

# The COVID-19 pandemic: diverse contexts; different epidemics – how and why?

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## ABSTRACT

It is very exceptional that a new disease becomes a true pandemic. Since its emergence in Wuhan, China, in late 2019, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes COVID-19, has spread to nearly all countries of the world in only a few months. However, in different countries, the COVID-19 epidemic takes variable shapes and forms in how it affects communities. Until now, the insights gained on COVID-19 have been largely dominated by the COVID-19 epidemics and the lockdowns in China, Europe and the USA. But this variety of global trajectories is little described, analysed or understood. In only a few months, an enormous amount of scientific evidence on SARS-CoV-2 and COVID-19 has been uncovered (knowns). But important knowledge gaps remain (unknowns). Learning from the variety of ways the COVID-19 epidemic is unfolding across the globe can potentially contribute to solving the COVID-19 puzzle. This paper tries to make sense of this variability—by exploring the important role that context plays in these different COVID-19 epidemics; by comparing COVID-19 epidemics with other respiratory diseases, including other coronaviruses that circulate continuously; and by highlighting the critical unknowns and uncertainties that remain. These unknowns and uncertainties require a deeper understanding of the variable trajectories of COVID-19. Unravelling them will be important for discerning potential future scenarios, such as the first wave in virgin territories still untouched by COVID-19 and for future waves elsewhere.

## INTRODUCTION

Late in 2019, a cluster of acute respiratory disease in Wuhan, China, was attributed to a new coronavirus,<sup>1–3</sup> later named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).<sup>4</sup> It was soon discovered that the virus is easily transmitted, can cause

## Summary box

- ▶ Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus that causes COVID-19, has spread to nearly all countries of the world in only a few months. It is unique that an emerging respiratory virus becomes a pandemic, and can continue human-to-human transmission unabated, probably permanently.
- ▶ Depending on the context, the trajectory and the impact of the COVID-19 epidemic vary widely across affected countries. This is in fact the case with most infectious diseases.
- ▶ Despite limited initial knowledge on COVID-19, most societies have deployed draconian measures, including lockdowns, to contain the virus and mitigate its impact. This had variable success, but invariably with profound socioeconomic collateral effects.
- ▶ Through research and rapid sharing of its findings, progressively more insights on SARS-CoV-2 and COVID-19 have been uncovered (knowns), mainly based on evidence from China, Europe and the USA; however, important knowledge gaps remain (unknowns).
- ▶ The different COVID-19 epidemics and the responses unfolding in the Global South are little described, analysed or understood. Insights from these less researched contexts are important for discerning potential future scenarios, not only for the first wave in virgin territories still untouched by COVID-19, but also for future waves.
- ▶ More understanding of lived experiences of people in a variety of contexts is necessary to get a full global picture and allow learning from this variety.
- ▶ BMJ Global Health and Emerging Voices for Global Health have launched a call for such on-the-ground narratives and analyses on the epidemics of, and responses to, COVID-19.



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**Table 1** Key events in the COVID-19 pandemic, December 2019–May 2020

Month	Key events
December 2019	<ul style="list-style-type: none"> <li>▶ Clusters of pneumonia of unknown origin in Wuhan, China.</li> <li>▶ Human infection probably began sometime between 9 October and 20 December 2019.<sup>69</sup></li> <li>▶ WHO alerted of a novel coronavirus on 31 December 2019.</li> <li>▶ Several cases in Hubei Province, China, and probably already spread to surrounding areas.</li> <li>▶ The virus may have already been spreading in France late December 2019.<sup>70</sup></li> </ul>
January 2020	<ul style="list-style-type: none"> <li>▶ First case outside China reported in Thailand on 13 January 2020.</li> <li>▶ Cases reported in at least 24 countries, mostly in South and Southeast Asia; also in Europe, the USA, Canada and the United Arab Emirates.<sup>71</sup></li> <li>▶ The ‘new disease’ declared a ‘Public Health Emergency of International Concern’ on 30 January 2020.</li> <li>▶ Mostly ‘imported cases only’, mainly travellers from China. Soon ‘export’ of virus from other countries started.</li> <li>▶ The Wuhan lockdown,<sup>72</sup> which later inspired a series of lockdowns across the world.</li> </ul>
February 2020	<ul style="list-style-type: none"> <li>▶ The new disease named COVID-19 on 11 February 2020.</li> <li>▶ Cruise ship Princess Diamond quarantined near Japan, sparking media attention.</li> <li>▶ Epidemic in China peaked with ~80 000 cases and 2900 deaths (80% of cases restricted to the Hubei Province).<sup>73</sup></li> <li>▶ Local epidemics of varying attack rates and case fatality rates in 58 countries with imported cases causing ‘local transmission’ reported from 20 countries.</li> <li>▶ South Korea, Italy and Iran emerged as new epicentres.</li> </ul>
March 2020	<ul style="list-style-type: none"> <li>▶ Europe engulfed with local epidemics.</li> <li>▶ Over 170 countries were affected worldwide.</li> <li>▶ The epidemic in China seemed to have plateaued.</li> <li>▶ WHO declared the epidemic a pandemic.</li> <li>▶ China partially lifted lockdown while India instituted the world’s biggest complete lockdown affecting ~1.4 billion people.<sup>74</sup></li> </ul>
April 2020	<ul style="list-style-type: none"> <li>▶ COVID-19 cases crossed 1 million with more than 50 000 deaths.</li> <li>▶ The US emerged as the most affected country with epicentre in New York.</li> <li>▶ Aerosols implicated in the transmission (prompting ‘mass masking’ of the general public).</li> <li>▶ WHO warned that Africa will be the future epicentre of COVID-19.</li> </ul>
May 2020	<ul style="list-style-type: none"> <li>▶ South America became the new epicentre of COVID-19.</li> <li>▶ More than 325 000 deaths globally with ~5 million cases in 216 countries/territories/areas.</li> <li>▶ At the time of writing (end of May 2020), no effective medication and/or vaccine exist.</li> <li>▶ The pandemic appeared to have slowed down in countries such as South Korea, Italy, Spain, France and the rest of Europe.</li> <li>▶ In Africa, the number of cases seemed to fall short of forecasts.</li> <li>▶ Tremendous socioeconomic fallouts after an estimated 4.5 billion persons (more than half of humanity) subjected to social distancing norms and/or lockdowns.<sup>75</sup></li> </ul>

severe disease and can be quite lethal especially in the elderly and those with comorbidities.<sup>5–8</sup> The new human disease is called COVID-19.<sup>9</sup> Soon it became clear that its global spread was unstoppable. Even with draconian containment measures, such as strict movement restrictions, the so-called lockdown, it spread, and within a few months reached almost all countries and was declared a pandemic by the WHO.<sup>10</sup> Table 1 summarises key events in the unfolding of the COVID-19 pandemic, from December 2019 to May 2020.

This progression is quite unique. New human pathogens emerge frequently from an animal host, but most cause only a local outbreak. Human-to-human transmission stops at some point, and the virus can only re-emerge as a human pathogen from its animal host. Only very rarely does an emerging pathogen become a pandemic. Over the past decades, a totally new pathogen emerged, caused serious disease, and spread around the

globe continuously only once before: the HIV. It seems increasingly likely that SARS-CoV-2 transmission will be continuing. All countries are now facing their own ‘COVID-19 epidemic’.

In only a few months, the scientific community has started to learn the virus’s characteristics and its manifestations in different contexts.<sup>11</sup> But we fail to understand fully why the virus spreads at different speeds and affects populations differently. Our main objective is to make sense of those different expressions of the COVID-19 pandemic, to understand why COVID-19 follows variable trajectories in ways that are often quite different from the collective image created by the mediatisation of the dramatic COVID-19 epidemics in densely populated areas.

We start by exploring the role of context, followed by a brief summary of what is already known at the time of writing about SARS-CoV-2 and COVID-19. We then

compare these knowns with what is known of some other viral respiratory pathogens and identify the critical unknowns. We also discuss the coping strategies and collective strategies implemented to contain and mitigate the effect of the epidemic. We finally look ahead to potential future scenarios.

### THE UNFOLDING COVID-19 PANDEMIC: IMPORTANCE OF CONTEXT

Initially, human-to-human transmission was documented in family/friends clusters.<sup>12–17</sup> Progressively, it became clear that superspreading events, typically during social gatherings such as parties, religious services, weddings, sports events and carnival celebrations, have played an important role.<sup>18–21</sup> Dense transmission has also been documented in hospitals<sup>22</sup> and nursing homes possibly through aerosols.<sup>23 24</sup>

SARS-CoV-2 has spread around the world through international travellers. The timing of the introduction of SARS-CoV-2 has largely depended on the intensity of connections with locations with ongoing COVID-19 epidemics; thus, it reached big urban centres first and, within these, often the most affluent groups. From there, the virus has spread at variable speeds to other population groups.<sup>25 26</sup>

As of May 2020, the most explosive COVID-19 epidemics observed have been in densely populated areas in temperate climates in relatively affluent countries.<sup>27</sup> The COVID-19 pandemic and the lockdowns have been covered intensively in the media and have shaped our collective image of the COVID-19 epidemic, both in the general public and in the scientific community.

The COVID-19 epidemic has spread more slowly and less intensively in rural areas, in Africa and the Indian subcontinent, and the rural areas of low and lower-middle income countries (LICs/LMICs). Not only the media but also the scientific community has paid much less attention to these realities, emerging later and spreading more slowly.

The dominant thinking has been that it is only a question of time before dramatic epidemics occur everywhere. This thinking, spread globally by international public health networks, has been substantiated by predictive mathematical models based largely on data from the epidemics of the Global North. However, what has been observed elsewhere is quite different although not necessarily less consequential.<sup>28</sup>

The effects of the COVID-19 epidemic manifest in peculiar ways in each context. In the early stages of the COVID-19 epidemic in sub-Saharan Africa, the virus first affected the urban elites with international connections. From there, it was seeded to other sections of the society more slowly. In contrast, the collateral effects of a lockdown, even partial in many cases, are mostly felt by the urban poor, as ‘stay home’ orders abruptly intensify hardship for those earning their daily living in the informal urban economy. Governments of LICs/LMICs lack the

budgetary space to grant generous benefit packages to counter the socioeconomic consequences. International agencies are very thinly spread, as the pandemic has been concurrent everywhere. Donor countries have focused mainly on their own COVID-19 epidemics.

The epidemic is thus playing out differently in different contexts. Many factors might explain SARS-CoV-2 transmission dynamics. Climate, population structure, social practices, pre-existing immunity and many other variables that have been explored are summarised in [table 2](#).

Although all these variables probably play some role, many uncertainties remain. It is difficult to assess how much these variables influence transmission in different contexts. It is even more difficult to assess how they interact and change over time and influence transmission among different social groups, resulting in the peculiar COVID-19 epidemic in any particular context.

### INSIGHTS FROM OTHER VIRUSES

We do not attempt to give a complete overview of viruses but select only those viruses that emerged recently and caused epidemics such as Ebola, that have obvious similarities in transmission patterns such as influenza and measles, or that are closely related such as other coronaviruses.

#### Emerging viral respiratory pathogens

Respiratory viruses such as severe acute respiratory syndrome coronavirus (SARS-CoV), Middle East respiratory syndrome coronavirus (MERS-CoV) and avian influenza A and also Ebola have originated from animal hosts and caused human diseases ([table 3](#)). These viruses do not continuously circulate from human to human. They create an outbreak only when there is interspecies cross-over transmission, most frequently from bats to another animal host.

The first human case of a disease from an emerging viral pathogen, the ‘index case’ or ‘patient zero’, is invariably someone in close contact with the originating animal host or an intermediary animal host. If this contact occurs in a remote rural community, the spread is usually slow, at low intensity, and could fade out before the pathogen gets a chance to spread to another community. The spread can suddenly intensify if seeded in a densely populated community, frequently in a particular context such as a hospital or during a social event, often referred to as a superspreading event. When the spread reaches a city, it can become a major outbreak, from where it can spread further; this happened with SARS-CoV in Hong Kong in 2003 and with Ebola in Conakry, Freetown and Monrovia in 2014–2016.<sup>29 30</sup> But at some stage human-to-human transmission is interrupted and the outbreak stops.

Only very exceptionally can a new viral pathogen sustain continuous human-to-human transmission. Other viral diseases such as measles and influenza are ‘old’ diseases; they have been studied in great depth. What can we learn from them?

**Table 2** Contextual variables potentially influencing transmission of severe acute respiratory syndrome coronavirus 2

Variable	Elements	Range (variation/extremes)	
Population density	<ul style="list-style-type: none"> <li>▶ People per km<sup>2</sup></li> <li>▶ People per household</li> <li>▶ Indoor space (m<sup>2</sup>) per person</li> </ul>	Big European/USA/ Chinese cities	Rural areas Megacities with urban slums
Social demography	<ul style="list-style-type: none"> <li>▶ Age structure: proportion of elderly and children</li> <li>▶ Household composition: nuclear versus multigenerational</li> <li>▶ Mixing patterns, including mode of transport</li> <li>▶ Forms of religious and social events</li> </ul>	Italy, Europe	Sub-Saharan Africa, Southeast Asia
Social practices	<ul style="list-style-type: none"> <li>▶ Mode of greeting and social contact (shaking hands, kissing, hugging, etc.)</li> <li>▶ Handwashing, water and sanitation</li> <li>▶ Ventilation and air conditioning</li> </ul>	High-income countries or areas	Slums
Geography	<ul style="list-style-type: none"> <li>▶ Climate</li> <li>▶ Urbanisation rate</li> <li>▶ Air traffic intensity</li> <li>▶ Population movements</li> <li>▶ Road networks</li> </ul>	Europe, USA	Sub-Saharan Africa, Brazil, India
Pre-existing immunity	<ul style="list-style-type: none"> <li>▶ Prior exposure to other coronaviruses, BCG vaccine, and so on.</li> <li>▶ Non-specific immunity?</li> </ul>	High-income countries	Low-income countries in tropical climates
Genetic factors	<ul style="list-style-type: none"> <li>▶ ACE variability</li> <li>▶ HLA variability</li> </ul>		

ACE, angiotensin-converting enzyme; HLA, human leucocyte antigen.

**Measles and influenza: the importance of context**

It is thought that measles emerged thousands of years ago in the Middle East. It is assumed that a cross-over occurred from the rinderpest virus,<sup>31</sup> to become the human measles virus. Measles has since spread around

the globe in continuous human-to-human transmission. When measles, along with other viruses such as smallpox and influenza, was introduced in the Americas by European conquerors, it contributed to a massive die-off of up to 90% of the original population.<sup>32</sup>

**Table 3** Examples of emerging human respiratory viral diseases without sustained human-to-human transmission

Virus	Originating animal host	Characteristics	No. of cases; CFR
SARS-CoV	Bat	<ul style="list-style-type: none"> <li>▶ First emerged in China in November 2002.<sup>76</sup></li> <li>▶ Causes severe acute respiratory syndrome (SARS).</li> <li>▶ Transmission through superspreading events in healthcare facilities.<sup>77</sup></li> </ul>	8422 cases; CFR:10% <sup>78</sup>
MERS-CoV	Bat	<ul style="list-style-type: none"> <li>▶ First emerged in the Middle East in 2012.<sup>79</sup></li> <li>▶ Causes Middle East respiratory syndrome (MERS).</li> <li>▶ Outbreaks from 2012 to 2019 in Saudi Arabia and one outbreak in South Korea (2015).</li> </ul>	2502 cases; CFR: 34% <sup>79</sup>
Avian influenza A (H5N1 and H7N9)	Birds/poultry	<ul style="list-style-type: none"> <li>▶ Subtypes of influenza viruses detected in birds (having killed millions of poultry) but with ‘pandemic potential’ (WHO).<sup>80</sup></li> <li>▶ H5N1 first detected in humans in 1997 in China with widespread emergence in 2003–2004; no sustained community-level transmission.<sup>80</sup></li> <li>▶ H7N9 first detected in humans in China in 2013.<sup>81</sup></li> </ul>	H5N1: 649 cases; CFR: 60% <sup>82</sup> H7N9: 571 cases; CFR: 37% <sup>81</sup>
Ebola virus	Bat	<ul style="list-style-type: none"> <li>▶ First appeared in 1976 and caused over 20 documented ‘major’ outbreaks.<sup>83</sup></li> <li>▶ Largest epidemics in 2014–2016 in Guinea, Liberia and Sierra Leone.</li> <li>▶ Ongoing epidemic in the Democratic Republic of Congo.</li> </ul>	Over 30 000 cases; average CFR: 50% <sup>83</sup>

CFR, case fatality rates.



**Box 1 Pandemic H1N1 influenza, 1918–2009**

- ▶ The 1918 H1N1 virus probably infected one-third of the world's population at that time (or ~500 million people).<sup>84</sup>
- ▶ The pandemic had three waves in quick succession; the second wave, in 1919, was worse than the first wave.<sup>84</sup>
- ▶ High mortality, especially in younger persons (5–15 years; ~25% of total deaths) in the 1918 pandemic, may have been due to antibody-dependent enhancement and 'cytokine storms'.<sup>84</sup> Another possible explanation is that older persons had some protective cross-immunity from previous influenza outbreaks while younger persons did not.
- ▶ H1N1 continued to circulate along with seasonal influenza viruses, often recombining to produce more severe local outbreaks, including other pandemics between 1918 and 2009, giving it the nickname 'mother of all pandemics'.
- ▶ The original 1918 H1N1 strain was replaced by A(H1N1)pdm09 virus that resulted from an antigenic shift and caused the 2009 H1N1 influenza pandemic.
- ▶ The 2009 H1N1 virus originated in pigs in central Mexico in March 2009 and was responsible for an estimated 284 000 deaths worldwide with an estimated CFR < 0.1%.<sup>85 86</sup>
- ▶ During the 2009 pandemic, mortality was much lower than in the 1918 pandemic. Higher mortality in persons younger than 65 years was related to cytokine storms.<sup>87</sup> A role of protective cross-immunity from previous influenza strains in older persons has been suggested.
- ▶ After August 2010, the A(H1N1)pdm09 virus appeared to have integrated with circulating strains of influenza and continues to cause localised seasonal influenza outbreaks worldwide.<sup>88</sup>

The transmission dynamics of SARS-CoV-2 can be compared with influenza. Influenza typically causes yearly epidemics in temperate climates during winter with less seasonal patterns in tropical or subtropical regions.<sup>33 34</sup> In hotter climates, such as in sub-Saharan Africa<sup>33</sup> or South and Southeast Asia,<sup>34</sup> it is transmitted year round, often not identified as influenza. Such different epidemic patterns of influenza are still incompletely understood but thought to be associated with temperature and humidity and human behavioural factors such as indoor crowding.<sup>35</sup>

But, in contrast to SARS-CoV-2, the influenza virus is not new. Influenza is a very old disease, certainly circulating for several centuries. It has infected most human beings living on the planet already, many of them several times, leaving some immunity but no durable protection. The virus also mutates, giving rise to a new dominant strain every influenza season. Influenza is every year a slightly different virus (due to antigenic drift as a result of progressive mutations) with major differences every few decades (antigenic shift as a result of recombination with novel strains).

One such antigenic shift resulted in the 1918 H1N1 'Spanish' Influenza pandemic, which had an estimated case fatality rate (CFR) of 2%–3%, killing millions.<sup>36</sup>

**Box 1** summarises some key facts about H1N1, including factors thought to be associated with its high CFR.

**Box 2 On the use of mathematical models during epidemics**

A dominant way of studying the transmission dynamics of an infectious disease such as COVID-19, and predicting the amplitude and peak of the epidemic in a population (city, province, country) and analysing the effect of control measures is using mathematical models. Based on available data and several assumptions, a model attempts to predict the course of the epidemic, the expected number of infections, clinical cases and deaths over time. Critical is the effective reproductive number ( $R_t$ ). When  $R_t > 1$ , the number of cases in a population increases; when  $R_t < 1$ , the number of cases decreases. A relatively simple and widely used model is the susceptible-exposed-infectious-recovered model, as used in the two papers recently published in *BMJ Global Health* on COVID-19 in Africa.<sup>67 89</sup> There are many more types of models, with varying degrees of complexity.

The use of such models has strengths and limitations. Building a mathematical model implies trade-offs between accuracy, transparency, flexibility and timeliness. A difficulty, in general, is that the parameters on which the model is based, the so-called assumptions are frequently uncertain (**table 7**) and predictions can vary widely if any of the parameters are modestly different. This uncertainty is captured in a sensitivity analysis, leading to various possible quantitative outcomes, usually expressed as a range of plausible possibilities, between 'worst-case' and 'best-case' scenarios.

With a new disease such as COVID-19, certainly at the start of the outbreak, the parameters had to be based on very limited data from a particular context. However, many variables can widely differ across communities as they critically depend on contextual factors (**table 2**). In mathematical models, all such uncertainties and unknowns are somehow hidden in the complex formulae of the model, as a quasi 'black box'. Few people have the knowledge and skill to 'open up the black box'.

As uncertainties in COVID-19 are large, the range of possibilities produced by a model is wide, with the worst-case scenario typically predicting catastrophic numbers of cases and deaths. Such predictions are often misunderstood by journalists, practitioners and policy-makers, with worst-case estimates getting the most attention,<sup>68</sup> not specifying the huge uncertainties.

A major difference between COVID-19 and influenza is that SARS-CoV-2 is a new pathogen and influenza is not. At the time of writing (May 2020), SARS-CoV-2 has triggered an immune response in over 5 million confirmed infections (and probably in many more), definitely too few to create anything close to herd immunity. Calculations using an estimated reproductive number ( $R_0$ ) for SARS-CoV-2 suggest that herd immunity would require at least 60% of the population to have protective immunity (see **box 2**).<sup>37</sup>

Like COVID-19, measles and influenza have different epidemic patterns in different contexts. This also is the case for cholera, tuberculosis, HIV/AIDS and most infectious diseases. The difference in patterns is most pronounced and so is easily understood with vector-borne and water-borne diseases. Epidemic patterns are also different for air-borne infections, although they are less easily understood. Transmission of respiratory viruses is influenced by factors related to the virus and

**Table 4** Factors related to transmission patterns and severity of respiratory viruses

Factor	Variables
Virus	<ul style="list-style-type: none"> <li>▶ Infection efficiency, transmissibility.</li> <li>▶ Capacity to survive outside the human body (including in aerosols, in droplets, on surfaces, in stools, in intermediate animal hosts, etc.)</li> <li>▶ Potential to shed virus from an infected person, asymptomatic or diseased.</li> <li>▶ Genetic stability or variability (affecting the potential of long-lasting immunity).</li> <li>▶ Viral load determines the incubation period with the formula high load -&gt;short incubation period -&gt;high severity.</li> </ul>
Human host	<ul style="list-style-type: none"> <li>▶ Human susceptibility to the virus; transfer of parental immunity to newborns.</li> <li>▶ Route and efficiency of human-to-human transmission.</li> <li>▶ Presence and capacity of asymptomatic carriers to transmit the virus.</li> <li>▶ Immunity created after infection, its robustness and how long-lasting it is.</li> <li>▶ Severity and duration of the disease: proportion symptomatic, lethality (CFR).</li> <li>▶ Pathogenicity and disease spectrum; disease pattern according to age and comorbidities, and related potential to spread.</li> </ul>
Natural environment	<ul style="list-style-type: none"> <li>▶ Temperature, humidity and seasonal changes in climate affecting the stability and transmission potential of the virus and human susceptibility.</li> <li>▶ Increasing extreme weather conditions such as droughts and severe storms, as well as global climate change may also affect transmission patterns.</li> <li>▶ Air pollution may also play a role in the transmission and stability of the virus.</li> </ul>
Human environment/social geography	<ul style="list-style-type: none"> <li>▶ Demographic variables such as population density, age structure and household composition.</li> <li>▶ Mixing patterns within households, including bed sleeping patterns, related to housing conditions and hygiene practices.</li> <li>▶ House construction with solid walls or permeable walls (thatched walls, straw mats).</li> <li>▶ Mixing patterns among households related to settlement patterns: social networks, urban–rural differences, working conditions, religious practices and commuting patterns.</li> <li>▶ Variables related to built environments, road infrastructure and socioeconomic conditions.</li> <li>▶ Mobility between communities, including international travel.</li> <li>▶ Crowding institutions: for example, elderly homes, extended families, boarding schools, child institutions, seclusion during tribal ceremonies, hospitals, nursing homes, military barracks and prisons.</li> </ul>

CFR, case fatality rate.

the human host but also by factors related to the natural and human environment (table 4).

However, we are quite unable to explain fully which factor has which influence, how these factors vary among different social groups and how interdependent or isolated they are. We are certainly unable to fully model all these variables mathematically to explain the epidemic pattern across a variety of different contexts. Too many variables and their interrelations are difficult to quantify, and when all these factors change over time while the pathogen continues to spread in diverse societies, the complexity becomes daunting.

Understanding transmission dynamics is a bit less daunting for measles, as several variables are well known and rather constant across individuals and contexts. The natural transmission pattern of measles, before the introduction of vaccines, has been well described. Measles is mostly a childhood disease, but this is not the case in very remote communities, where measles transmission had been interrupted for extended periods (such as the Faroe Islands).<sup>38 39</sup> Measles affected all age groups when reaching new territories, causing dramatic

first-wave epidemics, a phenomenon called ‘virgin soil epidemic’.<sup>40 41</sup> The latest stages of the global dissemination of measles have been well documented, including in Australia, the Fiji islands and the Arctic countries, where such virgin soil epidemics occurred in the 19th and the mid-20th centuries.<sup>32 42</sup> Fortunately, measles infection creates robust protective immunity and after a first wave becomes a typical childhood disease, affecting only those without any prior immunity.<sup>43</sup> Human-to-human transmission of measles virus in a community stops when the virus cannot find new susceptible human hosts and the so-called herd immunity is reached.<sup>44 45</sup> But transmission of measles continues elsewhere on the planet from where it can be reintroduced a few years later when the population without protective immunity has grown large enough to allow human-to-human transmission again.

The epidemic patterns of measles are easily understood as measles is highly infectious, creates disease in almost every infected person and leaves lifelong natural immunity. Measles circulation, prior to vaccination, was continuous only in large urban areas with high birth rates. Everywhere else reintroduction occurred typically every 3–5

years but sometimes only after 10 or 15 years in isolated rural communities (such as among nomadic groups in the Sahel), causing epidemics among all those without acquired immunity and having lost maternal antibodies.<sup>46</sup> These diverse patterns of measles epidemics have been fundamentally changed by variable coverage of measles vaccination. They can still help us make sense of the diversity of COVID-19 epidemics being observed in 2020.

Measles illustrates convincingly that the transmission pattern of a respiratory virus is strongly influenced by the demographic composition, density and mixing pattern of the population and the connectedness to big urban centres. Measles transmission is continuous only in some large urban areas. It presents in short epidemics everywhere else with variable periodicity. This transmission pattern may well be a bit similar for COVID-19. But it took thousands of years for measles to reach all human communities while SARS-CoV-2 spread to all countries in only a few months, despite measles being much more transmissible than SARS-CoV-2. Factors such as increased air travel and more dense community structures play bigger roles for SARS-CoV-2 than they did for measles.

### Comparison with other pathogenic coronaviruses

SARS-CoV-2 has many close relatives. Six other human coronaviruses (HCoV) are known to infect humans. SARS-CoV and MERS-CoV (causing SARS and MERS, respectively) are very rare and do not continuously circulate among humans. The other four (HCoV-229E, HCoV-OC43, HCoV-HKU1 and HCoV-NL63) cause the common cold or diarrhoea and continuously circulate and mutate frequently.<sup>47 48</sup> They can cause disease in the same person repeatedly. The typical coronavirus remains localised to the epithelium of the upper respiratory tract, causes mild disease and elicits a poor immune response, hence the high rate of reinfection (in contrast to SARS-CoV and MERS-CoV, which go deeper into the lungs and hence are relatively less contagious). There is no cross-immunity between HCoV-229E and HCoV-OC43, and new strains arise continually by mutation selection.<sup>49</sup>

### COPING STRATEGIES AND COLLECTIVE STRATEGIES

How a virus spreads and its disease progresses depend not only on the variables described above (table 4) but also on the human reactions deployed when people are confronted with a disease outbreak or the threat of an outbreak. All these variables combined result in what unfolds as ‘the epidemic’ and the diverse ways it affects communities.

What a population experiences during an epidemic is not fully characterised by the numbers of known infections and deaths at the scale of a country. Such numbers hide regional and local differences, especially in large and diverse countries. The epidemic reaches the different geographical areas of a country at different moments and with different intensities. It affects different communities in variable ways, influencing how these communities

perceive it and react to it. What constitutes a local COVID-19 epidemic is thus also characterised by the perceptions and the reactions it triggers in the different sections of the society.

Even before the virus reaches a community, the threat of an epidemic already causes fear, stress and anxiety. Consequently, the threat or arrival of the epidemic also triggers responses, early or late, with various degrees of intensity and effectiveness. The response to an epidemic can be divided into individual and household actions (coping strategies), and collectively organised strategies (collective strategies). Coping strategies are the actions people and families take when disease threatens and sickness occurs, including the ways they try to protect themselves from contagion. Collective strategies are voluntary or mandated measures deployed by organised communities and public authorities in response to an epidemic. These include, among others, isolation of the sick or the healthy, implementation of hygiene practices and physical distancing measures. They can also include mobility restrictions such as quarantine and *cordon sanitaire*. Coping strategies and collective strategies also include treatment of the sick, which critically depends on the availability and effectiveness of diagnostic and therapeutic tools, and performance of the health system. Collective strategies also include research being deployed to further scientific insight and the development of diagnostic and therapeutic tools, potentially including a vaccine.

Implementation of these measures depends not only on resources available but also on the understanding and interpretation of the disease by both the scientific community and the community at large, influenced by the information people receive from scientists, public authorities and the media. This information is interpreted within belief systems and influenced by rumours, increasingly so over social media, including waves of fake news, recently labelled ‘infodemics’.<sup>50</sup>

Coping strategies and collective strategies start immediately, while there are still many unknowns and uncertainties. Progressively, as the pandemic unfolds and scientists interpret observations in the laboratory, in the clinic, and in society, more insights are gained and inform the response.

Table 5 lists measures recommended by the WHO for preventing transmission and slowing down the COVID-19 epidemic.<sup>51–53</sup> ‘Lockdown’ first employed in early 2020 in Wuhan, China, is the label often given to the bundle of containment and mitigation measures promoted or imposed by public authorities, although the specific measures may vary greatly between countries. In China, lockdown was very strictly applied and enforced. It clearly had an impact, resulting in total interruption of transmission locally.<sup>54 55</sup>

This list or catalogue of measures is quite comprehensive; it includes all measures that at first sight seem to reduce transmission opportunities for a respiratory virus. However, knowledge is lacking about the effectiveness of each measure in different contexts. As a global health



**Table 5** Measures recommended by the WHO for preventing transmission and slowing down the COVID-19 epidemic, 2020

Implementation level	Intervention
Individual	<ul style="list-style-type: none"> <li>▶ Hand hygiene: handwashing or use of hydroalcoholic solution.</li> <li>▶ Physical distancing.</li> <li>▶ Respiratory etiquette.</li> <li>▶ Masks for infected and symptomatic individuals.</li> </ul>
Community	<ul style="list-style-type: none"> <li>▶ Mass masking with surgical and/or homemade masks by everyone in public spaces.</li> <li>▶ Avoid crowding and mass gatherings.</li> </ul>
Public authorities	<ul style="list-style-type: none"> <li>▶ Tracing, testing and isolating cases and providing them with appropriate care.</li> <li>▶ Tracking, quarantining and monitoring of asymptomatic contacts.</li> <li>▶ Protecting health workers and vulnerable groups.</li> <li>▶ Environmental cleaning and sanitising.</li> <li>▶ Closures of schools, places of worship, sporting events, non-essential shops.</li> <li>▶ Workplace closures and other measures: work from home where possible and/or reduction in workforce capacity.</li> <li>▶ Public transportation closures.</li> <li>▶ Stay-at-home orders.</li> <li>▶ Limiting national and international travel.</li> <li>▶ Maintaining essential health services.</li> <li>▶ Ensuring continuity of essential social and economic functions and services.</li> </ul>

agency, the WHO recommends a ‘generic catalogue’ of measures from which all countries can select an appropriate mix at any one time depending on the phase of the epidemic, categorised in four transmission scenarios (no cases, first cases, first clusters, and community transmission).<sup>52</sup> However, under pressure to act and with little time to consider variable options, public authorities often adopted as ‘blueprint’ with limited consideration for the socioeconomic context.<sup>53 56</sup>

The initial lockdown in China thus much inspired the collective strategies elsewhere. This has been referred to as ‘global mimicry’,<sup>57</sup>: the response is somehow partly ‘copy/paste’ from measures observed previously (strong path dependency).

Some epidemiologists in Northern Europe (including the UK,<sup>58</sup> Sweden<sup>59</sup> and the Netherlands<sup>60</sup>) pleaded against strict containment measures and proposed that building up herd immunity against SARS-CoV-2 might be wiser. Towards early April 2020, it became increasingly clear that reaching herd immunity in the short term was illusive. Most countries thus backed off from the herd immunity approach to combating COVID-19 and implemented lockdowns.<sup>61</sup> The intensity of the lockdowns has been variable, ranging from very strict (‘Chinese, Wuhan style’), over intermediary (‘French/Italian/New York City style’ and ‘Hong Kong style’), to relaxed (‘Swedish style’), or piecemeal.

The effectiveness of lockdowns largely depends on at what stage of the epidemic they are started, and how intensively they are applied. This is quite variable across countries, depending on the understanding and motivation of the population and their perceived risk (‘willingness to adhere’), on the trust they have in government advice (‘willingness to comply’), and on the degree of enforcement by public authorities. The feasibility for different population groups to follow these measures

depends largely on their socioeconomic and living conditions. It is obviously more difficult for people living in crowded shacks in urban slums to practise physical distancing measures and strict hand hygiene when water is scarce than for people living in wealthier parts of a city.

#### Collateral effects of the response

Every intervention against the COVID-19 epidemic has a certain degree of effect and comes at a cost with collateral effects. Each collective strategy (1) has intended and unintended consequences (some are more or less desirable); (2) is more or less feasible and/or acceptable in a given context and for certain subgroups in that society; (3) has a cost, not only in financial terms but in many other ways, such as restrictions on movement and behaviour, stress, uncertainty and others. These costs are more or less acceptable, depending on the perception of the risk and many societal factors; (4) can be implemented with more or less intensity; and (5) can be enforced more or less vigorously.

The balance between benefit and cost is crucial in judging whether measures are appropriate, which is very context specific. Furthermore, benefits and costs are also related to the positionality from which they are analysed: benefits for whom and costs borne by whom? More wealthy societies with strong social safety nets can afford increased temporary unemployment. This is much more consequential in poorer countries, where large proportions of the population live precarious lives and where public authorities cannot implement generous mitigation measures at scale.

The adherence to hygiene and distancing measures depends not only on living conditions but also on risk perception and cultural norms. Mass masking has been readily accepted in some Asian countries, where it was already broadly practised even before the COVID-19



epidemic. It remains more controversial in Western societies, some of which even have legal bans on veiling in public places.

Lockdowns are unprecedented and have triggered intensive public debate. Not surprisingly, the impact of lighter lockdowns on the transmission is much less impressive; they decrease transmission but do not stop it. Quite rapidly, the justification for lockdowns shifted from stopping transmission to ‘flattening the curve’. Also, once a lockdown is started, rationalised, explained and enforced, it is difficult to decide when to stop it. Exit scenarios, usually some form of progressive relaxation, are implemented with the knowledge that transmission will be facilitated again.<sup>62</sup>

## KNOWN AND UNKNOWN ABOUT SARS-COV-2/COVID-19

### What we already know

The available information on SARS-CoV-2 and the spectrum of COVID-19 disease is summarised in [tables 6 and 7](#). It is increasingly becoming clear that most transmission happens indoors and that superspreading events trigger intensive dissemination.

The virology and immunology of SARS-CoV-2/COVID-19 are being studied intensively. This is critical not only to understand what will potentially happen in future waves but also for the development of a vaccine. Some scientists and companies are very upbeat about the possibility of producing a vaccine in record time. Having a vaccine is one thing, but how effective it is, is quite another. As acquired immunity after a natural infection is probably not very robust ([table 6](#)), it will also be challenging to trigger robust immunity with a vaccine, but perhaps it is not impossible. Many questions remain, some of which are summarised in [table 8](#).

Regarding the severity of COVID-19, initial fears of very high mortality have also lessened. It has progressively become clear that many infections remain asymptomatic, that severe disease is rare in children and young adults, and that mortality is heavily concentrated in the very old and those with comorbidities. [Table 7](#) summarises a fuller overview of the present state of knowledge regarding COVID-19.

With COVID-19 epidemics unfolding rapidly, several of the variables in the transmission of SARS-CoV-2 and the disease spectrum of COVID-19 could be quantified. This allows for mathematical modelling. Several models have been quickly developed, leading to predictions of the speed of transmission and the burden of COVID-19 ([box 2](#)). Predictive models developed by the Imperial College<sup>63</sup>; the Center for Disease Dynamics, Economics & Policy and Johns Hopkins University<sup>28</sup>; the Institute for Health Metrics and Evaluation<sup>64</sup>; Harvard University<sup>65</sup>; and the WHO,<sup>66</sup> including an ‘African model’,<sup>67</sup> are a few that are influencing containment strategies around the world.

### Critical unknowns and uncertainties

Although the COVID-19 pandemic triggered unprecedented research efforts globally, with over 30 000 scientific papers published between January and April 2020, there are still critical unknowns and many uncertainties.

[Tables 6 and 7](#) summarise many of the knowns, but their relative importance or weight is not clear. For instance, the virus can spread via droplets, hands, aerosols, fomites and possibly through the environment. However, the relative importance of these in various contexts is much less clear. These factors undoubtedly vary between settings, whether in hospitals, in elderly homes, or at mass events. The weight of the variables also probably differs between the seeding and initial spread in a community and the spread when it suddenly amplifies and intensifies. The importance of each variable probably also depends on climatic conditions, not only outdoors, but also on microclimates indoors, influenced by ventilation and air conditioning and built environments.

We summarise the critical unknowns in [table 9](#) along some elements to consider in addressing the unknowns and thoughts on their importance.

Uncertainty remains, leading to controversy and directly influencing the choice of containment measures. Controversy continues regarding when and where lockdown or more selective measures are equally effective with lower societal effects.

### Relationship between the dose of the initial infectious inoculum, transmission dynamics and severity of the COVID-19 disease

New evidence is being discovered rapidly. Some evidence comes from field observations and ecological studies; other evidence results from scientific experiments or observations in the laboratory and the clinic. Sense-making by combining insights from different observations and through the lens of various disciplines can lead to hypotheses that can be tested and verified or refuted. One such hypothesis is that there is a relationship between the dose of virus in the infectious inoculum and the severity of COVID-19 disease. Several intriguing observations in the current pandemic could be (partially) explained by such a relationship. We develop this hypothesis in [box 3](#), as an example of possible further research, to create new insight which may influence control strategies.

This viral inoculum theory is consistent with many observations from the early stages of the COVID-19 pandemic, but it is not easy to test scientifically.

### POTENTIAL FUTURE SCENARIOS OF COVID-19

As COVID-19 is a new disease, we should make a distinction between (1) the current 2019–2020 ‘virgin soil pandemic’ caused by SARS-CoV-2, specifically in how it will further spread around the globe in the first wave, and (2) the potential future transmission in subsequent waves. In some countries, transmission will continue at lower levels. In other countries, such as China, the virus

**Table 6** Knowns, uncertainties and unknowns about severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), as of May 2020

Factor	Available information
Origin of SARS-CoV-2	<ul style="list-style-type: none"> <li>▶ Most probably from bats via intermediate animal hosts to index case.<sup>47 104</sup> All subsequent cases resulted from human-to-human transmission.</li> </ul>
Transmission	<ul style="list-style-type: none"> <li>▶ Mainly through respiratory droplets from infected persons<sup>105</sup>; by hands, after contamination at nose, mouth or eyes; also through air on exposure to sneezing or coughing from an infected person at close distance.</li> <li>▶ Through aerosols, while singing/talking loudly in congregations, groups, parties, karaoke, and so on, especially in poorly ventilated spaces.<sup>18 106</sup></li> <li>▶ Through fomites.<sup>107</sup></li> <li>▶ Possibly via faecal–oral route<sup>108 109</sup>; detection in sewage.<sup>110–112</sup></li> <li>▶ Related to peak in upper respiratory tract viral load prior to symptom onset in presymptomatic (paucisymptomatic) persons.<sup>106 113 114</sup></li> <li>▶ Transmission dynamics in asymptomatic persons not fully elucidated although viral shedding occurs.<sup>115</sup></li> </ul>
Influence of climate and/or air pollution on transmission	<ul style="list-style-type: none"> <li>▶ Influence of climate on the capacity of the virus to survive outside human body (in air, in droplets, on surfaces, etc.) and to spread has been speculative.</li> <li>▶ May spread more readily in milder/colder climate<sup>116 117</sup>; although variability of the reproductive number could not be explained by temperature or humidity.<sup>118</sup></li> <li>▶ Existing levels of air pollution may play a role; air pollutants, such as particulate matter, nitrogen dioxide and carbon monoxide, are likely a factor facilitating longevity of virus particles.<sup>119</sup></li> <li>▶ Elevated exposure to common particulate matter can alter host immunity to respiratory viral infections.<sup>119</sup></li> </ul>
Immunity—protective antibodies	<ul style="list-style-type: none"> <li>▶ IgM and IgA antibody response 5–10 days after onset of symptoms, does not depend on clinical severity, correlates with virus neutralisation; IgG is observed ~14 days after onset of symptoms,<sup>93 120</sup> may or may not correspond to protective immunity. Whether antibody response is long lasting has remained unclear.</li> <li>▶ Rechallenge in rhesus macaques showed immunity post primary infection.<sup>121</sup> How protective immunity after first infection is against subsequent infection with an identical or mutated strain has been uncertain.</li> <li>▶ Incidental reports showed recovered persons positive by real-time PCR,<sup>122 123</sup> later attributed to testing errors.</li> </ul>
Seroprevalence to SARS-CoV-2	<ul style="list-style-type: none"> <li>▶ Reported estimates for seroprevalence range between 0.4% and 59.3%<sup>124</sup>; differences in timing of the serosurvey, the use of assay kits with varying sensitivity/specificity, and different methods for detection may contribute to this large variation.<sup>125</sup></li> <li>▶ Seemingly high seroprevalence may be due to cross-reactive epitopes between SARS-CoV-2 and other HCoVs.<sup>126 127</sup></li> <li>▶ Whether seroprevalence implies immune protection is unclear, yet, some countries have considered use of ‘immunity passports’.<sup>128</sup></li> <li>▶ For herd immunity to be effectively achieved, an estimated seroprevalence of 60% of the population will be required.<sup>37</sup> Other studies estimate between 5.66% and 85% seroprevalence in different countries.<sup>129–131</sup></li> </ul>
Rate of variability/mutation in SARS-CoV-2	<ul style="list-style-type: none"> <li>▶ Mutation rate: ~10<sup>-3</sup> substitutions per year per site<sup>132 133</sup>; 13 mutation sites have been identified as of May 2020, suggesting selective mutations.<sup>134</sup></li> <li>▶ The low mutation rate suggests that a vaccine would be a single vaccine rather than a new vaccine every year like the influenza vaccine.<sup>135</sup></li> <li>▶ Ten different circulating clades (nextstrain.org; www.gisaid.org),<sup>136</sup> as of May 2020.</li> </ul>

HCoV, human coronaviruses.

may have been eliminated but can be reintroduced in identical or mutated form.

For the current first wave, using influenza and the common cold as reasonable comparisons, it is possible that the major epidemics, as witnessed in Wuhan, northern Italy, or New York, will typically occur in temperate climates in the winter season. Some predict that such epidemics will last between 8 and 10 weeks (but this is just a plausible and reasonable comparison

in analogy with seasonal influenza). It is possible that in hotter climates the transmission may become continuous, year round at lower levels. It is increasingly clear that hot climate does not exclude superspreading events as observed in Guayaquil, Ecuador and in various cities in Brazil. Ventilation, air-conditioning and crowded places may still create favourable environments for intensive transmission. It is also quite possible that the more difficult spread of SARS-CoV-2 in such climates may, in certain

**Table 7** Knowns, uncertainties and unknowns about COVID-19, as of May 2020

Factor	Available information
Disease spectrum	<ul style="list-style-type: none"> <li>▶ Many different estimates:</li> <li>▶ Initially, it was estimated that among infected, 30% remained asymptomatic, 55%–80% had mild/moderate disease, 10%–14% had severe disease, and 5%–6% became critically ill.<sup>73 90–92</sup></li> <li>▶ Very variable estimates for remaining totally asymptomatic (estimated 5%–80%<sup>93–96</sup>).</li> <li>▶ What determines that an infection remains asymptomatic?</li> <li>▶ Quasi-absence of disease in children: why?</li> </ul>
Case fatality rate (CFR)	<ul style="list-style-type: none"> <li>▶ Initial estimates CFR: 2%–3%; comparisons: influenza 0.1%; common cold: 0%; SARS: 9%–10%; MERS: 30%.<sup>97</sup></li> <li>▶ Calculated infection fatality rates (cIFR) and calculated CFR (cCFR) on the Princess Diamond were 1.3% and 2.6%, respectively (for all ages combined), and projected cIFR and cCFR for China were between 0.6%–0.66% and 1.2%–1.38%, respectively.<sup>90 98</sup> In Gangelt, Germany: cCFR of 0.37%.<sup>99</sup></li> <li>▶ CFR is influenced significantly by age; male sex; comorbidities; body mass index and/or fitness; and adequacy of supportive treatment, mainly oxygen therapy.<sup>100 101</sup> Also, as in certain other viral diseases such as measles, possibly influenced by the dose of virus in initial infectious inoculum (see <a href="#">Box 3</a>).</li> <li>▶ CFR and IFR vary depending on population distribution. March 2020, estimated IFR UK: 0.9%, Italy: 1.14%–6.22% initial estimate which increased to 9.26%, Spain: 6.16%, France: 4.21%.<sup>102 103</sup></li> </ul>
Medication/treatment options	<ul style="list-style-type: none"> <li>▶ Treatments being used: hydroxychloroquine and chloroquine, remdesivir, azithromycin, convalescent plasma and other antivirals.</li> <li>▶ At the time of writing (May 2020), no proven effective treatment. Many clinical trials ongoing.</li> <li>▶ Oxygen therapy most essential component of case management. Low oxygen saturation a dominant feature of COVID-19, curiously dissociated from dyspnoea. In most cases, oxygen can be administered through a facial mask. In very advanced disease, oxygen administered through artificial ventilation, requiring sophisticated equipment and highly skilled personnel.</li> </ul>

communities, be compensated for by human factors such as higher population density, closer human contacts and lesser hygiene (as, for instance, exist in urban slums in mega cities in low income countries). How all this plays out in sub-Saharan Africa, in its slums and remote areas, is still largely unknown. With SARS-CoV-2, transmission scenarios are mainly based on mathematical models despite their serious limitations ([box 2](#)).

As the virus continues to circulate, it will progressively be less of a ‘new disease’ during subsequent waves. The

immunity caused by the first epidemic will influence how the virus spreads and causes disease. Whether later waves will become progressively milder or worse, as observed in the 1918–19 Spanish influenza, is a matter of intense speculation. Both views seem plausible and the two are not necessarily mutually exclusive. Indeed, immunity should be defined on two levels: individual immunity and herd immunity. Individual immunity will dictate how mild or severe the disease will be in subsequent infections. Herd immunity could be defined in different communities/regions/

**Table 8** Questions and considerations in case a COVID-19 vaccine is developed

Question	Considerations
If a vaccine is developed?	<ul style="list-style-type: none"> <li>▶ What type of vaccine will it be (live/non-live, classic killed, DNA, or recombinant)?</li> <li>▶ Will it need special manufacture and transport conditions (such as cold chain)?</li> <li>▶ How robust will be vaccine-acquired immunity? After how many doses?</li> <li>▶ How protective will it be against infection?</li> <li>▶ For how long will vaccine-acquired immunity last? And hence: how often will the vaccine have to be administered? Only once? Or yearly?</li> <li>▶ Will there be any adverse effects?</li> </ul>
Acquired immunity is not very strong; hence, what is the consequence regarding herd immunity?	<ul style="list-style-type: none"> <li>▶ To achieve herd immunity, how efficient will the vaccine need to be?</li> <li>▶ What proportion of the population (critical population) will need to be vaccinated?</li> <li>▶ How long will it take to effectively vaccinate the critical population?</li> <li>▶ Will vaccination be acceptable in the population? Or will vaccine hesitancy reduce uptake?</li> </ul>
What are the socioeconomic implications?	<ul style="list-style-type: none"> <li>▶ Which countries will get the vaccine first (implications for LICs/LMICs)?</li> <li>▶ How expensive will the vaccine be?</li> <li>▶ Will vaccination be made mandatory, especially for international travel?</li> </ul>

LICs/LMICs, low and lower middle income countries.

**Table 9** Some critical unknowns in SARS-CoV-2 transmission

Critical unknowns	Considerations
Which transmission patterns will occur and will human-to-human transmission continue permanently?	<ul style="list-style-type: none"> <li>▶ Seasonal transmission in temperate climate?</li> <li>▶ Continuous tides, with ups and downs?</li> <li>▶ The experience from China and some other countries showed that ‘local elimination’ is possible but risk of reintroduction remains.</li> <li>▶ Increasingly unlikely that elimination everywhere is possible.</li> </ul>
This will strongly depend on:	
How strong will the acquired immunity after a first infection with SARS-CoV-2 be and how long will it last?	<ul style="list-style-type: none"> <li>▶ Evidence of acquired immunity against subsequent infections has been limited.</li> <li>▶ Measurable antibodies have been observed in most persons who have recovered from COVID-19,<sup>131</sup> and research in animal models has suggested limited possibility of reinfection.<sup>121</sup></li> <li>▶ It is still unclear as to how robust the immunity is and how long it will last.</li> <li>▶ Debate on use, practicality and ethics of ‘immunity passports’ for those recovered from COVID-19 has been ongoing.<sup>128 137</sup></li> </ul>
How stable is the virus (mutation) and do the different clades seen worldwide have any effect on the transmission potential/severity of the disease?	<ul style="list-style-type: none"> <li>▶ If the virus mutates quickly and different strains develop, then antibody-dependent enhancement might be an important risk, as in dengue with its four different strains. If so, then in subsequent waves progressively more severe cases could occur.</li> <li>▶ This has been reported for the Spanish influenza, where the second and third waves were characterised by a more severe disease pattern.<sup>36 84</sup></li> </ul>
What is the role of children in transmission?	<ul style="list-style-type: none"> <li>▶ Children have quasi-universally presented less severe disease. However, their susceptibility to infection remains unclear, with large heterogeneity reported between studies.<sup>138 139</sup></li> <li>▶ Their role in transmission has remained unclear, but evidence points to a more modest role in transmission than adults.</li> </ul>
How significant are asymptomatic carriers in transmission?	<ul style="list-style-type: none"> <li>▶ There have been several reports of asymptomatic transmission<sup>140 141</sup> and estimates based on modelling.<sup>114</sup></li> <li>▶ Increasing consensus that asymptomatic carriers play an important role in transmission.</li> </ul>

countries that, in theory, could be fenced off, allowing only limited interaction with other areas, impacting the spread of the virus to more vulnerable populations.

The future is unknown, but we can think of likely futures and critical elements therein.

Some obvious critical elements are:

- ▶ Will there be an effective vaccine? How soon? How effective? How available at scale? How acceptable?
- ▶ Will there be an effective treatment? How soon? How effective? How available at scale?

**CONCLUSION**

The current first wave is unfolding in the absence of effective biomedical tools (no vaccine, no effective antiviral or immune-modulating medicine, only supportive treatment such as oxygen therapy). This comes close to what can be called a ‘natural evolution’ of the COVID-19 pandemic, mostly modified by the containment measures deployed (table 5) and the effect of supportive treatment.

Progressively, we can learn more about the direct health effects of COVID-19 (morbidity and mortality), about appropriate individual and collective measures,<sup>68</sup> the various degrees of societal disruption and the collateral effects on other essential health services (eg, reluctance to use health services for other health problems,

because of ‘corona fear’). Our growing knowledge may enable us to progressively improve our response.

Learning from the variety of ways the COVID-19 epidemic is unfolding across the globe provides important ‘ecological evidence’ and creates insights into its epidemiology and impacts. Until now, the insights gained on COVID-19 have been largely dominated by the COVID-19 epidemics in the Global North. More understanding of lived experiences of people in a variety of contexts, where the epidemic is spreading more slowly and with different impacts, is necessary to get a full global picture and allow learning from this variety. This is an important missing piece of the COVID-19 puzzle.

BMJ Global Health and Emerging Voices for Global Health have launched a call (<https://blogs.bmj.com/bmjgh/2020/05/26/from-models-to-narratives-and-back-a-call-for-on-the-ground-analyses-of-covid-19-spread-and-response-in-africa/>) for such on-the-ground narratives and analyses of the spread of and response to COVID-19, local narratives and analyses that will hopefully help to further enrich our understanding of how and why the COVID-19 pandemic continues to unfold in multiple local epidemics along diverse trajectories around the globe.



### Box 3 Relationship between the dose of the initial infectious inoculum, transmission dynamics and severity of the COVID-19 disease

#### Hypothesis:

The dose of the virus in the initial inoculum may be a missing link between the variation observed in the transmission dynamics and the spectrum of the COVID-19 disease. It is plausible that:

- ▶ Viral dose in inoculum is related to severity of disease.
- ▶ Severity of disease is related to viral shedding and transmission potential.

This hypothesis plays out potentially at three levels:

- ▶ At individual level: a person infected with a small dose of viral inoculum will on average develop milder disease than a person infected with a high viral inoculum and vice versa.
- ▶ At cluster level: a person with asymptomatic infection or mild disease will on average spread lower doses of virus in droplets and aerosols and is less likely to transmit disease; when the person transmits, the newly infected person is more likely to have milder disease than if infected by a severely ill person, who spreads on an average higher doses of virus. This causes clusters and chains of milder cases or of more severe cases.
- ▶ At community level: in certain contexts, such as dense urban centres in moderate climates during the season when people live mostly indoors, the potential for intensive transmission and explosive outbreaks is high, especially during indoor superspreading events. In other contexts, such as in rural areas or in regions with hot and humid climate where people live mostly outdoors, intensive transmission and explosive outbreaks are less likely.

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#### REFERENCES

- 1 Lu H, Stratton CW, Tang Yi-Wei. Outbreak of pneumonia of unknown etiology in Wuhan, China: the mystery and the miracle. *J Med Virol* 2020;92:401–2.
- 2 Xinhuanet. New-type coronavirus causes pneumonia in Wuhan: expert; 9 January 2020, 2020. Available: [http://www.xinhuanet.com/english/2020-01/09/c\\_138690570.htm](http://www.xinhuanet.com/english/2020-01/09/c_138690570.htm) [Accessed 27 April 2020].
- 3 Zhu N, Zhang D, Wang W, *et al*. A novel coronavirus from patients with pneumonia in China, 2019. *N Engl J Med Overseas Ed* 2020;382:727–33.
- 4 Coronaviridae Study Group of the International Committee on Taxonomy of Viruses. The species severe acute respiratory syndrome-related coronavirus: classifying 2019-nCoV and naming it SARS-CoV-2. *Nat Microbiol* 2020;5:536–544.
- 5 Xu Z, Shi L, Wang Y, *et al*. Pathological findings of COVID-19 associated with acute respiratory distress syndrome. *Lancet Respir Med* 2020;8:420–2.
- 6 Ding Q, Lu P, Fan Y, *et al*. The clinical characteristics of pneumonia patients coinfecting with 2019 novel coronavirus and influenza virus in Wuhan, China. *J Med Virol* 2020;382. doi:10.1002/jmv.25781. [Epub ahead of print: 20 Mar 2020].

- 7 Wang D, Hu B, Hu C, *et al.* Clinical characteristics of 138 hospitalized patients with 2019 novel Coronavirus–Infected pneumonia in Wuhan, China. *JAMA* 2020;323:1061.
- 8 Li Q, Guan X, Wu P, *et al.* Early transmission dynamics in Wuhan, China, of novel Coronavirus–Infected pneumonia. *N Engl J Med Overseas Ed* 2020;382:1199–207.
- 9 World Health Organization. Naming the coronavirus disease (COVID-19) and the virus that causes it, 2020. Available: [https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-\(covid-2019\)-and-the-virus-that-causes-it](https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-guidance/naming-the-coronavirus-disease-(covid-2019)-and-the-virus-that-causes-it) [Accessed 17 Apr 2020].
- 10 World Health Organization. WHO Director-General's opening remarks at the media briefing on COVID-19 - 11 March 2020, 2020. Available: <https://www.who.int/dg/speeches/detail/who-director-general-s-opening-remarks-at-the-media-briefing-on-covid-19-11-march-2020> [Accessed 17 Apr 2020].
- 11 Lai C-C, Shih T-P, Ko W-C, *et al.* Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): the epidemic and the challenges. *Int J Antimicrob Agents* 2020;55:105924.
- 12 Ji L-N, Chao S, Wang Y-J, *et al.* Clinical features of pediatric patients with COVID-19: a report of two family cluster cases. *World J Pediatr* 2020;16:267–270.
- 13 Qian G, Yang N, Ma AHY, *et al.* A COVID-19 transmission within a family cluster by presymptomatic infectors in China. *Clin Infect Dis* 2020:ciaa316.
- 14 World Health Organization. Report of the WHO–China joint mission on coronavirus disease 2019 (COVID-19), 2020. Available: <https://www.who.int/docs/default-source/coronaviruse/who-china-joint-mission-on-covid-19-final-report.pdf> [Accessed 14 May 2020].
- 15 Danis K, Epaulard O, Bénet T, *et al.* Cluster of coronavirus disease 2019 (Covid-19) in the French Alps, 2020. *Clin Infect Dis* 2020:ciaa424.
- 16 Böhmer MM, Buchholz U, Corman VM, *et al.* Investigation of a COVID-19 outbreak in Germany resulting from a single travel-associated primary case: a case series. *Lancet Infect Dis* 2020.
- 17 Chan JF-W, Yuan S, Kok K-H, *et al.* A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster. *The Lancet* 2020;395:514–23.
- 18 Hamner L, Dubbel P, Capron I, *et al.* High SARS-CoV-2 attack rate following exposure at a Choir practice — Skagit County, Washington, March 2020. *MMWR Morb Mortal Wkly Rep* 2020;69:606–10.
- 19 Endo A, Abbott S, Kucharski AJ, *et al.* Estimating the overdispersion in COVID-19 transmission using outbreak sizes outside China. *Wellcome Open Res* 2020;5:67.
- 20 Kupferschmidt K. Why do some COVID-19 patients infect many others, whereas most don't spread the virus at all? *Science* 2020.
- 21 The Guardian. The cluster effect: how social gatherings were rocket fuel for coronavirus, 2020. Available: <https://www.theguardian.com/world/2020/apr/09/the-cluster-effect-how-social-gatherings-were-rocket-fuel-for-coronavirus#maincontent> [Accessed 1 May 2020].
- 22 Hu K, Zhao Y, Wang M, *et al.* Identification of a super-spreading chain of transmission associated with COVID-19. *medRxiv* 2020.
- 23 Wong BCK, Lee N, Li Y, *et al.* Possible role of aerosol transmission in a hospital outbreak of influenza. *Clin Infect Dis* 2010;51:1176–83.
- 24 Liu Y, Ning Z, Chen Y, *et al.* Aerodynamic analysis of SARS-CoV-2 in two Wuhan hospitals. *Nature* 2020;582:557–60.
- 25 Viens AM, Eyawo O. COVID-19: the rude awakening for the political elite in low- and middle-income countries. *BMJ Glob Health* 2020;5:e002807.
- 26 Wilson ME, Chen LH. Travellers give wings to novel coronavirus (2019-nCoV). *J Travel Med* 2020;27.
- 27 ourworldindata.org. Total confirmed COVID-19 cases per million vs GDP per capita, 2020. Available: <https://ourworldindata.org/grapher/total-confirmed-cases-of-covid-19-per-million-people-vs-gdp-per-capita> [Accessed 1 Jul 2020].
- 28 The Center For Disease Dynamics Economics & Policy. Modeling the spread and prevention of COVID-19, 2020. Available: <https://cdddep.org/covid-19/> [Accessed 15 May 2020].
- 29 Coltart CEM, Lindsey B, Ghinai I, *et al.* The Ebola outbreak, 2013–2016: old lessons for new epidemics. *Philos Trans R Soc Lond B Biol Sci* 2017;372:372.
- 30 Lam WK, Zhong NS, Tan WC. Overview on SARS in Asia and the world. *Respirology* 2003;8 Suppl:S2–5.
- 31 Furuse Y, Suzuki A, Oshitani H. Origin of measles virus: divergence from rinderpest virus between the 11th and 12th centuries. *Viral J* 2010;7:52.
- 32 McNeill WH. *Plagues and people*. New York: Anchor Press, 1976.
- 33 Hirve S, Newman LP, Paget J, *et al.* Influenza Seasonality in the Tropics and Subtropics - When to Vaccinate? *PLoS One* 2016;11:e0153003.
- 34 Young BE, Chen M. Influenza in temperate and tropical Asia: a review of epidemiology and vaccinology. *Hum Vaccin Immunother* 2020;1:1–9.
- 35 Leclerc QJ, Fuller NM, Knight LE, *et al.* What settings have been linked to SARS-CoV-2 transmission clusters? *Wellcome Open Res* 2020;5:83.
- 36 Taubenberger JK. The origin and virulence of the 1918 "Spanish" influenza virus. *Proc Am Philos Soc* 2006;150:86–112.
- 37 Altmann DM, Douek DC, Boynton RJ. What policy makers need to know about COVID-19 protective immunity. *Lancet* 2020;395:1527–9.
- 38 Panum PL. *Observations made during the epidemic of measles on the Faroe Islands in the year 1846*. New York: Delta Omega Society, 1940.
- 39 Rhodes CJ, Anderson RM. A scaling analysis of measles epidemics in a small population. *Philos Trans R Soc Lond B Biol Sci* 1996;351:1679–88.
- 40 Adels BR, FRANCIS JE, Gajdusek DC. Measles in Australasian indigenes. *Am J Dis Child* 1962;103:255–61.
- 41 Aaby Pet al. Epidemics among Amerindians and Inuits. A preliminary interpretation. In: Brøsted J, Dahl J, Gray A, *et al.*, eds. *Native power*. Bergen: Universitetsforlaget, 1985: 329–39.
- 42 Diamond J. *Chapter 11: lethal gift of livestock. guns, germs, and steel: the fates of human societies*. New York: W. W. Norton, 1997.
- 43 Krugman S, Giles JP, Friedmann H, *et al.* Studies on immunity to measles. *J Pediatr* 1965;66:471–88.
- 44 van den Driessche P, Watmough J. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math Biosci* 2002;180:29–48.
- 45 Fine P, Eames K, Heymann DL. "Herd Immunity": A Rough Guide. *Clinical Infectious Diseases* 2011;52:911–6.
- 46 Loutan L, Paillard S. Measles in a West African nomadic community. *Bull World Health Organ* 1992;70:741–4.
- 47 Z-W Y, Yuan S, Yuen K-S, *et al.* Zoonotic origins of human coronaviruses. *Int J Biol Sci* 2020;16:1686–97.
- 48 Su S, Wong G, Shi W, *et al.* Epidemiology, genetic recombination, and pathogenesis of coronaviruses. *Trends Microbiol* 2016;24:490–502.
- 49 Burrell C, Howard C, Murphy F. Chapter 31: Coronaviruses. In: *Fenner and white's medical virology*. 442. 5th Edition. Amsterdam: Elsevier, 2017.
- 50 Zarocostas J. How to fight an infodemic. *The Lancet* 2020;395:676.
- 51 World Health Organization. Responding to community spread of COVID-19: interim guidance, 7 March 2020, 2020. Available: [https://apps.who.int/iris/bitstream/handle/10665/331421/WHO-COVID-19-Community\\_Transmission-2020.1-eng.pdf](https://apps.who.int/iris/bitstream/handle/10665/331421/WHO-COVID-19-Community_Transmission-2020.1-eng.pdf) [Accessed 15 Apr 2020].
- 52 World Health Organization. Critical preparedness, readiness and response actions for COVID-19: interim guidance, 22 March 2020, 2020. Available: [https://apps.who.int/iris/bitstream/handle/10665/331511/Critical%20preparedness%20readiness%20and%20response%20actions%20COVID-10%202020-03-22\\_FINAL-eng.pdf?sequence=1&isAllowed=y](https://apps.who.int/iris/bitstream/handle/10665/331511/Critical%20preparedness%20readiness%20and%20response%20actions%20COVID-10%202020-03-22_FINAL-eng.pdf?sequence=1&isAllowed=y) [Accessed 15 Apr 2020].
- 53 World Health Organization. 2019 novel Coronavirus (2019-nCoV): strategic preparedness and response plan, 2020. Available: <https://www.who.int/publications-detail/strategic-preparedness-and-response-plan-for-the-new-coronavirus> [Accessed 15 May 2020].
- 54 Lai S, Ruktanonchai NW, Zhou L, *et al.* Effect of non-pharmaceutical interventions to contain COVID-19 in China. *Nature* 2020;41. doi:10.1038/s41586-020-2293-x. [Epub ahead of print: 04 May 2020].
- 55 Kucharski AJ, Russell TW, Diamond C, *et al.* Early dynamics of transmission and control of COVID-19: a mathematical modelling study. *Lancet Infect Dis* 2020;20:553–8.
- 56 Bedford J, Enria D, Giesecke J, *et al.* COVID-19: towards controlling of a pandemic. *Lancet* 2020;395:1015–8.
- 57 Piper K. The devastating consequences of coronavirus lockdowns in poor countries. *Vox* 2020.
- 58 Twitter. BBC Radio 4 Today (@BBCr4today) [Tweet]. Sir Patrick Vallance, the govt chief scientific adviser, says the thinking behind current approach to #coronavirus is to try and "reduce the peak" and to build up a "degree of herd immunity so that more people are immune to the disease", 2020. Available: <https://twitter.com/BBCr4today/status/1238390547783528448> [Accessed 15 May 2020].
- 59 Pancevski B. Inside Sweden's Radically Different Approach to the Coronavirus - No lockdown, no quarantines, just voluntary advice and a big dose of hope. *The Wall Street Journal* 2020.



- 60 Times NL. Coronavirus: Full Text of Prime Minister Rutte's National Address in English, 2020. Available: <https://nltimes.nl/2020/03/16/coronavirus-full-text-prime-minister-ruttes-national-address-english> [Accessed 16 Mar 2020].
- 61 National Geographic. The U.K. backed off on herd immunity. To beat COVID-19, we'll ultimately need it. National Geographic 2020 20 March, 2020. Available: <https://www.nationalgeographic.com/science/2020/03/uk-backed-off-on-herd-immunity-to-beat-coronavirus-we-need-it/> [Accessed 30 May 2020].
- 62 Gutiérrez P, Kirk A. Revealed: data shows 10 countries risking coronavirus second wave as lockdown relaxed, 2020. Available: <https://www.theguardian.com/world/ng-interactive/2020/jun/25/revealed-data-shows-10-countries-risking-coronavirus-second-wave-as-lockdown-relaxed> [Accessed 1 Jul 2020].
- 63 Ferguson NM, Laydon D, Nedjati-Gilani G, et al. Report 9: impact of non-pharmaceutical interventions (NPIs) to reduce COVID-19 mortality and healthcare demand. 2020 Imperial College London 16 March, 2020. Available: <https://spiral.imperial.ac.uk:8443/bitstream/10044/1/77482/14/2020-03-16-COVID19-Report-9.pdf> [Accessed 15 May 2020].
- 64 Institute for Health Metrics and Evaluation. COVID-19 projections, 2020. Available: <https://covid19.healthdata.org/united-states-of-america> [Accessed 20 May 2020].
- 65 Kissler SM, Tedijanto C, Goldstein E, et al. Projecting the transmission dynamics of SARS-CoV-2 through the postpandemic period. *Science* 2020;368:860–8.
- 66 World Health Organization. Novel coronavirus (COVID-19), 2020. Bull World Health Organ. Available: [https://www.who.int/bulletin/online\\_first/COVID-19/en/](https://www.who.int/bulletin/online_first/COVID-19/en/) [Accessed 30 May 2020].
- 67 Cabore JW, Karamagi HC, Kipruto H, et al. The potential effects of widespread community transmission of SARS-CoV-2 infection in the world Health organization African region: a predictive model. *BMJ Glob Health* 2020;5:e002647.
- 68 Van Damme W, Van Lerberghe W. Epidemics and fear. *Trop Med Int Health* 2000;5:511–4.
- 69 Fischetti M, Krzywinski M. Virus mutations reveal how COVID-19 really spread. *Sci Am* 2020.
- 70 Deslandes A, Berti V, Tandjauji-Lambotte Y, et al. SARS-CoV-2 was already spreading in France in late December 2019. *Int J Antimicrob Agents* 2020;55:106006.
- 71 World Health Organization. Coronavirus disease 2019 (COVID-19) - Situation Report – 12; 1 February 2020, 2020. Available: [https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200201-sitrep-12-ncov.pdf?sfvrsn=273c5d35\\_2](https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200201-sitrep-12-ncov.pdf?sfvrsn=273c5d35_2) [Accessed 7 Apr 2020].
- 72 Hamblin J. A Historic Quarantine: China's attempt to curb a viral outbreak is a radical experiment in authoritarian medicine. *Atlantic* 2020.
- 73 World Health Organization. Coronavirus disease 2019 (COVID-19) - Situation Report – 41, 2020. Available: [https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200301-sitrep-41-covid-19.pdf?sfvrsn=6768306d\\_2](https://www.who.int/docs/default-source/coronaviruse/situation-reports/20200301-sitrep-41-covid-19.pdf?sfvrsn=6768306d_2) [Accessed 7 Apr 2020].
- 74 Singh KD, Goel V, Kumar H, et al. India, Day 1: World's Largest Coronavirus Lockdown Begins, 2020. Available: <https://www.nytimes.com/2020/03/25/world/asia/india-lockdown-coronavirus.html> [Accessed 28 Apr 2020].
- 75 Twitter. AFP News Agency [Tweet], 2020. Available: <https://twitter.com/afp/status/1251556097539874818?lang=en> [Accessed 18 May 2020].
- 76 World Health Organization. Update 95 - SARS: Chronology of a serial killer, 2003. Available: [https://www.who.int/csr/don/2003\\_07\\_04/en/](https://www.who.int/csr/don/2003_07_04/en/) [Accessed 17 Apr 2020].
- 77 Centers for Disease Control and Prevention. Severe Acute Respiratory Syndrome - Singapore, 2003, 2003. Available: <https://www.cdc.gov/mmwr/preview/mmwrhtml/mm5218a1.htm>
- 78 World Health Organization. Summary table of SARS cases by country, 1 November 2002–7 August 2003, 2003. Available: [https://www.who.int/csr/sars/country/country2003\\_08\\_15.pdf?ua=1](https://www.who.int/csr/sars/country/country2003_08_15.pdf?ua=1) [Accessed 17 Apr 2020].
- 79 World Health Organization. MERS - Monthly Summary, January 2020, 2020. Available: <http://applications.emro.who.int/docs/EMCSR246E.pdf?ua=1> [Accessed 17 Apr 2020].
- 80 World Health Organization. Pandemic influenza risk management, 2017. Available: <https://apps.who.int/iris/bitstream/handle/10665/259893/WHO-WHE-IHM-GIP-2017.1-eng.pdf?sequence=1> [Accessed 17 Apr 2020].
- 81 World Health Organization. WHO Risk Assessment of Human infections with avian influenza A(H7N9) virus, 2015. Available: [https://www.who.int/influenza/human\\_animal\\_interface/influenza\\_h7n9/RiskAssessment\\_H7N9\\_23Feb20115.pdf?ua=1](https://www.who.int/influenza/human_animal_interface/influenza_h7n9/RiskAssessment_H7N9_23Feb20115.pdf?ua=1) [Accessed 17 Apr 2020].
- 82 World Health Organization. Human infection with avian influenza A(H5N1) virus - update (9 January 2014), 2014. Available: [https://www.who.int/csr/don/2014\\_01\\_09\\_h5n1/en/](https://www.who.int/csr/don/2014_01_09_h5n1/en/) [Accessed 17 Apr 2020].
- 83 World Health Organization. Fact sheet: Ebola virus disease, 2020. Available: <https://www.who.int/news-room/fact-sheets/detail/ebola-virus-disease> [Accessed 17 Apr 2020].
- 84 Taubenberger JK, Morens DM. 1918 influenza: the mother of all pandemics. *Emerg Infect Dis* 2006;12:15–22.
- 85 Trifonov V, Khiabani H, Rabadan R. Geographic dependence, surveillance, and origins of the 2009 influenza A (H1N1) virus. *N Engl J Med* 2009;361:115–9.
- 86 Dawood FS, Luliano AD, Reed C, et al. Estimated global mortality associated with the first 12 months of 2009 pandemic influenza A H1N1 virus circulation: a modelling study. *Lancet Infect Dis* 2012;12:687–95.
- 87 Writing Committee of the WHO Consultation on Clinical Aspects of Pandemic (H1N1) 2009 Influenza, Bautista E, Chotpitayasunondh T, et al. Clinical aspects of pandemic 2009 influenza A (H1N1) virus infection. *N Engl J Med* 2010;362:1708–19.
- 88 World Health Organization. H1N1 in post-pandemic period: Director-General's opening statement at virtual press conference, 2010. Available: [https://www.who.int/mediacentre/news/statements/2010/h1n1\\_vpc\\_20100810/en/](https://www.who.int/mediacentre/news/statements/2010/h1n1_vpc_20100810/en/) [Accessed 17 Apr 2020].
- 89 Diop BZ, Ngom M, Pougue Biyong C, et al. The relatively young and rural population may limit the spread and severity of COVID-19 in Africa: a modelling study. *BMJ Glob Health* 2020;5:e002699.
- 90 Verity R, Okell LC, Dorigatti I, et al. Estimates of the severity of coronavirus disease 2019: a model-based analysis. *Lancet Infect Dis* 2020;20:669–77.
- 91 Epidemiology Working Group for NCIP Epidemic Response - Chinese Center for Disease Control and Prevention. Epidemiological analysis of new coronavirus pneumonia. *Zhonghua Liu Xing Bing Xue Za Zhi (Chinese Journal of Epidemiology) [Chinese]* 2020;41:145–51.
- 92 Wu Z, McGoogan JM. Characteristics of and important lessons from the coronavirus disease 2019 (Covid-19) outbreak in China: summary of a report of 72 314 cases from the Chinese center for disease control and prevention. *JAMA* 2020. [Epub ahead of print: 24 Feb 2020].
- 93 Mizumoto K, Kagaya K, Zarebski A, et al. Estimating the asymptomatic proportion of coronavirus disease 2019 (COVID-19) cases on board the diamond Princess cruise ship, Yokohama, Japan, 2020. *Euro Surveill* 2020;25.
- 94 National Institute of Infectious Diseases (NIID). Field Briefing: diamond Princess COVID-19 cases, 2020. Available: <https://www.niid.go.jp/niid/en/2019-ncov-e/9417-covid-dp-fe-02.html> [Accessed 15 Apr 2020].
- 95 Nishiura H, Kobayashi T, Miyama T, et al. Estimation of the asymptomatic ratio of novel coronavirus infections (COVID-19). *Int J Infect Dis* 2020;94:154–5.
- 96 Heneghan C, Brassey J, Jefferson T, Centre for Evidence-Based Medicine, Nuffield Department of Primary Care Health Sciences, University of Oxford. COVID-19: What proportion are asymptomatic? : Oxford COVID-19 Evidence Service Team 2020.
- 97 Fauci AS, Lane HC, Redfield RR. Covid-19 - Navigating the Uncharted. *N Engl J Med* 2020;382:382–9.
- 98 Russell TW, Hellewell J, Jarvis CI, et al. Estimating the infection and case fatality ratio for coronavirus disease (COVID-19) using age-adjusted data from the outbreak on the diamond Princess cruise ship, February 2020. *Euro Surveill* 2020;25:pil000256.
- 99 Streeck H, Hartmann G, Exner M, et al. Preliminary result and conclusions of the COVID-19 case cluster study (Gangelt Municipality); land.nrw; 9 April, 2020. Available: [https://www.land.nrw/sites/default/files/asset/document/zwischenenergebnis\\_covid19\\_case\\_study\\_gangelt\\_en.pdf](https://www.land.nrw/sites/default/files/asset/document/zwischenenergebnis_covid19_case_study_gangelt_en.pdf) [Accessed 15 May 2020].
- 100 Docherty AB, Harrison EM, Green CA, et al. Features of 20133 UK patients in hospital with covid-19 using the ISARIC WHO Clinical Characterisation Protocol: prospective observational cohort study. *BMJ* 2020;369:m1985.
- 101 Banerjee A, Pasea L, Harris S, et al. Estimating excess 1-year mortality associated with the COVID-19 pandemic according to underlying conditions and age: a population-based cohort study. *The Lancet* 2020;395:1715–25.
- 102 Villa M. Covid-19 and Italy's Case Fatality Rate: What's the Catch? ISPI (Italian Institute for International Political Studies), 2020. Available: <https://www.ispionline.it/en/publication/covid-19-and-italys-case-fatality-rate-whats-catch-25586n1> [Accessed 15 Apr 2020].

- 103 Khafaie MA, Rahim F. Cross-Country comparison of case fatality rates of COVID-19/SARS-CoV-2. *Osong Public Health Res Perspect* 2020;11:74–80.
- 104 Cyranoski D. Mystery deepens over animal source of coronavirus. *Nature* 2020;579:18–19.
- 105 Asadi S, Wexler AS, Cappa CD, *et al*. Aerosol emission and superemission during human speech increase with voice loudness. *Sci Rep* 2019;9:2348.
- 106 Wei WE, Li Z, Chiew CJ, *et al*. Presymptomatic transmission of SARS-CoV-2 — Singapore, January 23–March 16, 2020. *MMWR Morb Mortal Wkly Rep* 2020;69:411–5.
- 107 van Doremalen N, Bushmaker T, Morris DH, *et al*. Aerosol and surface stability of SARS-CoV-2 as compared with SARS-CoV-1. *N Engl J Med* 2020;382:1564–7.
- 108 Gu J, Han B, Wang J. COVID-19: gastrointestinal manifestations and potential Fecal–Oral transmission. *Gastroenterology* 2020;158:30281–X;pii: S0016–1519. Mar 3.
- 109 Xu Y, Li X, Zhu B, *et al*. Characteristics of pediatric SARS-CoV-2 infection and potential evidence for persistent fecal viral shedding. *Nat Med* 2020;26:502–5.
- 110 Medema G, Heijnen L, Elsinga G, *et al*. Presence of SARS-Coronavirus-2 in sewage. *medRxiv* 2020.
- 111 Ahmed W, Angel N, Edson J, *et al*. First confirmed detection of SARS-CoV-2 in untreated wastewater in Australia: a proof of concept for the wastewater surveillance of COVID-19 in the community. *Sci Total Environ* 2020;728:138764.
- 112 Lodder W, de Roda Husman AM. SARS-CoV-2 in wastewater: potential health risk, but also data source. *Lancet Gastroenterol Hepatol* 2020;5:533–4.
- 113 Cheng H-Y, Jian S-W, Liu D-P, *et al*. High transmissibility of COVID-19 near symptom onset. *medRxiv* 2020.
- 114 Ferretti L, Wymant C, Kendall M, *et al*. Quantifying SARS-CoV-2 transmission suggests epidemic control with digital contact tracing. *Science* 2020;368:eabb6936.
- 115 He X, Lau EHY, Wu P, *et al*. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nat Med* 2020;26:672–5.
- 116 Araujo MB, Naimi B. Spread of SARS-CoV-2 coronavirus likely to be constrained by climate. *medRxiv* 2020.
- 117 Sajadi MM, Habibzadeh P, Vintzileos A, *et al*. Temperature, humidity and latitude analysis to predict potential spread and seasonality for COVID-19, 2020. Available: <https://ssrn.com/abstract=3550308> [Accessed 15 Apr 2020].
- 118 Luo W, Majumder MS, Liu D, *et al*. The role of absolute humidity on transmission rates of the COVID-19 outbreak. *medRxiv* 2020.
- 119 Martelletti L, Martelletti P. Air pollution and the novel Covid-19 disease: a putative disease risk factor. *SN Compr Clin Med* 2020;24.
- 120 Guo L, Ren L, Yang S, *et al*. Profiling early humoral response to diagnose novel coronavirus disease (COVID-19). *Clin Infect Dis* 2020;24.
- 121 Bao L, Deng W, Gao H, *et al*. Reinfection could not occur in SARS-CoV-2 infected rhesus macaques. *bioRxiv* 2020.
- 122 Yuan J, Kou S, Liang Y, *et al*. Pcr assays turned positive in 25 discharged COVID-19 patients. *Clin Infect Dis* 2020.
- 123 Lan L, Xu D, Ye G, *et al*. Positive RT-PCR test results in patients recovered from COVID-19. *JAMA* 2020;323:1502.
- 124 Bobrovitz N, Arora RK, Yan T, *et al*. Lessons from a rapid systematic review of early SARS-CoV-2 serosurveys. *medRxiv* 2020.
- 125 Okba NMA, Müller MA, Li W, *et al*. Severe acute respiratory syndrome coronavirus 2-specific antibody responses in coronavirus disease patients. *Emerg Infect Dis* 2020;26:1478–88.
- 126 Gorse GJ, Patel GB, Vitale JN, *et al*. Prevalence of antibodies to four human coronaviruses is lower in nasal secretions than in serum. *CVI* 2010;17:1875–80.
- 127 Theel ES, Slev P, Wheeler S, *et al*. The role of antibody testing for SARS-CoV-2: is there one? *J Clin Microbiol* 2020;00797–20.
- 128 World Health Organization. "Immunity passports" in the context of COVID-19, 2020. Available: <https://www.who.int/news-room/commentaries/detail/immunity-passports-in-the-context-of-covid-19> [Accessed 30 May 2020].
- 129 Britton T, Trapman P, Ball FG. The disease-induced herd immunity level for Covid-19 is substantially lower than the classical herd immunity level. *medRxiv* 2020.
- 130 Gomes MGM, Corder RM, King JG, *et al*. Individual variation in susceptibility or exposure to SARS-CoV-2 lowers the herd immunity threshold. *medRxiv* 2020. doi:10.1101/2020.04.27.20081893. [Epub ahead of print: 02 May 2020].
- 131 Kwok KO, Lai F, Wei WI, *et al*. Herd immunity – estimating the level required to halt the COVID-19 epidemics in affected countries. *Journal of Infection* 2020;80:e32–3.
- 132 Rambaut A. Phylogenetic analysis of nCoV-2019 genomes, 2020. Available: <http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356> [Accessed 15 Apr 2020].
- 133 Bar-On YM, Flamholz A, Phillips R, *et al*. SARS-CoV-2 (COVID-19) by the numbers. *eLife* 2020;9:e57309.
- 134 Wang C, Liu Z, Chen Z, *et al*. The establishment of reference sequence for SARS-CoV-2 and variation analysis. *J Med Virol* 2020;92:667–74.
- 135 Achenbach J. The coronavirus isn't mutating quickly, suggesting a vaccine would offer lasting protection. *The Washington Post* 2020 25 March, 2020. Available: [https://www.washingtonpost.com/health/the-coronavirus-isnt-mutating-quickly-suggesting-a-vaccine-would-offer-lasting-protection/2020/03/24/406522d6-6dfd-11ea-b148-e4ce3fbd85b5\\_story.html](https://www.washingtonpost.com/health/the-coronavirus-isnt-mutating-quickly-suggesting-a-vaccine-would-offer-lasting-protection/2020/03/24/406522d6-6dfd-11ea-b148-e4ce3fbd85b5_story.html) [Accessed 15 May 2020].
- 136 Nextstrain.com. Genomic epidemiology of novel coronavirus, 2020. Available: <https://nextstrain.org/ncov?r=location> [Accessed 30 May 2020].
- 137 Larremore DB, Bubar KM, Grad YH. Implications of test characteristics and population seroprevalence on 'immunity passport' strategies, 2020. Available: <http://nrs.harvard.edu/urn-3:HUL.InstRepos:42664007> [Accessed 30 May 2020].
- 138 Ludvigsson JF. Systematic review of COVID-19 in children shows milder cases and a better prognosis than adults. *Acta Paediatr* 2020;109:1088–95.
- 139 Viner RM, Mytton OT, Bonell C, *et al*. Susceptibility to and transmission of COVID-19 amongst children and adolescents compared with adults: a systematic review and meta-analysis. *medRxiv* 2020.
- 140 Bai Y, Yao L, Wei T, *et al*. Presumed asymptomatic carrier transmission of COVID-19. *JAMA* 2020;323:1406–7.
- 141 Rothe C, Schunk M, Sothmann P, *et al*. Transmission of 2019-nCoV infection from an asymptomatic contact in Germany. *N Engl J Med* 2020;382:970–1.