

Genomic trans-biopolitics: Why more-than-human geography is critical amid the COVID-19 pandemic

Gwendolyn Blue

University of Calgary, Canada

Melanie Rock

University of Calgary, Canada

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Abstract

The rapidity of technological change underpins the centrality of genomes in framing COVID-19 problems and proposals for remedies. We counter such framings through a critical perspective that seeks to infuse more-than-human geographies into public health.

Keywords

biopolitics, genomics, more-than-human geography, public health

Introduction

More-than-human geography is critical at a time when zoonotic disease is given a genomic fingerprint, and when the field of public health is turning toward genomic technologies to manage and anticipate the spread of zoonotic pathogens. By critical, we mean that more-than-human geography should play a significant role in advancing scholarship and practice in public health as well as generating novel insights about the governance of health and disease. In particular, more-than-human geography could help public health responses move beyond biomedical framings of health and illness, so as to address the multi-species contexts and situations that permeate bodies and lived experiences.

In this commentary, we highlight the extent to which COVID-19 interventions hinge on genomic

data. Since completion of the Human Genome Project in 2003, and with the development of increasingly sophisticated and affordable genome sequencing technologies, interest has grown in applying genomics – the examination of the entire genetic material of an organism – to the detection and management of infectious diseases (Gardy and Loman, 2018). With previous zoonotic pandemics, such as Ebola and H1N1, genomic applications enabled researchers to trace the origins and the transmission of pathogens as well as identify genetic factors associated with the severity of infection. In

Corresponding author:

Gwendolyn Blue, Department of Geography, University of Calgary, Calgary, AB T2N 1N4, Canada.

Email: ggblue@ucalgary.ca

response to COVID-19, genomic testing and tracing has received a global boost with respect to public attention and investments. Notwithstanding current and potential benefits, genomic technologies are neither innocent nor neutral.

In what follows, we build on the understanding that the deployment of genomic technologies for infectious diseases has far-reaching implications for blame, distribution of scarce resources, liability, privacy, and stigmatization (Boyce and Garibaldi, 2019; Geller et al., 2014). While important, these dimensions reflect a humanist orientation, which we find insufficient in the face of more-than-human challenges to public health (Rock et al., 2014). Our concern lies with how genomic technologies, when integrated into existing narratives in biomedicine and public health, reinforce a tendency to ignore cultural, social, and economic influences on health and illness (Craddock and Hinchliffe, 2015). An emphasis on genomic data already privileges certain types of geographical expertise, such as efforts to monitor pathogens and people. Even so, the critical sensibilities inherent to more-than-human geography also matter when envisioning policy measures to contain COVID-19. In this regard, critical geographers and other social scientists face a challenge: how to engage productively *with* public health (Mykhalovskiy et al., 2019). Amid the COVID-19 pandemic, we cannot stop at criticizing from afar. At the same time, we must find ways to counter-balance interventions that run counter to the pursuit of equity and justice.

Genomic trans-biopolitics and more-than-human public health

Over the past few decades, scholarship in health geographies has taken a more-than-human turn, in part stimulated by high-profile zoonotic infectious diseases such as SARS, H1N1, and BSE (Andrews, 2018; Braun, 2008; Friese and Nuyts, 2017; Hinchliffe et al., 2017). More-than-human approaches include animals and other nonhuman entities such as chemicals and technologies as active agents in the making of health and illness, and in constituting public matters of concern.

Writing in the context of a different zoonotic disease (BSE), we advanced the term trans-biopolitics to account for the complexity of human-nonhuman interactions enmeshed in technoscientific, industrial, and communications systems with global reach (Blue and Rock, 2011). Trans-biopolitics combines Foucault's attentiveness to the modern administration and management of life with Franklin's concept of trans-biology, which refers to the shaping of life at 'biological, technical, and informatic' intersections (Franklin 2006: 171). Trans-biopolitics provides a conceptual lens to help us examine the implications of genomic technologies that are rendering visible and viable the causal agent of COVID-19.

Genomic technologies allow scientists to produce genomic data faster and cheaper than ever before. In turn, open-data platforms and preprints provide rapid dissemination of preliminary results and interpretations. Consider that when the first coronavirus pandemic emerged in 2002, scientists took years to sequence, publish, and then replicate the viral genome (Becker et al., 2008). With COVID-19, by contrast, scientists published the nucleotide sequence of a novel coronavirus within weeks of reports that signaled an unusual respiratory disease in Wuhan, China (Wu et al., 2020). This genomic information confirmed the pathogen responsible for the disease. The genome sequences that followed suggested that the virus originated in an animal and then crossed into human populations, although the animal source remains inconclusive (Cyranoski, 2020). By the end of January 2020, the World Health Organization declared an emergency. By mid-February 2020, the Coronavirus Study Group of the International Committee on Taxonomy of Viruses named the causal agent: SARS-CoV-2, meaning Severe Acute Respiratory Syndrome Coronavirus 2. This name reflects the genetic similarities of SARS-CoV-2 with the virus underpinning the SARS pandemic of 2003 (i.e. SARS-CoV).

The identification of a virus is necessary but insufficient to determine causation of a disease like COVID-19. Other steps are common in biomedicine, such as reproducing a comparable disease in model organisms. Along these lines, scientists announced on 21 February 2020 that they had

engineered a chemically-synthesized clone of SARS-CoV-2 using nucleotide fragments generated from published genome sequences (Thao et al., 2020). Scientists are currently searching for, or using biotechnology to create, appropriate animal models for SARS-CoV-2 (Cohen, 2020).

Meanwhile, popular narratives have positioned genomic scientists as COVID-19 detectives. In these narratives, scientists decipher genome sequences and also guide strategies and policies to prevent deaths and disease. As one journalist described,

Those nucleotides conceal secrets of the virus' past, including its origins, its passage among families and its journey to distant ports. They signal how long it has been at large and whether it can hide by infecting people who show no outward signs of illness. And they can point the way to medicines, vaccines and public health strategies that might bring a runaway crisis under control (Healy, 2020).

Scientists themselves have publicly compared genomic data with barcodes on shipping labels (Ely and Carter, 2020). This comparison implies that scientists can decipher COVID-19 transmission routes readily and unambiguously. Taken together, these narratives suggest the continuation of a cultural primacy granted to genetic material as privileged sources of information about life.

From our perspective, efforts to fingerprint and recreate SARS-CoV-2, and the narratives that accompany these efforts, reinforce a tendency in public health circles to focus on pathogens and technological fixes, rather than on sophisticated accounts of more-than-human life (Rock et al., 2014). Note that COVID-19's genomic fingerprint grounds measures such as testing, contact tracing, and advisories such as physical distancing. Yet, viruses are endemic in bodies and ecologies. As such, the presence of a virus alone is insufficient to cause illness. Genomic sequence information can flatten and even erase the material, political, social, and geographical factors that contribute to the spread, uptake, and lived experience of zoonotic infections.

In our view, more-than-human geographies can inform genomic responses to COVID-19 by challenging dualistic categories (nature/technology; human/

animal; animate/inanimate) and by foregrounding the complex connections among humans and nonhumans, including animals, chemicals, and technologies. Viruses are boundary-crossing organisms that are simultaneously biological, technical, informatic, and agential. Since viruses cannot reproduce or spread apart from a host organism, human and animal relations inhere in zoonotic viral transmission. Human-animal-viral relations are also part of socio-technical and cultural systems that play a significant role in fostering and responding to illness. Advances in genomic technologies are further enabling the *de novo* synthesis of viruses, in part and in whole, and novel animals to serve as model organisms. These developments constitute new possibilities, risks, relations, and dilemmas for public health that require more-than-human theoretical sensibilities.

Beyond genomic responses to COVID-19

In an era when biomedical initiatives loom large in framing and responding to zoonotic diseases, the ascendance of genomic technologies in infectious disease management can enroll social scientists in locating and tracking pathogens or in translating genomic discoveries into public health applications. Indeed, the sheer quantity of genomic data and the speed with which it is generated leaves little time for critical reflection, sustained formal peer review, or public deliberation. Real-time analysis of viral genomes has already contributed to spurious and potentially harmful scientific interpretations of COVID-19 that have gone 'viral' on social media (Kupferschmidt, 2020).

Genomic sciences are important but insufficient to make sense of the interconnected, meaning-laden, and context-dependent relations among humans and with other species. Just as scientists are routinely encouraged to step outside of the lab to support evidence-based decision-making in a more public way, we call for better recognition of and support for theoretically-informed approaches to public health that open consideration of the diverse ways in which humans and other critters live with viruses and infectious disease. Public health and biomedicine have long been informed by a humanist ethos

that places a premium on human life and that separates humans from other nonhuman entities. These strong humanist tendencies exist alongside the rapid generation of data and interpretations fostered by genomic science. As such, creativity and persistence will be required to infuse the insights and ethos of more-than-human geographies into COVID-19 science and public debates.

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