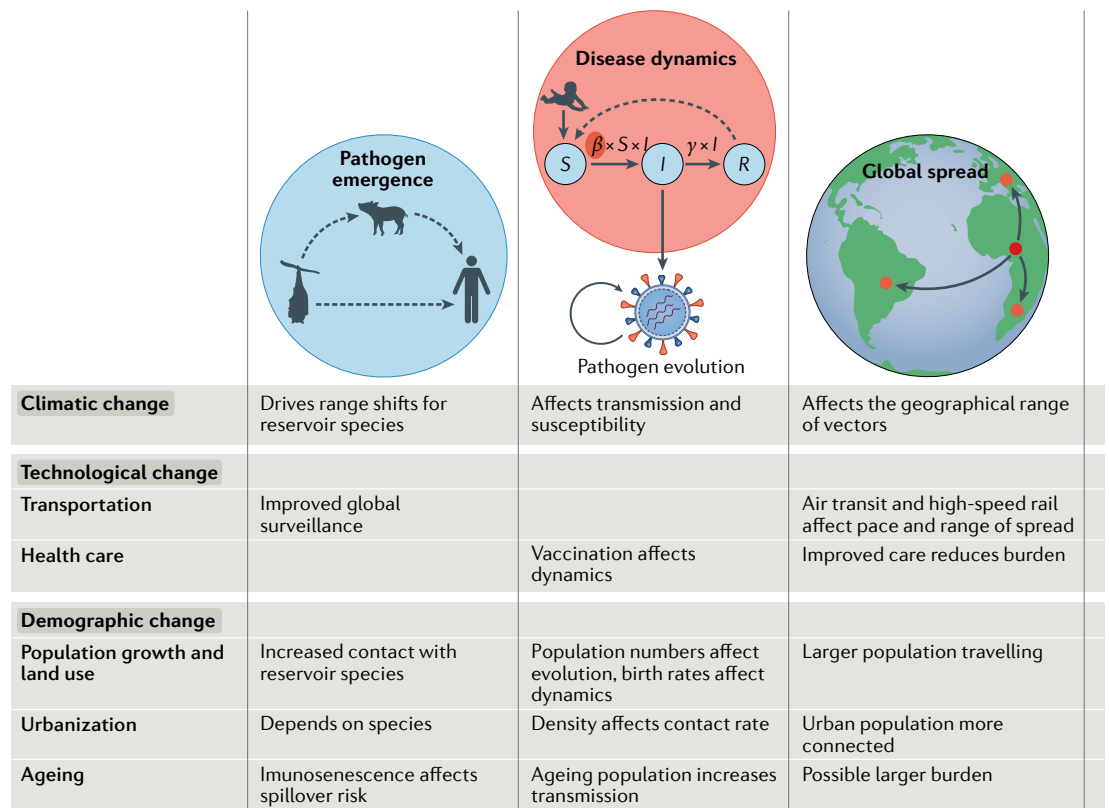|	Pathogen emergence	Disease dynamics / Pathogen evolution	Global spread
Climatic change	Drives range shifts for reservoir species	Affects transmission and susceptibility	Affects the geographical range of vectors
Technological change			
Transportation	Improved global surveillance		Air transit and high-speed rail affect pace and range of spread
Health care		Vaccination affects dynamics	Improved care reduces burden
Demographic change			
Population growth and land use	Increased contact with reservoir species	Population numbers affect evolution, birth rates affect dynamics	Larger population travelling
Urbanization	Depends on species	Density affects contact rate	Urban population more connected
Ageing	Imunosenescence affects spillover risk	Ageing population increases transmission	Possible larger burden

Fig. 3 | **Effects of climatic, technological and demographic change on disease emergence, dynamics and spread.** The table summarizes select recent global changes (rows) and their impacts on disease emergence, local-scale dynamics and global spread (columns). An example susceptible (S), infected (I), recovered (R) model is shown, where β represents the transmission rate and γ is the recovery rate.
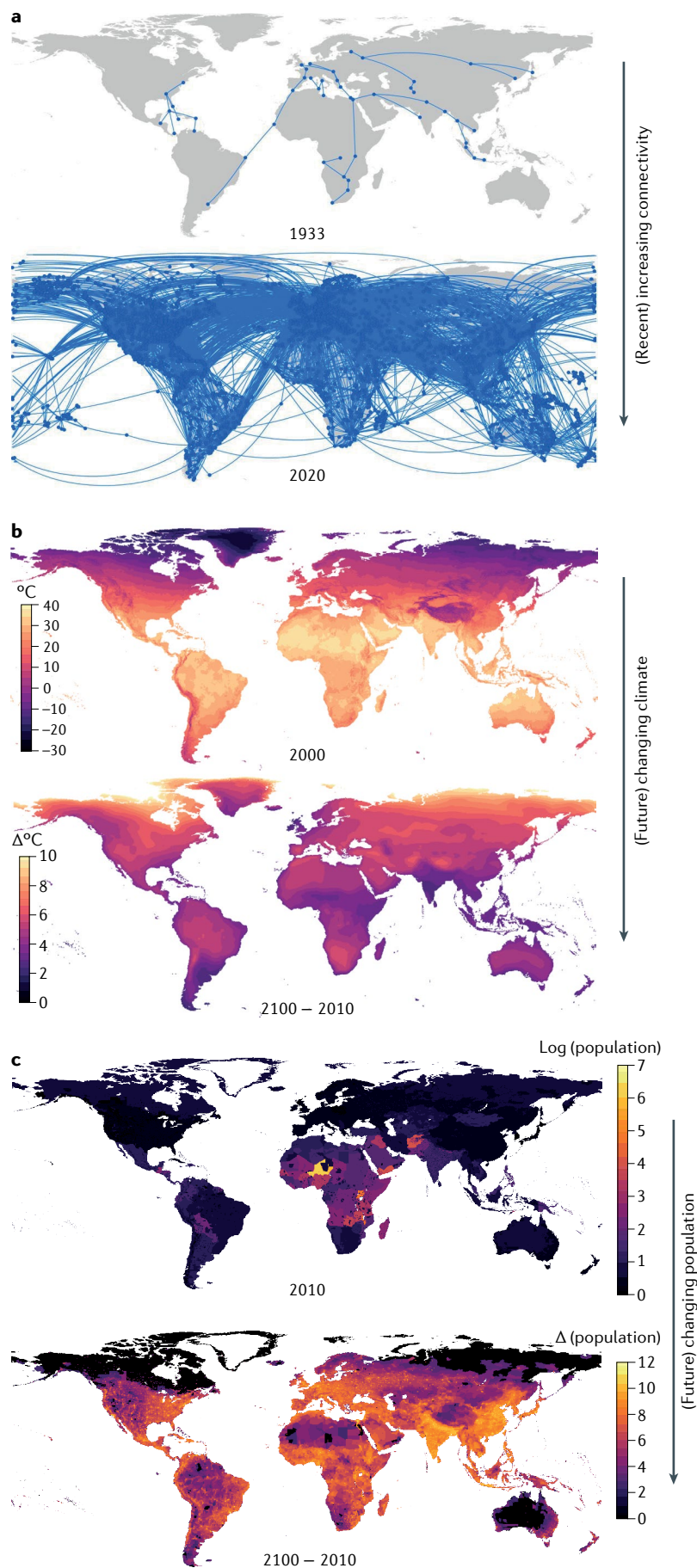
Fig. 4 | **Mapping changes to travel and climate.**
a | The global international air travel network expanded substantially from 1933 to 2020 (data from WorldPop and REF.[131]). **b** | Average monthly maximum temperature in 1970–2000) and difference between 2070–2100 and 1970–2000 averages (data from WorldClim, Shared Socioeconomic Pathway 3 (SSP3)). **c** | Population projections under SSP3 in 2010 and relative population change projected until 2100 (source NASA Socioeconomic Data and Applications Center (REF.[132])). Part **a** adapted with permission from REF.[131], OUP.

International travel can lead to the global spread of vector-borne diseases via the introduction of new vectors into regions with suitable environmental conditions or the introduction of new pathogens into native and invasive vector populations. Historically, vectors have been introduced via trade routes: ships are thought to have been key to the global dispersal of *Ae. aegypti* and *Ae. albopictus*, which then became established in locations with appropriate environmental conditions[72,73]. *Anopheles gambiae*, the primary vector of malaria in Africa, was introduced into Brazil in the 1930s and became established in a region with a climate similar to that of its native Kenya[74]. Although malaria was already endemic in Brazil at the time, *An. gambiae* proved a much more effective vector, leading to a severe outbreak and a costly (but successful) eradication campaign[73]. There has been relatively little documented evidence of the introduction of new vectors via air travel. This is likely due to the low probability of vectors surviving the flight, and disembarking in a suitable region, in sufficient numbers to establish and drive an epidemic[75]. However, cases of 'airport malaria', that is, malaria transmitted within international airports, even outside endemic regions, are rare but becoming more common[76].

A more feasible scenario is that air travel can bring an infected human host into contact with a native or invasive vector population that then establishes local transmission. Climate change has driven a shift in the range of several key vectors, which may make this introduction more likely. The range of the biting midge *Culicoides imicola*, a vector of bluetongue virus, which causes disease in ruminants, has expanded over the past few decades from sub-Saharan Africa and the Middle East into Europe, bringing a wave of bluetongue epidemics[77]. Following this expansion, bluetongue virus then spread outside the range of *C. imicola* into native populations of *Culicoides* spp. in more northerly regions of Europe. In terms of air travel, the 2015 Zika virus disease epidemic in the Americas may provide a recent example of a pathogen spreading into a susceptible vector population, likely facilitated by high connectivity[78]. Zika virus is thought to have been introduced to Brazil from French Polynesia and vectored by *Aedes* spp., although the volume of air travel during this period makes it almost impossible to conclusively determine the origin[78]. Similarly, it is hard to pinpoint the pathway via which West Nile virus was introduced into the USA in the 1990s; however, transport by either shipping (transporting vectors) or aircraft (transporting a human host) is likely[79]. After introduction, West Nile virus spread in the native *Culex* spp. mosquito population. More broadly, climate change

Box 2 | **Will there be another pandemic like COVID-19?**

COVID-19 has had an unprec-edented impact on both human lives and our society, and we will likely be dealing with the consequences for decades to come. As we reckon with these con-sequences, one concern is that a suite of global changes has increased the risk from emerging pathogens, such that pandemics similar to COVID-19 could be a more frequent occurrence. However, there are biological features of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) that have made the pathogen distinctly diffi-cult to control, primarily the virus's ability to spread asym-ptomatically and presympto-matically. Many pathogens do not exhibit these features, which may be a cause for cautious optimism going forward.

The expansion of regional and global air travel, along with the increasing development of high-speed railway networks, has resulted in a substantial degree of connectivity between human populations[73]. At the same time, land-use change and climate change may have increased the risk of pathogen emergence. In combination, these drivers imply an era where pathogens are more likely to emerge, and more likely to spread globally on emergence. However, while the last century bore witness to several pandemics (FIG. 1), SARS-CoV-2 is unrivalled in its rapid, global reach. A key question is why SARS-CoV-2 was so successful at spreading globally and whether this was due to recent increases in global connectivity as opposed to epidemiological and biological characteristics of the virus itself[145].

A clear distinction between SARS-CoV-2 and other recently emerged pathogens (for example, SARS-CoV and Ebola virus) is that an individual infected with SARS-CoV-2 may become infectious before developing symptoms[146]. This presents a unique challenge from a disease control perspective. A standard approach for limiting the onward spread of a new outbreak is to isolate infected individuals when they show symptoms. Case isolation proved successful in mitigating earlier SARS[147] and Ebola virus disease[148] outbreaks. However, symptoms for SARS-CoV-2 infection likely occur after an individual is already infectious[146]. This possible presymptomatic spread limits the efficacy of case isolation interventions as by the time the infected individual is isolated, the person may have already spread the pathogen to others[149]. In the figure, we plot the time to infectiousness (latent period) against the time to symptom onset (incubation period) for four pathogens that have caused severe outbreaks in recent decades. When the latent period equals the incubation period (dashed line in the figure), symptoms occur at a similar time to infectiousness (for example, influenza). The shaded region to the right of this line in the figure indicates possible presymptomatic spread, which may be uniquely difficult to control.

The 2–3-day delay between infectiousness and symptom onset provides ample time for long-distance spread of the disease, given current transport networks (see the figure). Control policies, such as testing before travel, provide a more effective option in this context, yet developing and distributing a test takes time, during which time the disease may spread rapidly. The good news is that this presymptomatic spread appears somewhat unique to SARS-CoV-2, at least compared with other acute infections such as influenza, SARS and Ebola virus disease (FIG. 4). In comparison, asymptomatic spread explains some of the difficulty in controlling acquired immunodeficiency syndrome before antiretroviral measures were available.

complicates the picture in terms of possible future intro-ductions. As the range of locations with environmental suitability for certain vector species changes, successful introductions of pathogens into these vector populations may become more likely[80]. At the same time, changes to population structure (for example, via urbanization) may alter the suitability of an environment for vector reproduction (FIG. 2).

Migration and local mobility. Human migration is an intrinsic component of population dynamics driven by socio-economic, political and environmental factors,

and one that has undergone considerable upheaval in the modern era. It is estimated that globally the number of international migrants, those who intentionally relo-cate to a country other than their birth country, is almost 272 million, representing 3.5% of the world's population. By contrast, temporary migration, often considered 'sea-sonal migration', is driven largely by economic patterns, including agricultural seasons that require short peri-ods of intense labour. The rate of migration continues to increase owing to both social, economic, political and environmental drivers in origin countries and economic opportunities, physical safety and security in destination
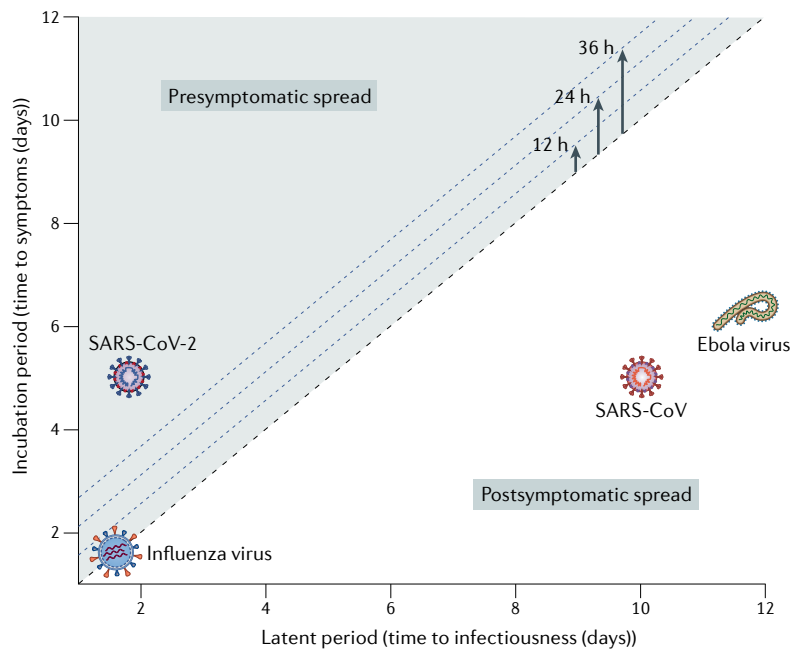
countries. Projections for migration are unclear, with the UN projecting stable rates after 2050 (REF.[81]). However, climate change will likely provide an escalating push factor, with sea level rise and extreme weather events leading to forced migration from exposed regions[82].

Given the movement of people between countries, there remain risks of introduction of infectious diseases, including those common and uncommon in the country of migration[83]. It is possible for a infectious disease common in the source country, such as latent tuberculosis, malaria, viral hepatitis and infection with intestinal parasites, to be imported via this mechanism[84–86]. For example, in many destination countries, a large proportion of cases of tuberculosis are observed in the foreign-born population. However, the ultimate impact of these introduction events will depend largely on the population-level susceptibility and environmental suitability for sustained transmission in the destination country. More importantly, migrant groups often have more limited access to health care, treatment and resources, particularly those displaced, who are often provided with limited options to safely seek care and treatment[87]. Minimizing the impact of these possible disease threats depends on providing appropriate health care to these high-risk groups that takes into account the multifaceted social, political and economic components[88].

Within-country population mobility can also play a key role in disease spread; however, it is typically difficult to track these movements. Aggregated mobile phone data are a valuable tool for tracing patterns of local mobility and predicting future outbreaks[89]. In recent work, mobility data have been shown to be predictive of inequities in COVID-19 burden in the USA[90]. Similarly, population mobility was found to predict the spread of the 2011 dengue epidemic in Pakistan[91], while local travel following the Eid holidays was found to predict the spread of the chikungunya outbreak in 2017 in Bangladesh[92]. As the trend of urbanization continues, mobility to and from dense urban centres (that is, megacities) will likely play a future role in local spread of infections[92]. Better tracking of within-country population mobility, using novel data streams, may present an opportunity for forecasting future outbreaks[93].

Intensification of animal and plant trade

International trade has expanded rapidly in the modern era and has been matched by a global proliferation of infectious diseases affecting not only humans but also animals and plants[94,95]. Trade drives this pattern by facilitating the translocation of hosts and pathogens across the geographical and ecological boundaries that constrain their spread. The economic and environmental threats posed by trade-driven infectious diseases of plants and animals are increasingly being recognized, and calls for more stringent containment measures have intensified in recent years[96,97].

Plant trade. Deliberate transport of plant products has existed since the emergence of trade. Increases in the speed of transport during modern times have allowed more live plant tissue, and as a result more viable pathogen propagules, to be transported over long distances.

Combined with the intensification of trade at the global scale, this pattern has driven a rise in long-distance transmission and disease emergence[98,99]. Trade drives the emergence of novel plant diseases by creating novel interactions between hosts and pathogens[100]. One pathway through which this can occur is the introduction of novel pathogens to native plants. For example, *Xylella fastidiosa*, a generalist bacterium vectored by xylem-feeding insects, was introduced into Europe in 2013 from the USA, likely as a result of trade. In Italy, *X. fastidiosa* is causing an ongoing epidemic of 'olive quick decline syndrome', resulting in severe losses of an economically and culturally important crop[101,102]. Trade can also drive the emergence of plant disease by introducing novel hosts to native pathogens. Eucalyptus rust, a disease caused by the fungal pathogen *Austropuccinia psidii*, emerged when the pathogen transferred from its native South American hosts in the myrtle family (Myrtaceae) to non-native *Eucalyptus* trees (which also belong to the myrtle family) being grown on plantations[103]. The disease now threatens to 'spill back' into naive endemic *Eucalyptus* populations in Australia.

Animal and animal-product trade. Animal trade has contributed to multiple outbreaks and emergence events globally, which have had major consequences for the agricultural sector as a whole and pose substantial risk for animal and public health. Large numbers of livestock are traded annually between countries and may facilitate the spread of pathogens. Rift Valley fever, for example, is a zoonotic vector-borne viral disease causing abortion and high neonatal mortality in domestic ruminants. The disease is widespread on the African continent and has recently been detected in Saudi Arabia and Yemen. Live cattle movement between East Africa and the Arabian peninsula or from the Union of Comoros to Madagascar is thought to have contributed to the introduction of Rift Valley fever virus and caused outbreaks in these locations in 2000 (Arabian Peninsula) and 2008 (Madagascar)[104,105].

Additionally, the trade of animal-derived products such as meat may enable the movement of pathogens over large distances and between continents. For instance, African swine fever is a highly contagious viral disease affecting several members of the family Suidae, including domestic pigs and wild boars. Infection by African swine fever virus may result in up to 100% morbidity and mortality in affected pig herds and substantial economic losses for producers. In 2007, the accidental introduction of African swine fever virus to Georgia led to the first outbreak of African swine fever in Europe since the early 1990s[106]. The virus, which used to occur primarily in sub-Saharan Africa, was allegedly introduced to the Caucasian peninsula through meat products contaminated with viruses closely related to the ones found in Madagascar, Mozambique or Zambia[107]. Despite efforts to contain the virus, the disease has spread to more than 20 countries in Europe and Asia[108,109].

Similarly, in recent decades there has been an expansion in infections of *Vibrio parahaemolyticus* — a bacterial pathogen found in shellfish and the leading

Propagules
Pathogen units responsible for infection, such as a fungal spore or viral particle.

Recent technological advances in collecting, sharing and processing large datasets, from satellite images to genomes, represent a new opportunity to answer critical questions in global health. However, challenges remain, including the uneven geographical distribution of available data as well as biases in representative sampling. We highlight three areas of future growth.

Serological surveys
Serological surveys detect the presence of antibodies in blood — recent advances in testing now enable the detection of exposure to multiple pathogens with use of a small sample of blood[150]. Serological surveys have attracted attention during the COVID-19 pandemic as a means to track population exposure given under-reporting, although test performance characteristics differ widely between epidemiological contexts as well as the choice of assay used[151]. Historically, serological surveys have been financially and logistically expensive to run, but declining costs are leading to increased availability of serological data.

Genomic surveillance systems
Genomic surveillance systems are able to characterize and track the emergence of novel variants (for example, during the COVID-19 pandemic). Undoubtedly these data have enabled the rapid development of diagnostics and vaccines and, when combined with epidemiological information, are able to provide a more detailed picture of ongoing transmission dynamics. Efforts to develop national and international genomic surveillance networks are varied but with clear success stories[152,153] even in low-resources settings[154]. However, resource limitations, including sequencing platforms, bioinformatic pipelines and the regular collection of samples for processing, continue to limit the global expansion of sequencing.

Artificial intelligence and machine learning
These techniques are frequently proposed as tools for answering key public health questions, yet specific use cases remain elusive[155]. Using these tools to predict viral emergence, for example, may prove difficult due to microbiological complexities and the cost of data collection[156], yet could prove valuable for targeting sampling efforts[157]. In terms of uncovering population-level drivers of disease transmission, statistical approaches, including machine learning, can be used to leverage novel, and high-volume, data streams. However, more classical, mechanistic models may provide a more robust framework for projecting future outcomes for the disease system under demographic, technological and climatic change. Future work should aim to improve the integration of machine learning approaches within the traditional mechanistic modelling frameworks to rapidly and accurately assess prospective challenges.

cause of seafood-related illness globally. The pathogen is endemic to regions of the US Pacific Northwest but has recently spread to other parts of the USA, Europe and South America[110,111]. The concerning increase in *V. parahaemolyticus* infection is expected to have several drivers connected to global change. Declines in sea ice have increased ship traffic through the Bering Strait, with cargo ships possibly transporting *V. parahaemolyticus* in ballast water. At the same time, increasing sea temperatures may have increased the global environmental suitability for *V. parahaemolyticus* in the marine environment[110]. Finally, dispersal of the pathogen may have occurred via increasing global trade in shellfish, with evidence suggesting possible dispersal via Manila clams introduced into Spain from Canada[111]. This combination of possible drivers speaks to the complexity of understanding infectious disease risk in an era of global change, and the necessity of exploring concurrent changes.

Transboundary spread of diseases through legal and illegal trade of live animals may also have important consequences for biodiversity on a global scale. For example, the amphibian trade contributed to the expansion of novel strains of the fungal pathogen genus *Batrachochytrium* into naive hosts, devastating wild amphibian populations globally[112]. Conversely, infectious diseases also hamper trade, resulting in indirect economic losses in affected populations. Foot and mouth disease virus is a major reason for trade restrictions on livestock. While endemic in certain countries in Asia and Africa, foot and mouth disease virus causes outbreaks in naive populations, resulting in large economic losses[113]. While trade is a major driver of pathogen spread, food animal production has transformed in recent history into large-scale intensified systems with high-density, genetically homogenous populations, ideal for pathogen emergence and maintenance[114]. Critically, animal production systems often serve as the interface between wild and human populations, and multiple viral spillover events have occurred at this nexus. Nipah virus spilled over from fruit bats to the domestic pig population multiple times before subsequently infecting humans[115]. Pandemic variants of human influenza A virus are often the result of reassortment between human and avian viruses, with both domestic poultry and wild birds posited to play a role[116–118]. A non-viral example is the spillover of antimicrobial-resistant pathogens from livestock into humans: intensive antibiotic use in industrialized and smallholder livestock production systems to promote growth and prevent infections has been linked to the emergence of antibiotic resistance in humans[119]. Tackling emergence and disease spread in animal systems will require rethinking both food animal production and global trade of animals.

A new era of infectious disease

In recent decades, declines in mortality and morbidity, particularly childhood mortality, have been one of the great triumphs of public health. Greater access to care, such as therapeutics (including antibiotics), improved sanitation and the development of vaccines[120] have been core drivers of this progress. Even as medical advances in the twenty-first century have spurred advances in population health, inequalities in access to these advances remain widespread between and within countries[121]. Reducing inequities in access to health care and improving surveillance and monitoring for infectious diseases in low-income and middle-income countries, and in underserved populations within countries, should be a priority in tackling pathogen emergence and spread.

While life expectancy continues to increase, and life years lost to infectious diseases decline, the new threat of infectious disease will likely come from emerging and re-emerging infections. Climate change, rapid urbanization and changing land-use patterns will increase the risk of disease emergence in the coming decades. Climate change, in particular, may alter the range of global pathogens, allowing infections, particularly vector-borne infections, to expand into new locations. A continued uptick in global travel, trade and mobility will transport pathogens rapidly, following emergence. However, there are counterpoints to this trend: the rapid growth of connectivity observed in the early twenty-first century may stabilize, and structural changes wrought during the COVID-19 pandemic may persist[122]. Increased investment in outbreak response, such as the recent formation of the WHO Hub for Pandemic and Epidemic

Reassortment
The mixing of genetic material of different pathogens within an infected cell.

Multiplex serology
The measurement of antibody responses to multiple pathogens simultaneously.

Intelligence, could help mitigate the threat from future emerging infections. In addition, efforts to develop universal vaccines (that is, vaccines that engender immunity against all strains of influenza viruses or coronaviruses, for example) could provide a monumental leap forward in tackling present and future infections[123].

A changing world requires changing science to evaluate future risks from infectious disease. Future work needs to explicitly address concurrent changes: how shifting patterns of demographic, climatic and technological factors may collectively affect the risk of pathogen emergence, alterations to dynamics and global spread. More forward-looking research, to contend with possible future outcomes, is required in addition to the retroactive analyses that typically dominate the literature. Increasing attention needs to be paid to pathogens currently circulating in both wild and domestic animal populations, especially in cases where agriculture is expanding into native species' habitats and, conversely, invasive species are moving into populous regions due to climate change. As the battle against certain long-term endemic infections is won, institutional structures built to address these old enemies can be co-opted and adapted for emerging threats. At the same time, new technologies, including advances in data collection and surveillance, need to be harnessed (BOX 3). There is much recent innovation around surveillance, from reinterpreting information available from classic tools such as PCR[124] to leveraging multiplex serology approaches to identify anomalies that might suggest pathogen emergence, and there is increasing interest in integrating multiple surveillance platforms (from genomic to case data) to better understand pathogen spread. Finally, future research needs to align with a global view of disease risk. In an increasingly connected world, the risk from infectious disease is globally shared. The COVID-19 pandemic, including the rapid global circulation of evolved strains, highlights the need for a collaborative, worldwide framework for infectious disease research and control.

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