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# Sociocultural, behavioural and political factors shaping the COVID-19 pandemic: the need for a biocultural approach to understanding pandemics and (re)emerging pathogens

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## ABSTRACT

Although there has been increasing focus in recent years on interdisciplinary approaches to health and disease, and in particular the dimension of social inequalities in epidemics, infectious diseases have been much less focused on. This is especially true in the area of cultural dynamics and their effects on pathogen behaviours, although there is evidence to suggest that this relationship is central to shaping our interactions with infectious disease agents on a variety of levels. This paper makes a case for a biocultural approach to pandemics such as COVID-19. It then uses this biocultural framework to examine the anthropogenic dynamics that influenced and continue to shape the COVID-19 pandemic, both during its initial phase and during critical intersections of the pandemic. Through this understanding of biocultural interactions between people, animals and pathogens, a broader societal and political dimension is drawn as a function of population level and international cultures, to reflect on the culturally mediated differential burden of the pandemic. Ultimately, it is argued that a biocultural perspective on infectious disease pandemics will allow for critical reflection on how culture shapes our behaviours at all levels, and how the effects of these behaviours are ultimately foundational to pathogen ecology and evolution.

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## Introduction: the case for a biocultural framework for studying pandemics

### *COVID-19 and a biocultural approach*

Attention has been drawn to the COVID-19 pandemic due to its unprecedented scale and potential to completely overwhelm public health systems internationally. In the midst of co-contagions of misinformation and fear (Depoux et al., 2020; Törnberg, 2018), questions have arisen as to how and why such a pandemic could have emerged. Approaches from which to approach this topic are diverse within the context of research on infectious disease pandemics. But whilst ecological and climatic factors have been the focus of numerous investigations, sociocultural factors have been slower to be incorporated into this mix. This may in large part be due to traditional subject boundaries between the social and natural sciences. The role of 'biocultural' dynamics in human–pathogen interactions therefore deserves further exploration, both as an interdisciplinary

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approach and specifically in providing an overview of emerging patterns in the COVID-19 pandemic.

### ***Approaches to situating the sociocultural within pandemics***

Current approaches to examining the interaction of sociocultural factors with disease more generally are numerous. From a social science perspective they include health sociology, medical psychology, medical anthropology, urban studies and health geography, to name a few. Within the natural sciences, social epidemiology, evolutionary epidemiology and network modelling approaches are prominent, whilst One Health and Ecosocial approaches are notable in attempting to bridge the social-natural sciences divide. One Health, the study of epi/pandemics through linking multiple disciplines, has become particularly prominent and is closely aligned to biocultural approaches (Ahmad & Hui, 2020; Conrad et al., 2013). However work in this area tends to be heavily focused on ecology or eco-social dynamics, with comparatively less focus on the biological outcomes of sociocultural variables themselves.

Social epidemiology has also emerged out of a similar interest in understanding how social environments impact differential disease burdens. Work in this field has particularly highlighted how structural violence and inequalities in the form of socioeconomic and racial categories produce differentially poorer health outcomes (Bauch & Galvani, 2013). However, studies within social epidemiology often have a heavy focus towards non-communicable disease, with the exception of HIV/AIDS. They also favour an epidemiological, quantitative approach to specific (bio)social variables that can be difficult to apply to complex multispecies and cultural interactions. Another approach that has been suggested to bridge this gap is that of cultural epidemiology (Bhui, 2009; DiGiacomo, 1999) as an idea to unite epidemiology and anthropology (Barbosa, 1998). However, this has largely failed to gain popularity in comparison with social epidemiology, possibly due to fears of disciplinary 'reductionism' (C. Benson, 1982). Meanwhile, health psychology tends to focus on population-level psychosocial variables rather than locally constructed phenomena. Health sociology on the other hand often employs quantitative approaches that capture in detail specific behaviours but not always the broader cultural context in which such behaviours are constructed.

Mathematical modelling studies form a baseline for theorising how human behavioural patterns influence predicated epidemic spread. However, in doing so they may make assumptions on human behavioural dynamics that are necessarily simplistic and not always well-defended from a social science or anthropology perspective. This is not to say at all that advances in modelling behavioural factors in infectious disease epidemiology have not made immense strides in the last few decades. Several studies have examined the effects of network dynamics as a broad proxy for social dynamics and their effects on epidemics (Barrett et al., 2008; Cauchemez et al., 2011; Christley et al., 2005; Eubank et al., 2004; Stattner & Vidot, 2011). Within evolutionary epidemiology, genuinely insightful use has been made of 'big data', to combine behavioural data such as flight connections with phylogeographic data on pathogen behaviour (Grubaugh et al., 2017; Salami et al., 2020; Tian et al., 2017). Such work has also demonstrated how host shifts in network dynamics have the potential to create fundamental selective (Buckee et al., 2004; Leventhal et al., 2015) and epidemiological pressures (Pellis et al., 2015) on pathogens, being largely constrained within such networks.

### ***Biocultural approaches in the context of infectious disease***

Biocultural approaches have already been cited across disciplinarily diverse studies, but what constitutes culture and the biological within this approach has been ambiguous (Wiley & Cullin, 2016). Dressler (2016) has argued that culture can be situated within the biocultural though the concept of cultural consonance: how well an individual is able to mirror beliefs and behaviours within their social environment. Low cultural consonance has been shown to result in poorer health outcomes, through mechanisms such as stress (Copeland, 2018). Whilst this model can be applied directly to

infectious disease, via the immunosuppressant effects of stress and likely higher infection, this is a host-centred perspective. This article proposes an approach that extends work on biocultural approaches to include a more pathogen-centred perspective. This has traditionally been an exclusively biological and medical science focus, examining selective ecological and evolutionary pressures on the pathogen. However, recent work in medical anthropology has begun to shift this dynamic by producing multi-species ethnographies that move away from privileging only the human perspective. Celia Lowe for example, in her work on avian influenza (H5N1) discusses the idea of viral and multispecies ‘clouds’ (Lowe, 2010), whilst Alex Nading explores how pathogen, mosquito and human ecologies are ‘entangled’ (Nading, 2012). This work represents a clear move towards a biocultural approach, with consideration not merely of how human social landscapes are impacted by epidemics, but how vector and pathogen socioecological realities are impacted by human behaviours. Additionally, researchers within areas such as urban studies and health geography have begun to incorporate more ‘epidemiological thinking’ into their analysis of how human landscapes impact disease. One example of this is Ali and Keil’s (2006) work on SARS, illustrating how global city networks, through their historical-cultural and economic linkages, produce physical ‘disease spaces’ via the movement of ‘microbial traffic’.

Broader examples of the impact of sociocultural phenomena on pathogen dynamics relevant to the COVID-19 pandemic include spheres such as consumption and mobility patterns. The role of consumption patterns more generally in structuring viral pandemics has already been amply demonstrated from work on Ebola and H5N1. Research on Ebola for example indicates that bushmeat, a potential source of such zoonotic pathogens, is often considered healthier or of better quality than commercial alternatives (Chausson et al., 2019). Within a more general context bushmeat is linked to cultural heritages in specific ecosystems such as rainforests as well as to consumer preference over intensively farmed species (van Vliet, 2018). Socioeconomic and ecological factors also impinge on this relationship, as whilst consumer preference for bushmeat amongst the wealthy households remained more stable during Ebola outbreaks, poorer households may rely on hunting wild animals for income (Ordaz-Németh et al., 2017). This coupled with intensification of land exploitation such as logging intensifies wildlife-human transmission networks through consumption patterns (Wolfe et al., 2005). Avian influenza is another example, where relations between poultry and humans have been highlighted by Natalie Porter’s work as key in navigating the H5N1 outbreak in Vietnam (Porter, 2013). Porter describes how the close relations between villagers and chickens were maintained by a constructed system of disease risk that viewed locally produced chickens as healthy, and industrially produced chickens as an unhealthy ‘other’. This was linked to conflict between public health actors and small-scale poultry producers in complying with culls and vaccinations. This can itself be contrasted to One Health approaches which have indeed linked intensive animal raising practices in developed countries to zoonotic disease outbreaks such as Q fever (van der Hoek et al., 2012) and Nipah virus (Jones et al., 2013), as well as to the potential for the spread of antibiotic resistance in the environment (Manyi-Loh et al., 2018).

It has also long been recognised that mobility patterns play a key role in pandemic emergence. Historical examples linking sociocultural practices, mobility and pandemics include plague outbreaks in Europe such as the ‘Black Death’, where navigable rivers on trade routes have been statistically correlated with outbreak patterning (Yue et al., 2017). Similar examples of large scale migratory movements linked to outbreaks are the introduction of diseases such as smallpox to the Americas during European colonisation (Ramenofsky, 2003) and the 1918 influenza pandemic (the ‘Spanish Flu’) linked to the mass movements of soldiers and poor trench conditions during the First World War (Wever & van Bergen, 2014). More recent studies have begun to turn attention not only to airborne infections but also vector-borne diseases such as dengue. Work on this area has increasingly found that human, rather than mosquito, spatial networks are a key factor in structuring dengue infection risk (Reiner et al., 2014; Wen et al., 2012). In the case of zoonotic diseases, work on SARS from a health geography and urban studies perspective

has also suggested that connections both within and between cities are important predictors of pandemic outbreak dynamics (Ali & Keil, 2006).

Drawing on such work, this paper echoes Dressler's call to 'operationalize' culture in a way that can be used to directly examine its effects on measurable biological outcomes. This also echoes calls for a 'cultural epidemiology', but which hinged on the same issue: that many of these perspectives are operationalised for non-communicable diseases. Understandings of multi-species entanglements continue to provide excellent insights into 'cloudy' biosocial realities but they do not provide measurable outcomes from the perspective of the pathogen. That is to say, how do the cultural and behavioural phenomena described in such ethnographies precisely shape the epidemiology and evolution of such pathogens? It is suggested that to understand this two shifts be made when applying a biocultural framework to infectious disease.

Firstly, that 'biocultural' be extended, as proposed by Leatherman and Goodman (2019), over a broad level: to examine for example, how political and socioeconomic dynamics may have cultural underpinnings and biological consequences. This would allow for diverse factors that may shape host transmission networks and dynamics to be examined: visualisation of such networks as pathogen 'habitats' would allow for operationalisation of multispecies entanglements. In this sense culture is viewed through an ethnological lens, as specific systems of behaviours that are socially constructed and locally transmitted within a group. But that it is also, linking to the concept of cultural consonance, the medium through which a group understands norms of interaction and constructs categories and relations with the physical environment. Work by Celia Lowe (2010) has already encapsulated this general idea into more integrative approaches by analysing how international inequalities around biosecurity compound differences in infection risk between developed and developing nations. Beisel's (2015) work on malaria in Ghana also demonstrates how socioeconomic factors such as commercialisation of mosquito nets and neocolonial power structures can impact mosquito biology. This is also touched on in work by Kelly and Lezaun (2014), where urban dynamics in Tanzania are described as both a sociohistorical narrative of inequality and the fabric for mosquito reproduction, shaping the connection between both species.

Secondly, that infectious disease epidemiology be the source of the 'measured biological outcome (s)' proposed by Dressler. This distinguishes such an approach from some medical sociology and psychology studies, which tend to examine psychosocial responses to pandemics. By contrast a biocultural approach to pandemics would focus on how existing sociocultural structures may select for eco-epidemiological outcomes at the pathogen level. This extends Margret Lock's conception of 'local biologies' from human embodiment of differential eco-social landscapes (Lock, 2017) to a conception of humans themselves as a shifting eco-social landscape of pathogen embodiment. This requires drawing on both multispecies entanglements in anthropology and evolutionary epidemiological understandings of pathogen as the 'unstable bodies' described by Palsson (2016). Human bodies themselves are therefore the vehicle for pathogen embodiment of cultural dynamics.

## Emerging biocultural narratives in the COVID-19 pandemic

Whilst the COVID-19 epidemic, traced to crossover between bats and intermediate hosts via live animal markets (Ji et al., 2020; Zhu et al., 2020), appeared in some ways to 'come out of nowhere', it is perhaps not so surprising in the wake of the H1N1 and H5N1 outbreaks. As has often been repeated, around 75% of emerging diseases are zoonotic pathogens (Woolhouse, 2002), representing crossover from animals to humans. On top of this, although antibiotic resistance represents one of the most pressing public health concerns in the field of infectious diseases globally (Roca et al., 2015; Zhang et al., 2006), viruses are arguably a far more pressing threat in the context of *emerging* infectious diseases. This is especially true of RNA viruses, of which COVID-19 is one, due to their high mutation rate and thus fast evolutionary 'pace' of adaptation (Peck & Luring, 2018) and high taxonomic flexibility (host range) (Johnson et al., 2015). This may contribute to their potential for

pathogenic changes such as ‘host jumping’ or changes in virulence patterns (Woolhouse et al., 2005).

Biocultural hubs such as markets represent heightened risk for novel pathogen behaviours and host crossovers due to their capacity to link sociocultural and eco-biological networks. Similar to the idea of ‘superspreaders’ (Stein, 2011) they represent ‘superconnected axes’ linking potentially diverse habitats. For example, in countries with high diversities of ecosystems, such as in and around the Amazon, markets can form a direct link between habitats such as tropical forest and mountainous regions (Uhart et al., 2012). There are also clear links between biodiversity and potential for transference events from one host species to another (K. E. Jones et al., 2008; World Health Organization & Convention on Biological Diversity, 2018). Additionally, human disruptions to ecosystems have the potential to form ‘triggering events’ for host jumping, whilst psychological stress in captive animals has been linked to immunosuppression (de Passillé & Rushen, 2005). Zoonotic host-jumping events in hotspots of socioecological interchange have already been observed during the Ebola (Alexander et al., 2015; Meseko et al., 2015) and Nipah virus (Daszak et al., 2013) outbreaks, and with other coronaviruses such as SARS (Sims & Peiris, 2013) and MERS-CoV (Zumla et al., 2016).

Focus has been put on the role of bats in zoonotic diseases, due to the high diversity of viruses found in bat populations (Hayman, 2016; Moratelli et al., 2015). The long evolutionary history, high species and ecological diversity of bats has been suggested to account in part for this (Brook & Dobson, 2015; Wang et al., 2011). In particular through their greater co-evolutionary history with many viruses, particularly coronaviruses (Cui et al., 2019), emerging work suggests that they have developed high tolerance of viral infection, resulting in little to no disease outcomes such as inflammation (Ahn et al., 2019; Hayman, 2019). There is even evidence that such viruses may even confer some symbiotic benefits such as strengthening bat immune systems against other pathogens (Wang et al., 2011). However, this balance may become disturbed under conditions of stress (Chua, 2003; Chua et al., 2002), which is of particular importance in biocultural context. This is because human changes in local habitats, or trade in animals such as bats, may induce stress-related immunological changes that favour increased virus shedding. But it is unhelpful in a wider public and One Health sense for two reasons. Firstly, it draws attention away from the likely principle causative reasons for the emergence of the pathogens in sustained human transmission networks at specific intervals, which is human sociocultural dynamics and not simply bat biology. Secondly, it filters into the public perception in a way that could be very damaging to fragile ecosystems that depend on bats for several ecosystem services (Williams-Guillén et al., 2016). Consequent ‘reprisal’ killing of species such as bats – as occurred with pigs during the H1N1 pandemic (Leach & Tadros, 2014, p. 1) – could ironically could trigger further host-jumping events either indirectly through ecosystem disruption, or directly through contact with bat faeces or tissues.

Barriers to banning live animal markets however, despite previous coronavirus outbreaks from these sources (Woo et al., 2006), also have a cultural source. Traditional medicine, including medicines from a variety of wild animal products (Still, 2003), has a central role in Chinese society that is deeply historically and culturally routed and therefore arguably reaches far beyond Western alternative medicine equivalents (Cheung, 2011; Hsu, 2008; Kim & Han, 2012). This is reflected economically, in the value of traditional medicine and the trade of animal products used in traditional medicine estimated in the billions of dollars (Xu & Xia, 2019). It can also be seen through research investment into the pharmacological activity of a range of traditional Chinese medicine products (Li et al., 2012; Ma et al., 2013; Qiu, 2007; Wang et al., 2006) and the widespread co-use of both traditional and modern medicines (Park et al., 2012; Xu & Yang, 2009). A further aspect concerns differences in perceptions of pollution and safety. Whilst in in some cultural contexts the killing of live animals would be unacceptable, equally in a Chinese context the idea of buying meat of uncertain provenance might equally be viewed as suspect or even dangerous, since the origin, quality and freshness might be unclear (Keck, 2012; Liu, 2008; Lynteris, 2016; Webster, 2004). These factors can be seen to magnify on a national level, where the wildlife trade is worth billions

of dollars (Engler, 2008). Wet markets also act as important nexuses for local farmers and producers, even if such markets are themselves in the hands of state-owned or private companies (Si et al., 2016). Beyond their socioeconomic value, research has highlighted how supermarkets do not replace wet markets: rather, markets have an important cultural value that is enacted through the experience of visiting itself, such as interacting with vendors (Si et al., 2019). Additionally, although intense focus in the wake of the pandemic has been put on wet markets as a purely Chinese phenomenon, wet markets can in fact be found all over the world – albeit within differential socio-cultural contexts that may impinge on pathogen emergence. This is especially the case in areas with high biodiversity (Uhart et al., 2012), despite research tending to centre around those in Asian contexts (Nhung et al., 2018; Rahman et al., 2018; Ribas et al., 2016). This goes a little way to understanding the biocultural placement of the outbreak, both within its local context and the wider context of markets as biocultural nexuses of pathogen emergence and divergence. Additionally, although China has now banned wild animal markets (Li et al., 2020), the possible impact of continued black market trade will be a question for future analysis.

The timing of the COVID-19 outbreak also appears to have intimate cultural links: coinciding with Spring Festival, millions of people working in Wuhan dispersed across China to be with their families before quarantine measures were imposed. This is significant, not merely as a biocultural superspreading event that may have been fundamental in the difficulty containing the COVID-19 pandemic (Zhong et al., 2020), but also because of the specific sociocultural networks involved. That is to say, predominantly younger (working age) people, potentially carrying the virus asymptotically to older relatives (those most at risk of severe infection outcomes) for weeks of cohabitation. This ‘perfect storm’ of factors was also able to reach a critical stage in part due to the initial governmental suppression of information indicating that a new infectious agent linked to a wet market in Wuhan could be causing a surge in pneumonia-related deaths. It has been suggested that early restrictions on epidemiological data were themselves in part created by the lack of autonomy between epidemiologists and the government (Gu & Li, 2020).

Some debate in journalistic literature has also focused on possible cultural reasons for the high case numbers and difficulty in containing the epidemic in the case of Italy (‘Why is Italy’s coronavirus fatality rate so high?’ n.d.). One example is the issue raised of high vaccine scepticism in the context of seasonal flu, which along with a co-epidemic of COVID-19 has the potential to overwhelm health systems as well as the potential for coinfection (Stefanska et al., 2013; Wu et al., 2020). This is perhaps mirrored in the academic literature by discussion of the complex state-society dynamics influencing vaccine confidence (Kieslich, 2018). These include suggested correlative links between rises in populism and vaccine scepticism (Kennedy, 2019), as well as the role of the H1N1 pandemic in bolstering the vaccine scepticism movement due to concerns that the vaccine had not been adequately tested (Verger et al., 2018). However, it is important to distinguish between vaccine scepticism and actual vaccination rates in vulnerable groups, i.e. those in older age groups and those with chronic health conditions. Whilst uptake of seasonal influenza vaccine has been shown to be alarmingly low for older people in Italy (Manzoli et al., 2018; Marano et al., 2020), vaccination coverage remains low in several European countries, including countries that have drastically lower uptake rates than Italy (ECDC, 2018; Jorgensen et al., 2018). The role of seasonal influenza vaccination uptake in contributing to mortality during the COVID-19 epidemic should therefore be weighed in the context of other factors, such as flight connectivity, movement patterns, and health system capacity. However, it is worth considering this as a risk factor for capacity of health systems to cope with possible mortality in countries with very low seasonal influenza uptake. It has also been suggested that the demographic structure (high elderly population) coupled with the sociocultural network dynamics – with more frequent interactions between the young and old within families – increased the potential for spread between densely populated areas with younger asymptomatic carriers travelling to surrounding zones (‘Why is Italy’s coronavirus fatality rate so high?’ n.d.). Whilst this is not supported by data on cohabitation patterns for older adults in the wider European context (Eurostat, 2015), there is research to suggest increased

social contact networks between older parents and children in Italy specifically (Albertini & Kohli, 2013; Floridi, 2018; Kalmijn & Saraceno, 2008). Emerging demographic research suggests that the age structure of populations could play a large causative role in COVID-19 mortality patterns by country (Dowd et al., 2020), whilst large-scale social network studies as illustrated by the BBC Pandemic Project (Klepac et al., 2020) could be useful in further illustrating the social network dynamics within such structures.

The impact of school closures potentially bringing younger and older individuals into closer contact through childminding roles has also been highlighted (Dowd et al., 2020). A further topic for analysis in this area will also be intergenerational network shifts in light of quarantine and containment measures. For example, whether younger populations may decide to move back to family homes within or between countries during quarantine measures or the effects of assisting older individuals, (such as younger individuals delivering shopping). These issues may be further exacerbated by the recovering nature of health systems in Southern Europe, having been amongst the countries whose health systems and economics were more severely affected by the 2008 financial crisis (OECD, 2011; Serapioni, 2017).

## **Effects of biocultural inequalities on differential pandemic burden**

### ***Intersections of vulnerability in times of coronavirus***

Within the context of the current COVID-19 pandemic, despite gaps in the social epidemiology literature, we can reasonably expect differential effects of such sociocultural inequalities on infection risk as well as burden and outcomes. Although data specifically on COVID-19 is just beginning to emerge, work on intersectional vulnerabilities in epidemics can help us to gain an idea of those who may be more affected. The idea of intersectionalities of vulnerabilities in health is relatively recent and can be seen as an important advance on the general concept of social epidemiology (Bauer, 2014). However, as with the majority of social epidemiological work, and with the prominent exception of HIV (Rodríguez & Velázquez, 2017), most research attention has been focused on non-communicable diseases. This has often been within fairly narrow categories of socioeconomic class and sometimes self-identified ethnicity reflecting a highly quantitative epistemological framework, sometimes reducing such categories to naturalistic fixed values rather than constructed cultural relations within a socially produced context. This obscures more complex interplays of biocultural inequalities during epidemics, since how cultural constructions such as gender and ethnicity interact with variables like socioeconomic opportunity. Such interactions may produce compounding inequalities that are often complex and multi-faceted, making them difficult to capture using only qualitative techniques; partly due to the potentially 'unexpected' nature of some of these effects.

The role of ethnicity is somewhat better researched within social and infectious disease epidemiology literature, largely due to the diffusion of literature on HIV vulnerabilities in African-American and Hispanic communities in the USA (Bowden et al., 2006; Jarama et al., 2007). Again, much of the causative mechanisms involved focus around the complex biosocial dynamics of structural violence in the context of ethnicity, such as higher social vulnerability, poor socioeconomic conditions in predominantly African-American or Hispanic neighbourhoods, and lower education and access to medical care (Bauch & Galvani, 2013; Marmot & Bell, 2016; Miller et al., 2007; Poundstone et al., 2004; Shedlin et al., 2005). In the context of racism and increased social epidemiological risk, consideration within COVID-19 should also be given to the increased incidences of racism recorded against Asian communities in places such as the United States and Europe (Wen et al., 2020). Similarly, China itself reported similar discrimination on a national level against those from Wuhan, the epicentre of the outbreak (Ren et al., 2020). Work on indigenous communities has also linked ethnicity and associated structural violence issues to health inequalities, with research pointing to higher rates of infection for diseases such as HIV (Negin et al., 2015),

tuberculosis (Romero-Sandoval et al., 2007; Tuite et al., 2017), malaria (Donnelly et al., 2016) and streptococcal Infections (Bocking et al., 2017). For communities that not only suffer stigma, but also live in poor socioeconomic conditions, or in remote communities (the protective effect of which will likely depend on long-distance social connections), access to medical aid and information in the context of COVID-19 may be problematic. Intersecting at an overarching level will also be the role of socioeconomic status and stability:: whilst there has been concern voiced over the economic effects of quarantine on job stability, issues of more severe poverty raise pressing questions. A prominent example of this is the potential impact on the homeless and their higher vulnerability at times of crisis, including obvious issues such as the inability to self-quarantine, (Tsai & Wilson, 2020).

### ***The role of gender: men as superspreaders, women as invisible caregivers?***

Within the context of the current outbreak gender merits further discussion, but gaps within the context of epidemics and gender have been highlighted on several occasions. Specifically, the lack of awareness in crisis and humanitarian settings of the need to fundamentally integrate differential gender vulnerabilities, and the lack of gender analysis in health and epidemic policy documents (Smith, 2019). When gender is included, it can tend towards something of a 'token gesture', focusing largely on a narrow and stereotyped view of largely non-white, non-occidental women (Syed & Ali, 2011) in their role as mothers, or mothers-to-be. Within the context of infectious disease epidemics, the literature is scarcer still, despite lessons from the Ebola and Zika epidemics, both from the perspective of under-researched differential infection risk, and differential burden of suffering during the crises (Davies & Bennett, 2016). This further impinged on the conditions of severe socioeconomic deprivation in which women most impacted by the crises lived (Vélez & Diniz, 2016). Indeed early epidemiological results linking greater zika prevalence to higher socioeconomic brackets have been shown to reflect the differential ability of women to pay for screenings, with adjusted rates demonstrating a clear link between poverty and zika seroprevalence (Lee et al., 2017).

The issue of gender gaps however, is separate (though related) to differential gender burden highlighted from gender analyses in epidemic or crisis policy, since it is rooted firmly in the *biocultural* and not merely the cultural. This in practice means that an epidemiological difference observed between males and females, in the absence of a purely biological causative explanation (which would be a sex, and not a gender, gap), is primarily caused by differential patterns in risk behaviours. These are transmission-related behaviours which though enacted on a physical, social level, are themselves constructed through gendered culture. It is important to recognise this is not the same, and in fact COVID-19 illustrates this very well: a male-predominated gender gap has been observed (Zhao et al., 2020), which suggests that behavioural patterns associated with 'male' gender predispose men to higher infection risk. Even given this, however, it has still been suggested in the literature that women are at higher differential risk of adverse effects. This may be due not only to their socioculturally more vulnerable positions, again largely as caregivers (Wenham et al., 2020), but also given the potential for gender violence and abuse during epidemics and their aftermath, as seen during the co-epidemic of sexual and gender violence during the 2013–2015 Ebola outbreak (Menéndez et al., 2015; Minor, 2017; Onyango et al., 2019).

One caveat should be noted in the study of gender in epidemics: that is that epidemiological reporting statistics do not necessarily reflect a 'true' epidemiological reality at the population level, and that is because they are largely a reflection of the number of hospital register cases. This means that people who are asymptomatic, or do not report to hospitals (for example because they cannot afford time off work in the case of mild to moderate symptoms, or do not rate them as important), will not be registered in such statistics. These measures therefore reflect rather a combination of both the likely true distribution of cases and the behaviour of people reporting to medical services. However, most research has strongly argued that this effect is more strongly seen in

women, that is to say, that women are characterised in health psychology studies as more risk-averse and generally more risk-aware (Harrant & Vaillant, 2008), thus they report to hospital more. This has been argued to be the core reason for some gender gaps, such as in arboviruses, in the past (Casapulla et al., 2018), although a link between risk aversion and differences in hospital treatment seeking behaviours is not always well-supported (Hunt et al., 2011). However, this same ‘universal’ (i.e. psychological not cultural) argument is hard to employ in the case of COVID-19, since the gender gap shows that men, rather than women, register more cases, despite evidence from Chinese surveys that men employ more risk-avoidance behaviours in the case of COVID-19 (Zhan et al., 2020). This echoes to some extent tuberculosis gender gaps, where both seroepidemiological and epidemiological studies have shown higher proportions of males, largely argued to result from differential patterns in smoking (Watkins & Plant, 2006), another biocultural activity. In the context of the COVID-19 outbreak therefore, this may be a factor, although if it is we might expect to see the same inter-country differences in the COVID-19 gender gap as for tuberculosis. An initial study in this area found a weak but not significant correlation between smoking and infection severity (Zhang et al., 2020), but it should be noted that the small sample size was likely a constraining factor. An additional possibility may be differences in gender-based transmission networks; for example, higher superspreading due to different working conditions for men than women. It remains to be seen from potential seroepidemiological studies of COVID-19 therefore, how well these reporting distributions may reflect population level distributions of infection.

### **International inequalities as a biocultural framework for structural risk in context of pandemics**

One of the themes well-illustrated by the COVID-19 outbreak is equally true for many other pandemics: the issue of inequality on an international level and its relation with the differential impact of such pandemics. This differential impact is reflected not only in potential economic costs, – as it can reasonably be assumed that this this will be much greater in weakened economic areas such as Latin America than in Western European nations and the United States – but also bioculturally. In countries with higher burdens of corruption, the potential COVID-19 burden may be particularly great in poorer communities with less capacity to access healthcare and given social security during such outbreaks is likely to be especially weak. Such effects may be mediated through existing implementation failures of infrastructure budgets (Gillanders, 2014), resulting in communities exposed to higher differential infection risk, even if direct public health spending has a complex relationship with corruption measures (Factor & Kang, 2015; Swaleheen et al., 2019).

This means that during quarantine measures social support, if advanced at all, may not reach the most vulnerable communities and individuals. The link between socioeconomic inequality and disease burden has already been well established in social epidemiology (Marmot & Bell, 2016). In recent years, reviews have also tentatively advanced the same link between infectious diseases epidemics and socioeconomic status (Houweling et al., 2016), albeit without necessarily expanding greatly on social–biological linkages that might provide causative mechanisms. However, in slum communities we can reasonably draw some broad hypotheses, such as the lack of treated water, lack of consistent water supply, lack of reliable infrastructure for solid waste disposal, lack of drainage systems, poor housing quality and high population density (Butala et al., 2010; Turley et al., 2013). In the context of the current outbreak, this also has implications in terms of being able to contain the spread of the epidemic, since it is unlikely that the inhabitants of such areas will be able to afford personal protective equipment, highlighting a primary socioeconomic inequality in risk.

Secondly, poor sanitation and water supplies in these areas will complicate the need for frequent hand washing and cleaning of shared surfaces, potentially increasing the role of indirect transmission networks, which has already in higher income settings been shown to be significant (Cai et al., 2020). Issues with sanitation are also relevant in the context of uncertainties regarding

oral–faecal transmission (Gu et al., 2020), which in low-resource and slum settings has the potential to further spread the virus, even with quarantine measures in place. Since many people in these areas need to work on a daily basis to support themselves and their families, implementing quarantine will be especially challenging.

Such measures will therefore take a disproportionate social, economic and health toll on the poorest communities and this will be further underlined in countries that may not have the budgets to invest in systems of emergency social support. The World Health Organisation COVID-19 Solidarity Response Fund that has been established to tackle shortcomings and gaps in managing the pandemic is therefore important in this regard, but its distribution and careful follow-up of funds to ensure they are reaching communities most in need will be critical in minimising human suffering during the outbreak. In the context of more extreme measures such as quarantine, ensuring that most vulnerable groups such as women and girls in the poorest communities receive adequate support will be important. This will help avoid a repeat of abuses that occurred during Ebola quarantine measures, such as sexual violence, inability to access basic maternity care and reports of women trading sex for basic necessities during quarantine (Davies & Bennett, 2016; Eba, 2014; Korkoyah & Wreh, 2015; Minor, 2017; Onyango et al., 2019).

It is worth mentioning that the distribution of cases and deaths has so far at the time of writing shown great variation. Several explanations have already been put forward to explain this, such as flight connectivity (especially with reference to China) and reporting bias (Niehus et al., 2020) – that is to say, the stronger economies will be more likely to have adequate public health reporting systems. In countries with high political instability, there is also the potential for this data to be actively suppressed by governmental sources, as has been suggested to be the case currently in Syria (Gharibah & Mehchy, 2020). A less extreme version of this can however, be seen in highly developed countries such as the United States, where early reports of COVID-19 were rebuffed by the president as politically motivated conspiracies (Dyer, 2020). The interaction of political and medical factors therefore may be critical in determining the early course of the pandemic on a country level.

What should also be noted is that there has been a marked lack in the literature so far of collaborations between those analysing capacity and health system inequalities in developing countries' abilities to cope with COVID-19 (Gilbert et al., 2020), and those working in climatic modelling (Araujo & Naimi, 2020). This leaves gaps in the ability to identify zones that have intersecting socio-economic, cultural and climatic vulnerabilities and further highlights the need for interdisciplinary work in the context of pandemics.

Other key areas of differential biocultural risk within societies include conflict zones, fragile states with weakened health systems, refugee camps and areas experiencing mass exoduses of people – the latter of which is ongoing from Venezuela and has already been linked to increases in infectious disease incidence (Rodriguez-Morales et al., 2020). The impact of infectious diseases in relation to these other factors is complex and has been less explored, although there is some evidence that the poor conditions and lack of medical supplies in conflict zones and refugee camps are associated with increased epidemic outbreaks. For example, the re-emergence of leishmaniasis in the Middle East in the wake of the war in Syria (Alawieh et al., 2014) and increases in tuberculosis and cholera in refugee camps (Cookson et al., 2015; Phares & Ortega, 2014). In the context of the COVID-19 outbreak, both of these examples are relevant, due to established droplet transmission and also for possible oral–faecal transmission if sanitation is not adequate – both of which may be amplified in conditions of overcrowding.

### ***Pandemic politics as biocultural dynamics writ large***

Wider biocultural dimensions impinge on the biopolitics of pandemics: international governmental cultures and their interactions may ultimately produce changes in pathogen dynamics through policy decisions. For example, one important issue to draw on from previous pandemics is

government-level ‘hoarding’ of supplies such as personal protective equipment, even in the context of severe shortages in other countries. This was illustrated during the H5N1 epidemic, when Material Transfer Agreements between the World Health Organization (WHO) and pharmaceutical companies were made without the involvement of the most impacted countries that had provided viral samples such as Indonesia. Such moves allowed wealthier nations to hoard vaccine capacity through pre-production agreements, despite their proportionally lower risk (Kamradt-Scott & Lee, 2011). This raises important questions for the distribution of potential antiviral drugs in the context of narratives concerning global health inequalities at a political level in pandemic policies. This is underlined by questions of international cooperation between non-allied countries, such as the United States and Iran, where the impact of sanctions has been blamed for severe shortages of medical and laboratory supplies and consequently for the severity of the COVID-19 epidemic in Iran (Takian et al., 2020).

Further topics to explore in the context of potential differential burdens of COVID-19 internationally include the politics of vaccine and drug development, which currently rest largely in the hands of pharmaceutical companies (Chakravarthy et al., 2016). The research priorities of such companies are naturally shaped by expected financial returns on investment, to the detriment of diseases that do not impact the richest nations, regardless of estimates of need or mortality (Trouiller et al., 2002). This further adds to global biopolitical inequalities in the context of pandemics, where the richest populations will also be prioritised in terms of research and development, rather than those most at risk. Additionally, in the context of a public health crisis, it has the potential to slow responses if the financial return is uncertain due to the lack of investment into potential drug and vaccine solutions. This further highlights the importance of emerging models of broad public–private collaborations such as Coalition for Epidemic Preparedness Innovations (CEPI), one of the sources of research and funding for COVID-19 vaccine candidates (Brende et al., 2017; Cohen, 2020). Ensuring that all countries have fair and economically adjusted access to antiviral drugs and potential vaccines against COVID-19 – as well as reviewing such research relationships in the context of future preparedness responses – will therefore be vital areas of policy focus.

## Conclusion

The biocultural spans those dynamics of human behaviour that are socially constructed in nature, and how such factors fundamentally shape and direct the co-evolution of pathogen behaviours. This is necessarily very broad in scope, uniting as it does many constructed identities, realities and inequalities, from a highly local to international level, from the individual to the international relations sphere of nations and organisations. In this way, academia and global health policy – still western-dominated institutions – can simultaneously examine the cultural and geopolitical assumptions in which they are themselves constructed whilst pursuing an understanding of bio-social relationships and inequalities in individual communities. Now that we must apply such understandings to a pandemic like COVID-19 and not merely an epidemic, such an inclusive view will be especially important. Ultimately, a biocultural view emphasises what the COVID-19 pandemic has reinforced in our current understandings of pathogen–human dynamics: that our behaviours, our cultures and societies, are fundamental drivers of pathogen emergence. We are in many ways therefore, the architects of our own pandemics: understanding how and why may help us to tackle not only the COVID-19 pandemic but better anticipate the sources and dynamics of future pandemics.

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