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Securitising infectious disease outbreaks: The WHO and the visualisation of molecular life

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Abstract

Following its exceptional response to the 2003 severe acute respiratory syndrome (SARS) outbreak, the World Health Organization (WHO) gained new powers to securitise infectious disease outbreaks via the revised 2005 International Health Regulations (IHRs) and the ability to declare a Public Health Emergency of International Concern (PHEIC). This article investigates the declaration of a PHEIC in relation to the 2009 H1N1 flu pandemic, the 2014–16 Ebola outbreak, and the ongoing COVID-19 pandemic. It argues that the securitisation of these outbreaks was dependent upon global surveillance networks that utilised genetic technologies to visualise the molecular characteristics and spread of the pathogen in question. Genetic evidence in these cases facilitated the creation of a securitised object by revealing the unique and 'untypable' nature of the H1N1 and SARS-CoV-2 viruses and made visible the widespread prevalence of Ebola across the population of West Africa. The power of this evidence draws from a societal perception of science as producing objective 'facts' about the world that *objectivise* their objects of concern and empower political actors in the implementation of their security agendas. As a result, scientific evidence provided by genetic technologies now plays a *necessary* and indispensable role in the securitisation of infectious disease outbreaks.

Keywords: Global Health Security; Molecular Life; Securitisation; Surveillance; Visibility; World Health Organization

Introduction

Following its response to the 2003 severe acute respiratory syndrome (SARS) crisis and the publication of the revised 2005 International Health Regulations (IHRs), the World Health Organization (WHO) gained new powers to declare a disease outbreak a Public Health Emergency of International Concern (PHEIC). This declaration gives the WHO the ability to securitise infectious disease outbreaks.[1] Declaring a PHEIC communicates to countries around the world that a disease outbreak represents an extraordinary event and a public health risk,[2] bringing into play the use of extraordinary measures, including increased disease surveillance, quarantine, border closures, the invocation of pandemic preparedness plans and the emergency

[1]See Tine Hanrieder and Christian Kreuder-Sonnen, 'WHO decides on the exception? Securitization and emergency governance in global health', *Security Dialogue*, 45:4 (2014), pp. 331–48.

[2]Lucia Mullen, Christina Potter, Lawrence O. Gostin, Anita Cicero, and Jennifer B. Nuzzo, 'An analysis of international health regulations emergency committees and public health emergency of international concern designations', *BMJ Global Health*, 5 (2020), p. 1; WHO, *International Health Regulations (2005)* (Geneva: WHO, 2008), p. 9.

use of novel vaccines or therapeutics.[3] This declaration also generates increased levels of urgency and support from the international community, including financial resources, enhanced diplomatic efforts, and security.[4]

This article investigates three cases in which the WHO has declared a PHEIC. It looks at the H1N1 outbreak of 2009, the Ebola outbreak that occurred in West Africa from 2014–16 and the ongoing outbreak of coronavirus disease 2019 (COVID-19) caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It analyses these cases in terms of the declaration of a PHEIC and the securitisation of each outbreak and the response. In doing so, it engages with work focused on the securitisation of infectious disease that has increasingly highlighted the way in which this process occurs along a continuum and emphasises the significant role that evidence now comes to play in the (de)securitisation process.[5]

Thinkers within this field have set out to explore with greater precision how evidence within certain contexts promotes, fosters, or limits a specific outcome of securitisation.[6] This article contributes to this endeavour via an investigation into these three cases and the combined role that global surveillance networks and genetic technologies played in the declaration of PHEICs. It argues that the securitisation of these outbreaks was dependent upon global and regional surveillance networks that utilised genetic technologies to make visible and intelligible the molecular characteristics and spread of the threat in question. In other words, they facilitate the creation of viruses as a threatening object to be securitised.[7] In 2009, genome sequence data was used to reveal the unique and 'untypable' nature or inherent characteristics of this swine flu virus. In 2014, reverse transcription polymerase chain reaction tests (RT-PCR) were used to make intelligible the widespread prevalence of Ebola across the population of West Africa. In 2020, a combination of RT-PCR tests and genome sequence data were used to reveal the unique nature of SARS-CoV-2.

Drawing from the literature focused on the role of science in securitisation efforts, this article demonstrates the power that genetic evidence exerts in the process through which infectious diseases are securitised. This power draws from a social perception of science as producing technical expertise and objective 'facts'[8] about the world that *objectivise* – define and categorise – their objects of concern. The effect is not only that political issues can be depoliticised but that political actors can also be empowered in the implementation of their security agendas via the mobilisation of these facts.[9] In the cases of H1N1, Ebola, and SARS-CoV-2 genome mapping and RT-PCR tests revealed the novel molecular characteristics and spread of these viruses across various populations. This *objectification* led to their categorisation and securitisation in terms

[3]WHO, *Strengthening Response to Pandemics and Other Public Health Emergencies: Report of the Review Committee on the Functioning of the International Health Regulations (2005) and on Pandemic Influenza (H1N1) 2009* (Geneva: WHO, 2011), pp. 32–3.

[4]The Lancet, 'The politics of PHEIC', *The Lancet*, 393 (2019), p. 2470.

[5]See Rita Abrahamsen, 'Blair's Africa: The politics of securitization and fear', *Alternatives*, 30:1 (2005), pp. 55–80; Thierry Balzacq, 'The three faces of securitization: Political agency, audience and context', *European Journal of International Relations*, 11:2 (2005), pp. 171–201; Thierry Balzacq, 'A theory of securitization: Origins, core assumptions, and variants', in Thierry Balzacq (ed.), *Securitization Theory: How Security Problems Emerge and Dissolve* (Abingdon, UK: Routledge, 2010), pp. 1–30; Thierry Balzacq, Sarah Léonard, and Jan Ruzicka, '"Securitization" revisited: Theory and cases', *International Relations*, 30:4 (2016), pp. 494–531; Catherine Lo Yuk-Ping and Nicholas Thomas, 'How is health a security issue? Politics, responses and issues', *Health Policy and Planning*, 25 (2010), pp. 447–53; Colin McInnes and Simon Rushton, 'HIV, AIDS and security: Where are we now?', *International Affairs*, 86:1 (2010), pp. 225–45; Colin McInnes and Simon Rushton, 'HIV/AIDS and securitization theory', *European Journal of International Relations*, 19:1 (2013), pp. 115–38.

[6]Balzacq, Léonard, and Ruzicka, '"Securitization" revisited: Theory and cases', p. 504.

[7]Mark B. Salter and Can E. Mutlu, 'Securitisation and Diego Garcia', *Review of International Studies*, 39 (2013), p. 815.

[8]Ole Wæver, 'Politics, security, theory', *Security Dialogue*, 42:4–5 (2011), p. 474.

[9]Trine Villumsen Berling, 'Science and securitization: Objectivation, the authority of the speaker and mobilization of scientific facts', *Security Dialogue*, 42:4–5 (2011), pp. 390–3.

of the threat that they posed to the health of the international community. In all three cases the WHO Director-General and the Emergency Committee mobilised this 'objective' evidence to support their securitisation decision.

The result is an investigation that advances securitisation theory by demonstrating the way that evidence of the nature and spread of these pathogens provided by genetic technologies and gathered by fixed surveillance networks now plays a necessary and indispensable role in the securitisation of infectious disease outbreaks. There is, of course, no direct causal mechanism between the use of genetic technologies, the objectivation of scientific objects, the mobilisation of scientific 'facts' and successful securitisation.[10] Yet, the scientific evidence provided by genetic technologies now plays a *necessary* role in the declaration of PHEIC by the WHO and the securitisation of infectious disease outbreaks.

This argument is set out in the following steps. The first section details the way in which the securitisation theory of the Copenhagen School has been extended and adapted in its application to the study of infectious disease outbreaks and scientific evidence. In this application, scientific evidence is highlighted as having particularly powerful effects in shaping the securitisation of disease outbreaks. The second section details the WHO's response to the SARS outbreak and the new set of IHRs that would give the WHO increasing powers to categorise disease outbreaks as international emergencies and securitise them in response. The next section investigates the field of surveillance studies and the global networks supported and developed by the WHO to gather information on disease outbreaks. Focusing mainly on influenza, these fixed networks contrast with liquid forms identified in this area. They gather, analyse, and share physical samples in real time and make visible the genetic sequence data on emerging viruses. This data facilitates the creation of disease as a securitised object by identifying viruses with pandemic potential and it is also used to develop RT-PCR tests to aid diagnosis and population surveillance efforts. The final three sections detail the sole and combined role that genetic sequence data and RT-PCR tests played in the securitisation of the three outbreaks noted above. The conclusion details the wider implications that this analysis has on our understandings of securitisation outside of European and North American contexts.

Securitisation theory and infectious disease

The securitisation theory of the Copenhagen School analyses the application of a securitising logic that runs across different sectors.[11] Though not without criticism,[12] this approach frames security as an intersubjective field of social interaction with a specific set of actions and codes that are known by a set of agents in this field.[13] Security problems not only undercut the 'normal' political order but are often initiated by states that can then claim a special right of exceptional and extraordinary action.[14] The internalist reading of this approach emphasises the role of the speech act. Political elites have the ability to declare an issue to be a security concern. A securitising speech act is successful when its demands follow the accepted grammar of security, the

[10]Ibid., p. 393.

[11]Ole Wæver, 'Securitization and desecuritization', in Ronnie Lipshutz (ed.), *On Security* (New York, NY: Columbia University Press, 1995), p. 51.

[12]See Alison Howell, 'The global politics of medicine: Beyond global health, against securitisation theory', *Review of International Studies*, 40 (2014), pp. 961–87; Alison Howell and Melanie Richter-Montpetit, 'Is securitization theory racist? Civilizationism, methodological whiteness, and antiblack thought in the Copenhagen School', *Security Dialogue*, 51:1 (2020), pp. 3–22.

[13]Wæver, 'Securitization and desecuritization', p. 51; Barry Buzan, Ole Wæver, and Jaap de Wilde, *Security: A New Framework for Analysis* (London, UK: Lynne Rienner Publishers, 1998), p. 19.

[14]Wæver, 'Securitization and desecuritization', p. 54; Buzan, Wæver, and de Wilde, *Security*, p. 21.

securitising actor has sufficient authority to make the statement, the threat stated has features that either support or impede securitisation and the relevant audience accepts the claim and the issue as such a threat.[15] In addition to a securitising agent and a receptive audience, securitising moves also often require a threatening object to be securitised.[16]

Applying this approach to the securitisation of infectious disease in the international arena, Colin McInnes and Simon Rushton have identified in the securitisation of HIV/AIDS a much more nuanced process. Drawing from Thierry Balzacq, these authors have argued that in this case, the process of securitisation represents a continuum and that empirical evidence plays a more significant role than previously argued and understood.[17] For Balzacq and his externalist and sociological reformulation of securitisation,[18] this approach is best utilised as a strategic (pragmatic) practice that occurs within, and 'as part of, a configuration of circumstances, including the context, the psycho-cultural disposition of the audience, and the power that both speaker and listener bring to the interaction'.[19] This strategic practice is aimed at convincing a target audience to 'accept, based on what it knows about the world, the claim that a specific development (oral threat or event) is threatening enough to deserve an immediate policy to alleviate it'.[20] By emphasising these elements of securitisation theory, Balzacq places securitisation in its social context, recognising the intersubjective field of power struggles that surround it and that the securitising actors and audience find themselves within.[21]

Balzacq's position emphasises the use of securitising language in alignment with an external reality and context that is of concern to a particular audience.[22] Crucially, this external context and reality is also independent from the use of language.[23] For McInnes and Rushton this is important as it 'opens the door for empirical "evidence" in support of the securitising claims to play a much more significant role'.[24] These authors note that the types of evidence required will depend upon the types of securitising claim being made. In the securitisation of HIV/AIDS such claims were linked to the evidence surrounding HIV prevalence and state stability, on prevalence rates among militaries and other uniformed services, and on the claim that armed conflict is a vector of HIV transmission.[25] This evidence presented HIV/AIDS as a threatening object and played a vital role in the process through which our understanding of this disease was reshaped leading to its securitisation and the passing of Security Council Resolution 1308 in January of 2000.[26] The emergence of novel viruses too can provide the material event and evidence allowing disease outbreaks to move further along the continuum of securitisation.[27] The result is that securitisation must now be understood not as self-referential and performative but as an argumentative process[28] in which debate and dialogue takes into consideration the evidence regarding the external reality of a situation or threat in an attempt to convince a particular audience. One of the key forms of evidence investigated in this article is that provided by scientific tools and in particular genetic technologies.

[15]Buzan, Wæver, and de Wilde, *Security*, pp. 24–5, 33.
[16]Salter and Mutlu, 'Securitisation and', p. 815.
[17]Abrahamsen, 'Blair's Africa', p. 59; McInnes and Rushton, 'HIV/AIDS and securitization theory', pp. 117–8.
[18]Balzacq, 'A theory of securitization', p. 26.
[19]Balzacq, 'The three faces of securitization', p. 172.
[20]Ibid., p. 173.
[21]Balzacq, 'The three faces of securitization', p. 173; Balzacq, 'A theory of securitization', p. 3.
[22]Balzacq, 'A theory of securitization', p. 13; Balzacq, 'The three faces of securitization', p. 182.
[23]Balzacq, 'The three faces of securitization', p. 173.
[24]McInnes and Rushton, 'HIV/AIDS and securitization theory', p. 120.
[25]Ibid., p. 120.
[26]Ibid., p. 122.
[27]Adam Kamradt-Scott and Colin McInnes, 'The securitisation of pandemic influenza: Framing, security and public policy', *Global Public Health*, 7:sup2 (2012), p. S104.
[28]Balzacq, 'A theory of securitization', p. 22.

Science and securitisation

For thinkers investigating the power that scientific actors and evidence plays in the securitisation of political issues, the work of Bourdieu has been informative. For Trine Villumsen Berling, Bourdieu is valuable for his explicit focus on the role of science and expertise in the constitution of the social realm, making his thoughts important for understanding the role of science in society. Further, his focus on fields as structuring social reality and social universes can provide tools that enable us to better understand the external dimension of securitisation theory: the context in which securitisations take place.[29] The notion of the field allows us to break away from the societal view of science as 'pure' in that it produces technical expertise and objective 'facts'[30] about the world in an apolitical way[31] unconcerned with power. A view that not only disguises the political interests of those drawing from the objective authority of 'scientific evidence'[32] but that also occludes the falsification, dissent, and controversy integral to the workings of science itself.[33] Bourdieu's explicit focus on the role of agency and strategic manoeuvring also connects well with the image of the securitising actor within this approach and makes important insights into how agents strive to become successful in securitisation attempts.[34] In this way, Bourdieu gives us insight into the role that scientific actors and evidence plays in both the external and internal mechanisms through which securitisation occurs.[35]

One of the key external factors identified in the role of science in securitisation processes concerns the way that science *objectifies* its object of study. For Bourdieu, the veil of scientific objectivity is a social product of its field.[36] This generates a practice of objectification by scientific researchers, which leads to the systematic categorisation and rationalisation of human practice and solid conclusions regarding the natural world.[37] Such practical activity as an object of observation, analysis, and representation[38] risks destroying its object or creating pure artefacts whenever it is applied without critical reflection.[39] As Berling notes, the scientist consecrates social reality with a scientific status, making it very difficult to change while also potentially *prescribing* action that exercises a specific kind of symbolic violence.[40] The consequence of objectivation – the power to define and categorise – shapes political discussion and can close down controversy. This adds a significant contextual dimension to the political process in that science can exert a considerable degree of influence on what is being said and what is not.[41] It has particular power in (co)determining the setting and the issues deemed legitimate and 'true' as objects of security.[42] As we will see, genetic technologies demonstrate a particular power of objectivation in that they literally make intelligible the nature of viruses that would otherwise remain unknowable.

One of the key internal factors identified in the role of science in securitisation processes concerns the mobilisation of scientific facts to suit particular political agendas. Facts, scientific

[29]Berling, 'Science and securitization', p. 388.
[30]Wæver, 'Politics, security', p. 474.
[31]Adam Kamradt-Scott, 'The politics of medicine and the global governance of pandemic influenza', *International Journal of Health Services*, 43:1 (2013), p. 113.
[32]Adam Kamradt-Scott, 'Evidence-based medicine and the governance of pandemic influenza', *Global Public Health*, 7: sup2 (2012), p. S118.
[33]See Bruno Latour, *Science in Action: How To Follow Scientists and Engineers Through Society* (Cambridge, MA: Harvard University Press, 1987).
[34]Berling, 'Science and securitization', p. 388.
[35]Ibid.
[36]Pierre Bourdieu, *Science of Science and Reflexivity* (Cambridge, UK: University of Chicago Press, 2004), p. 71.
[37]Berling, 'Science and securitization', p. 391.
[38]Pierre Bourdieu, *Outline of a Theory of Practice* (Cambridge, UK: Cambridge University Press, 1977), p. 2.
[39]Pierre Bourdieu, *Practical Reason* (Cambridge, UK: Polity, 1998), p. 130.
[40]Berling, 'Science and securitization', p. 391.
[41]Ibid.
[42]Ibid.

models, and data can all be mobilised strategically by agents in political struggles in their efforts to secure for themselves the power to impose the legitimate version of the social world and its divisions.[43] These efforts also close off debate and create *doxic* or taken for granted practices that also objectivise the understanding of a threat or situation. Framed in technical terms, the knowledge about this relation can only be challenged by those with scientific capital using similar vocabulary or technological techniques.[44] For Berling, the value ascribed to scientific facts should be kept in mind when analysing securitisation attempts and this constitutes a key internal mechanism of science in relation to securitisation.[45]

Importantly though, there is no causal mechanism or direct relationship between the objectivation of scientific objects, the mobilisation of scientific 'facts' and successful securitisation. These two elements do not guarantee success but are certainly important factors to be reckoned with.[46] Indeed, as this article argues, scientific evidence provided by genetic technologies is now a *necessary* part of the process through which infectious disease outbreaks are securitised by the WHO in the declaration of PHEIC. Clearly, these technologies alone are not sufficient to determine the securitisation of infectious disease outbreaks, yet we must understand the vital role they now play. As we will see now, the WHO's response to the SARS outbreak of 2003 would give it new powers to categorise the outbreaks of particular viruses as potential PHEIC.

The IHRs, WHO, and the securitisation of infectious disease

As part of the revised 2005 IHRs the WHO gained new powers to securitise infectious disease outbreaks via the declaration of a PHEIC. These new powers would allow it to declare a public health emergency in relation to a number of events, including in direct response to the emergence of novel pathogens and the re-emergence of known ones. These events are collected, shared, and made intelligible via the national surveillance systems supported by the WHO. The WHO's surveillance capabilities have developed over time in relation to the IHRs and other international initiatives, including the Pandemic Influenza Preparedness (PIP) Framework. As many commentators have noted, the WHO's exceptional efforts in dealing with the SARS outbreak of 2003 set the ground for the revision of IHRs that followed.[47]

The revised IHRs were adopted by the World Health Assembly (WHA), the policymaking arm of the WHO, in May of 2005.[48] Reflecting the active role the WHO had played in the SARS outbreak a few years earlier, the new IHRs introduced the notion of the PHEIC, giving this organisation new powers to categorise the spread of disease as an international emergency. Via the declaration of a PHEIC, the WHO could also now issue non-binding temporary recommendations to States Parties concerning how they should respond to such emergencies and routine public health risks.[49]

A PHEIC has been defined as an extraordinary event that constitutes a public health risk to other states through the international spread of disease and that may require a coordinated international response.[50] Its purpose is to focus international attention on acute public health risks that require the coordinated mobilisation of extraordinary resources by the international

[43]David Swartz, *Culture and Power: The Sociology of Pierre Bourdieu* (Chicago, IL and London, UK: University of Chicago Press, 1997), p. 89, cited in Berling, 'Science and securitization', p. 393.

[44]Berling, 'Science and securitization', p. 393.

[45]Ibid.

[46]Ibid.

[47]Hanrieder and Kreuder-Sonnen, 'WHO decides on the exception?', p. 337.

[48]David P. Fidler, 'From international sanitary conventions to global health security: The new international health regulations', *Chinese Journal of International Law*, 4:2 (2005), p. 325.

[49]Ibid., pp. 358, 377.

[50]Mullen, Potter, Gostin, Cicero, and Nuzzo, 'An analysis of', p. 1; WHO, *International Health Regulations*, p. 9.

community to prevent and respond to disease outbreaks.[51] The declaration of a PHEIC brings into play extraordinary measures, including increased disease surveillance, restrictions on international travel and trade, such as border closures and quarantine, the invocation of national influenza pandemic preparedness plans, and the emergency use of novel vaccines or therapeutics.[52] Such trade and tourism restrictions can cause significant harm to a country's economy. This declaration has also been associated with increased levels of urgency and support from the international community, including financial resources, enhanced diplomatic efforts and security.[53]

The WHO's failure to consistently invoke a PHEIC has led to criticisms asserting that the implementation process appears 'more political than technical'.[54] It's decision-making power in this regard is so significant, then, as the failure to declare a PHEIC sends a message to the international community that the situation is not an international emergency and so does not require a surge response and the mobilisation of global resources and communities.[55]

In a dramatic shift away from the previous regulations, a PHEIC and its recommendations can now be declared without obtaining the permission of State Parties potentially harmed by such actions.[56] The determination and declaration of the existence of a PHEIC represented a new power to securitise infectious disease outbreaks. As Tine Hanrieder and Christian Kreuder-Sonnen note, this is delegated to the WHO Director-General, who 'shall make the final determination on this matter'.[57] This decision is made in coordination with the views of an Emergency Committee whose members are selected by the Director-General from the IHRs expert roster.[58] However, recent investigations have shown that this is not always the procedure.[59] As set out in the IHRs, the discovery of human influenza caused by a new subtype or unknown virus, the re-emergence of the Ebolavirus and any event of potential international public health concern, including those of unknown causes or sources such as the emergence of the SARS-CoV-2 virus responsible for COVID-19, may alone represent the basis and impetus for the declaration of a PHEIC.[60]

As we shall see, the declaration of PHEICs in response to the 2009 H1N1, 2014–16 Ebola, and ongoing COVID-19 outbreak were underpinned by surveillance networks and molecular technologies that made visible and intelligible the nature and spread of these viruses, respectively, making possible their understanding as objects to be securitised. Crucially, these technologies made the inherent characteristics or nature[61] of the threat in question visible and intelligible to the audience charged with assessing the severity of an outbreak and declaring a PHEIC.

Recognising the essential reliance that any WHO declaration has upon disease surveillance networks and the sharing of information by its member states with it, the revised IHRs also set out a range of new capabilities for the organisation and responsibilities for member states in relation to surveillance. The dramatic expansion of the scope of the IHRs included the creation

[51]David N. Durrheim, Laurence O. Gostin, and Keymanthri Moodley, 'When does a major outbreak become a Public Health Emergency of International Concern?', *The Lancet*, 20 (2020), p. 888.

[52]WHO, *Strengthening Response to Pandemics*, pp. 32–3.

[53]The Lancet, 'The politics of PHEIC', p. 2470.

[54]Durrheim, Gostin, and Moodley, 'When does a major', p. 888; see Mark Eccleston-Turner and Clare Wenham, *Declaring a Public Health Emergency of International Concern: Between International Law and Politics* (Bristol, UK: Bristol University Press, 2021).

[55]Durrheim, Gostin, and Moodley, 'When does a major', p. 888.

[56]Fidler, 'From international sanitary conventions', p. 378.

[57]Hanrieder and Kreuder-Sonnen, 'WHO decides on the exception?', p. 338; WHO, *International Health Regulations*, p. 32.

[58]WHO, *International Health Regulations*, pp. 31–2.

[59]Eccleston-Turner and Wenham, *Declaring a Public Health Emergency*, pp. 148–9.

[60]WHO, *International Health Regulations*, p. 43.

[61]See Christopher Long, 'Challenging contingency: Viruses and the nature of molecular life', *Security Dialogue*, 51:4 (2020), pp. 323–39.

of obligations on State Parties to develop minimum core surveillance and response capacities.[62] As we will see now, one of the core components of any surveillance mechanism is its ability to make the objects of concern visible and intelligible in relation to their external environment.

Global disease surveillance and molecular technologies

Surveillance and visualisation

Surveillance, facilitated by technologies such as communication networks, has been analysed as being inherently tied to the creation of regimes of in/visibility.[63] These regimes are vital to wider political and security projects focused on identifying, managing and classifying people into groups in relation to levels of threat.[64] The surveillance of disease at the level of the population too is tied to technologies such as statistical analysis that make visible its prevalence across different age groups.[65] New technologies in the molecular sciences and in the form of algorithms have intensified the search to make visible and intelligible the occurrence of disease and its classification into new objects of knowledge.

With regard to algorithms, syndromic surveillance systems have emerged as routine rapid detection devices. Syndromic surveillance marks a departure from more traditional and fixed forms of public health surveillance, which tended to rely upon the reporting of official scientific and statistical health information to guide responses to emergent health emergencies.[66] The flows of data from hospital emergency departments, hospital admissions, sales of medicines from pharmacies, telephone calls to health advice providers, levels of absenteeism at school and/or workplaces, etc. are continuously monitored and captured in tools such as HealthMap to gather early indications of a new disease outbreak or bioterrorist attack.[67]

Molecular and genetic technologies have also made it possible for us to visualise and intervene in life at the molecular level.[68] We can now analyse viruses and bacteria in terms of their genetic sequences that reveal their nature or inherent characteristics. The data of these sequences, particularly that of viruses and other pathogens of concern can be used to reconstruct any virus for which an accurate genetic sequence exists.[69] These sequences can also be rapidly shared via the Internet. Organisations such as the Global Initiative on Sharing All Influenza Data (GISAID) and EpiFlu™, form repositories of high-quality influenza genetic sequence data that can be shared between scientists at the click of a mouse in efforts to create new medicines.[70]

For some commentators such as Zygmunt Bauman and David Lyon the increasing speed and flexibility with which information can be gathered and shared between networks represents a fundamental shift from previous notions regarding the workings of surveillance. One conception, captured in Bentham's panopticon, is a modern form of surveillance that worked according to fixed understandings of time and space for both inmates and surveillants.[71] Supported by transnational and instantaneous communication networks as revealed by Edward Snowden, surveillance now takes on a liquid form in its flexibility, collapsing traditional notions of time,

[62]WHO, *International Health Regulations*, pp. 40–2.

[63]See David Lyon, 'Liquid surveillance: The contribution of Zygmunt Bauman to surveillance studies', *International Political Sociology*, 4:4 (2010), pp. 325–38.

[64]David Lyon, *Surveillance Studies* (Cambridge, UK: Polity Press, 2007), p. 61.

[65]Michel Foucault, *Security, Territory, Population* (New York, NY: Palgrave Macmillan, 2009), pp. 59–61.

[66]Steven Roberts and Stefan Elbe, 'Catching the flu: Syndromic surveillance, algorithmic governmentality and global health security', *Security Dialogue*, 48:1 (2017), p. 47.

[67]Ibid., pp. 47–8.

[68]See Christopher Long, *The Molecularisation of Security* (Abingdon, UK: Routledge, 2022), pp. 24–40.

[69]Christopher Long, 'Biosecurity and biodefense', in S. Romaniuk, M. Thapa, and P. Marton (eds), *The Palgrave Encyclopedia of Global Security Studies* (Cham: Palgrave Macmillan, 2019), p. 7.

[70]See Stefan Elbe, 'Bioinformational diplomacy: Global health emergencies, data sharing and sequential life', *European Journal of International Relations*, 27:3 (2021), pp. 657–81.

[71]Zygmunt Bauman, *Liquid Modernity* (Cambridge, UK: Polity Press, 2000), pp. 9–10.

distance, and space. It is now mobile and all encompassing.[72] The world of fixity and enclosure has dissolved into global and local flows across networks.[73] The body along with its pathogens are reduced to data in the creation of the doppelgänger data-double.[74]

In contrast to these liquid forms of disease surveillance this section will now detail the WHO surveillance networks set up to gather and share information on disease threats, particularly that posed by the influenza virus. These networks, just like those detailed above, rely upon technologies to make the pathogenic threat visible, intelligible and categorisable as an object of knowledge. Yet, they also rely upon the collection of physical samples in order to carry out their analysis and threat classification. This necessitates the creation of fixed nodes in a surveillance network that are subject to the traditional constraints of distance and that are linked in 'real time'[75] in the collection and sharing of samples. As this section will show, genetic sequence data reveals the occurrence of a novel virus outside of known classifications and RT-PCR tests reveal the prevalence and rate of known viruses across and within a population. The visibility of the genetic constitution of molecular life has now become a necessary tool in generating evidence regarding the nature and spread of an outbreak that can be mobilised in the declaration of a PHEIC and the securitisation of a disease threat.

The WHO's pandemic influenza surveillance network

The WHO's ability to determine the severity of a disease outbreak for the international community and securitise it via the declaration of a PHEIC is directly linked to the surveillance networks that feed into and share information with it. The largest network created by the WHO is that focused on the early detection of influenza. At the core of this network is the WHO's Global Influenza Programme (GIP), initiated in 1947. One of the most important goals of this programme is the monitoring and tracking of influenza outbreaks. To facilitate this the GIP provides Member States with strategic guidance, technical support, and the coordination of activities to help make their health systems better prepared against seasonal and pandemic influenza threats. This section will outline the essential elements in the WHO's influenza surveillance network along with the role that genetic sequence data plays within it in the generation of scientific evidence that identifies viruses with pandemic potential and contributes to the development of RT-PCR tests.

In order to monitor and track influenza outbreaks, since 1952, global influenza surveillance has been conducted through the WHO's Global Influenza Surveillance and Response System (GISRS). This system, one of the partners in the Global Outbreak Alert and Response Network (GOARN) and formerly known as the Global Influenza Surveillance Network up until 2011, is a global alert mechanism focused on the emergence of influenza viruses with important features, including those that represent new seasonal variants and those with pandemic potential.[76] It is set up to provide early warning of genetic changes in influenza viruses circulating in the global population, to help mitigate the consequences of potential pandemics and maintain the efficacy of seasonal influenza vaccines.[77]

[72]Zygmunt Bauman and David Lyon, *Liquid Surveillance* (Cambridge, UK: Polity Press, 2013), p. 3; Tim Stevens, 'Security and surveillance in virtual worlds: Who is watching the warlocks and why?', *International Political Sociology*, 9:3 (2015), pp. 230–47.

[73]Bauman and Lyon, *Liquid Surveillance*, pp. 55, 134.

[74]Lyon, *Surveillance Studies*, p. 352.

[75]Bruce Braun, 'Biopolitics and the molecularization of life', *Cultural Geographies*, 14:1 (2007), p. 20.

[76]WHO, *Pandemic Influenza Preparedness Framework for the Sharing of Influenza Viruses and Access to Vaccines and Other Benefits* (Geneva: WHO, 2011), p. 49.

[77]Alan J. Hay and John W. McCauley, 'The WHO global influenza surveillance and response system (GISRS): A future perspective', *Influenza and Other Respiratory Viruses*, 12 (2018), p. 551.

One of the ways in which GISRS acts as an early warning mechanism is by identifying and tracking the genetic changes that are occurring in the genomes of influenza viruses that can make them more virulent and transmissible in human populations. This is done through a network of laboratories that collect and share information on viruses circulating across the globe. The GISRS network is made up of WHO designated National Influenza Centres (NICs), WHO Collaborating Centres on influenza (WHO CCs), H5 Reference laboratories (H5RLs), and Essential Regulatory Laboratories (ERLs) that are coordinated by the GIP.

As of 2018, GISRS comprised of 152 institutions, including seven WHO CCs, four ERLs, 13 H5RLs, and 144 NICs in 114 countries, with about 60 per cent of WHO member states participating in global influenza surveillance.[78] These GISRS laboratories conduct research on influenza viruses received for public health surveillance purposes and also submit and share genetic sequence data to GISAID, Genbank and other similar public databases.[79] ERLs exist in the US, UK, Japan, and Australia. They are formally associated with national regulatory agencies and have a critical role in developing, regulating, and standardising influenza vaccines for H5N1 and other influenza viruses that have pandemic potential.[80]

The vast majority of viruses shared through GISRS are those that cause seasonal influenza outbreaks, with 28,000 of these shared annually with WHO CCs.[81] As viruses mutate, seasonal vaccines must be updated. This means that the bulk of GISRS's work is focused on assessing the threat that any new virus may pose. This activity necessitates seasonal risk assessment, virus characterisation, recommendations for seasonal vaccines, and the development of candidate vaccine viruses for use in these vaccines. This work is of critical importance to the effective and robust production of seasonal influenza vaccines. It is also essential to pandemic preparedness, as the same facilities will be used to manufacture any vaccine developed to combat viruses with pandemic potential.[82]

The network of WHO laboratories plays a vital role in the analysis of the changes that are occurring to the genetic makeup of viruses circulating the globe. The year-round surveillance of seasonal influenza by the NICs provides the bedrock of the global virological surveillance system and its ability to respond to a pandemic.[83] Virological surveillance represents the ongoing and systematic collection and analysis of viruses in order to monitor their genetic characteristics.[84]

This system begins with NICs when they receive physical clinical specimens collected from patients with influenza-like illness or severe acute respiratory infections and perform initial identification for the presence of influenza virus and attempt virus isolation.[85] In the identification of relevant influenza viruses, NICs perform virus culture and genetic characterisation by sequence analysis.[86] Next generation genetic sequencing is used by NICs primarily for virological surveillance, but it may also be used for research or outbreak investigations[87] as was the case with SARS-CoV-2. NICs that lack access to appropriate biocontainment facilities or relevant

[78]Hay and McCauley, 'The WHO global influenza surveillance', p. 555; WHO, *Review of the Pandemic Influenza Preparedness Framework* (Geneva: WHO, 2016), pp. 10–11.

[79]WHO, *Pandemic Influenza Preparedness Framework*, p. 41.

[80]Ibid., pp. 57–60.

[81]WHO, *Review of the Pandemic Influenza*, p. 34.

[82]Ibid.

[83]Hay and McCauley, 'The WHO global influenza surveillance', p. 553.

[84]WHO, *WHO Global Influenza Surveillance Network: Manual for the Laboratory Diagnosis and Virological Surveillance of Influenza* (Geneva: WHO, 2011), p. vi.

[85]WHO, *Operational Guidance on Sharing Seasonal Influenza Viruses with WHO Collaborating Centres (CCs) under the Global Influenza Surveillance and Response System (GISRS)* (Geneva: WHO, 2017), p. 4.

[86]Ibid., p. 5.

[87]WHO, *Next-Generation Sequencing of Influenza Viruses: General Information for National Influenza Centres* (Geneva: WHO, 2019), p. 6.

experience of working with highly pathogenic avian influenza viruses may be unable to isolate viruses, so increasing the need to rapidly share physical samples.[88]

Of particular concern to this network are viruses that are categorised as un-subtypeable and associated with human infection.[89] NICs select and share physical samples of these types of viruses with the seven WHO CCs that exist in Memphis, Koltosov, Atlanta, Beijing, London, Melbourne, and Tokyo and that then carry out detailed antigenic, genetic, and biological characterisation.[90] This analysis supports the determination of a number of factors related to public health risk assessment and risk management. This includes assessing and monitoring viral evolution and antiviral drug susceptibility and updating protocols for global virus detection.[91] The collection and analysis of the genetic sequence data of circulating viruses is essential then to the general global health security architecture dedicated to influenza pandemic preparedness and the identification of viruses that may pose a pandemic threat.

Viruses with pandemic potential

Demonstrating the objectivating power of science and as set out in the 2005 IHRs, the emergence of human influenza caused by a new or unknown subtype of virus, termed un-subtypeable, can form the basis of the declaration of a PHEIC.[92] These unclassifiable viruses are also categorised as viruses with pandemic potential. The random emergence of novel influenza viruses results from the process through which they replicate. One unfortunate characteristic of the influenza virus is its inability to accurately reproduce its genetic code when it replicates. As DNA replicates inside human cells, it is accompanied by a proofreading activity that assists this process by removing incorrectly incorporated nucleotides.[93] Nucleotides, also known as nucleotide bases, make up genetic sequences in DNA and RNA. In DNA they are represented by adenine, cytosine, guanine, and thymine with uracil taking the place of thymine in RNA. The RNA-based influenza virus lacks such a proofreading process and this results in the accumulation of point mutations during replication that lead to changes in the sequence of nucleotides and the reassortment and mutation of genes that in turn produce different proteins.

Some of the most important genes in the molecular surveillance and assessment of the pandemic potential of influenza viruses are those that determine the structure and function of the haemagglutinin (HA) and neuraminidase (NA) surface proteins. These proteins are responsible for viral entry into human cells and their release from the surface of human cells, respectively. The mutations that occur during viral replication and the changes to the sequence of nucleotides are so significant as they contain the genetic information that determines the physical biological characteristics and infectivity of a virus, demonstrated in the structure of the HA and NA surface proteins.[94]

When a virus replicates using the genetic machinery of its host it not only shares its genetic material with the host, but host DNA is also incorporated into the viral genome.[95] In this way, as viruses spread, they carry this material with them, transferring DNA and RNA from

[88]WHO, *Operational Guidance on Sharing Influenza Viruses with Human Pandemic Potential (IVPP) under the Pandemic Influenza Preparedness (PIP) Framework* (Geneva: WHO, 2017), p. 6.

[89]WHO, *Operational Guidance on Sharing Seasonal Influenza Viruses with WHO*, p. 4.

[90]WHO, *Operational Guidance on Sharing Influenza Viruses with Human Pandemic Potential*, p. 6; WHO, 'WHO Collaboration Centres' (2022), available at: {https://www.who.int/initiatives/global-influenza-surveillance-and-response-system/who-collaboration-center-erl} accessed 16 December 2022.

[91]WHO, *Operational Guidance on Sharing Seasonal Influenza Viruses with WHO*, p. 4.

[92]WHO, *International Health Regulations*, p. 43.

[93]Anna Bębenek and Izabela Ziuzia-Graczyk, 'Fidelity of DNA replication: A matter of proofreading', *Current Genetics*, 64 (2018), p. 985.

[94]WHO, *Pandemic Influenza Preparedness Framework*, p. 8.

[95]John Dupré, *Processes of Life* (Oxford, UK: Oxford University Press, 2014), p. 92.

one organism to another. The mutations and reassortments that result from this exchange lead to changes in the amino acids in the antigenic or infective portions of the viral HA and NA surface glycoproteins that may give selective advantages to a strain by allowing it to evade pre-existing immunity and host immune responses.[96] Subtle changes and genetic mutations are termed antigenic 'drift', with more substantial ones given the moniker antigenic 'shift'. The former give rise to novel seasonal variants of the influenza virus while the latter generate potentially pandemic forms.

Surveillance of the genetic changes to influenza viruses is so important as pandemics often occur when an influenza virus of a new subtype to which most humans have little or no existing immunity 'shifts' to acquire the ability to cause sustained human-to-human transmission leading to global community-wide outbreaks.[97] Such a virus is not only able to evade pre-existing immunity and our pharmaceutical defences but also transmit efficiently between humans. This potential was realised with the emergence of the H1N1 influenza pandemic virus in 2009. The H5N1 and H7N9 viruses have also evolved the ability to move from animals to humans but luckily have not yet been found to spread easily from human to human.[98] As a result, the GISRS global system of monitoring and surveillance detailed above has been set up to identify, visualise, and assess the specific molecular characteristics of influenza viruses in order to determine those that may have the potential to cause a global pandemic. In other words, to categorise, objectify, and determine the nature of the threat.

As part of this system, the WHO has created global pandemic influenza virus risk assessments to inform decision-making for influenza viruses with pandemic potential.[99] A virus with pandemic potential is defined as one that 'must, at the least, have a haemagglutinin gene and potentially also other genes that are distinct from those in seasonal influenza viruses so as to indicate that the virus has potential to spread within human populations'.[100] This includes viruses isolated from animals that have spread from animal reservoirs to humans and caused zoonotic infections, such as avian influenza H5N6 and the swine-origin H3N2 virus.[101] It also includes viruses that previously circulated in humans but no longer do so, such as the H2N2 virus.[102] A novel virus with distinctive genes representative of a new subtype combined with the ability to spread effectively in humans represent key red flags in the determination of whether this scientific object constitutes a PHEIC and should be securitised.

Genetic sequence data and RT-PCR tests

Sequence data is not only used to determine the danger a virus represents, but it is also used to design primers for surveillance and diagnostic tools such as RT-PCR tests that can tell if someone is infected with a particular virus and thus make measurable and visible infection rates across a population.[103] Fast, accurate, and comprehensive diagnostic tools such as this are central to the surveillance of emerging and re-emerging viruses, outbreak management, as well as for early antiviral treatment, prophylaxis, and infection control.[104]

[96]Jeffery K. Taubenberger and Scott P. Layne, 'Diagnosis of influenza virus: Coming to grips with the molecular era', *Molecular Diagnosis*, 6:4 (2001), p. 293.

[97]WHO, *Tool for Influenza Pandemic Risk Assessment (TIPRA)* (Geneva: WHO, 2020), p. 5.

[98]Ibid.

[99]Ibid., p. 7.

[100]Ibid., p. 8.

[101]Ibid.

[102]Ibid.

[103]WHO, *Review of the Pandemic Influenza*, p. 49; See WHO, *WHO Information for the Molecular Detection of Influenza Viruses* (Geneva: WHO, 2021).

[104]Ruixue Wang and Jeffery K. Taubenberger, 'Methods for molecular surveillance of influenza', *Expert Review of Anti-infective Therapy*, 8:5 (2010), p. 518.

This technology detects parts of the genome and particular genes of the virus in question.[105] Our understanding of the full genome sequence of a virus is therefore important in the development of RT-PCR tests and the designing of PCR primers that determine the region of DNA to be detected and amplified.[106] The most frequently implemented RT-PCR diagnostic tests for the Zaire ebolavirus responsible for the 2014–16 outbreak targeted conserved (constant) domains within genes for structural elements of this virus including the glycoprotein that is involved in the infection of cells and spread of the disease in the body.[107] Tests that recognise these genes also form part of the confirmatory strategy for US cases and for samples referred to the US Centers for Disease Control (CDC) as a WHO CC for Viral Haemorrhagic Fevers.[108]

RT-PCR capitalises on the function of one enzyme – DNA polymerase – to add nucleotides to a single strand of DNA. This enzyme is normally used to facilitate cell division, as when a cell divides the DNA must be duplicated. In this process the two-stranded DNA helix will separate and the DNA polymerase will add the relevant nucleotides to each single strand in the creation of a new double-stranded helix and a duplicate of the cell's DNA. As the Ebola virus has a genome that consists of RNA, the RT-PCR tests must create a complementary DNA strand from an RNA template, a process termed reverse transcription using the enzyme reverse transcriptase.[109]

Once the DNA strand has been created, the polymerase enzyme then amplifies a specific part of this strand (such as the conserved domains) creating many copies, in a process known as polymerase chain reaction, which can serve as a clear and visible identifier of infection. This method of analysis is not, however, fool proof as any errors in the reverse transcription process will also be amplified by the DNA polymerase enzyme.[110]

As we will see in the next three sections, this diagnostic test and genomic analysis played essential roles in the WHO's declarations of PHEIC in response to the H1N1, Ebola, and SARS-CoV-2 outbreaks. These technologies categorised and objectivised the virus of concern making either its nature or spread visible and intelligible so creating evidence of a threatening object that could be utilised by the WHO in its securitisation of these outbreaks via the declaration of a PHEIC. In the analysis of these cases I draw from publicly available reports to demonstrate the process through which the nature and spread of these viruses became understood scientifically and then securitised.

Genome sequence data and the securitisation of H1N1

On the 25 April 2009, in response to the global spread of the H1N1 'swine flu' virus, the WHO declared a PHEIC, recognising that the situation represented an extraordinary event requiring immediate emergency actions on an international scale.[111] On the 11 June 2009, after thirty thousand cases had been confirmed across 74 countries, a global pandemic was declared, the first of the twenty-first century.[112] On the 24 April 2009, the full genome of this newly identified influenza virus was sequenced by the US WHO CC in Atlanta and was subsequently made publicly

[105]M Goeijenbier, J. J. A. van Kampen, C. B. E. M. Reusken, M. P. G. Koopmans, and E. C. M. van Gorp, 'Ebola virus disease: A review on epidemiology, symptoms, treatment and pathogenesis', *The Netherlands Journal of Medicine*, 2:9 (2014), p. 444.

[106]Declan Butler, 'Swine flu goes global', *Nature*, 458 (2009), p. 1083.

[107]Tara K. Sealy, Bobbie R. Erickson, Céline H. Taboy, Ute Ströher, Jonathan S. Towner, Sharon E. Andrews, Laura E. Rose, Elizabeth Weirich, Luis Lowe, and John D. Klena, 'Laboratory response to Ebola: West Africa and United States', *MMWR*, 65:3 (2016), p. 46; Long, 'Challenging contingency', pp. 333–4.

[108]Sealy et al., 'Laboratory response to Ebola', p. 47.

[109]Willard M. Freeman, Stephen J. Walker, and Kent E. Vrana, 'Quantitative RT-PCR: Pitfalls and potential', *BioTechniques*, 26 (1999), p. 113.

[110]Ibid., p. 112.

[111]WHO, *Strengthening Response to Pandemics*, pp. 32, 42.

[112]Seth J. Sullivan, Robert M. Jacobson, Walter R. Dowdle, and Gregory A. Poland, '2009 H1N1 influenza', *Mayo Clinic Proceedings*, 85:1 (2010), p. 64.

available on the GISAID sequence database.[113] Studies quickly made visible the nature of the threat that manifested in the 'unique genome constellation'[114] of the virus that was genetically 'untypable'[115] and unclassifiable. As detailed above, human influenza caused by a new and unknown subtype of virus is a key factor in the IHRs decision instrument, guiding the assessment and notification of incidents that may constitute an exceptional event and PHEIC and that should be communicated to the WHO by affected countries.[116]

Viruses that are untypable or 'un-subtypable' cannot be matched to the catalogue of known viruses or subtypes. Influenza A viruses are divided into subtypes based on the 18 different haemagglutinin and 11 different neuraminidase surface proteins found in the natural world to date.[117] As detailed above, 'un-subtypable' viruses often have this characteristic after they have undergone substantial antigenic or genetic changes. Following detailed genetic analysis, it was soon revealed that this H1N1 virus contained the genetic components of three distinct organisms: humans, pigs, and birds.[118] Pigs have been identified as the ideal mixing vessels for the generation of new viruses as they are not only susceptible to infection by swine viruses but also bird and human influenza viruses too.[119]

As word spread among the international community that a novel virus was now circulating widely, the WHO began to assemble an Emergency Committee from the IHR Roster of Experts.[120] Once assembled, the Committee focused on collecting more detailed information on the epidemiology, virology, and clinical characteristics of this new virus before advising the Director-General on the announcement of the PHEIC. In line with the IHRs, Committee members advised the Director-General on the announcement of the PHEIC that was carried through on the 25 April.[121] As a result, over the next few days and as the disease spread, the Director-General recommended that all countries intensify surveillance for unusual outbreaks of influenza-like illness and severe pneumonia. As the virus had already spread widely by this time, the strategy of containment and the more stringent security measures of quarantine, border closures, and restrictions on international trade and travel were rejected in favour of recommendations focused on mitigation. This was not followed by every country or region, though, with Hong Kong implementing quarantine measures and China doing the same to Mexican or Canadian nationals arriving from their home countries or already present in China.[122]

Over the months leading up to the Emergency Committee's final meeting on the 10 August 2010, countries were encouraged to maintain their surveillance measures. At this time more than 214 countries and overseas territories or communities had reported laboratory confirmed cases of pandemic H1N1.[123] Based on the global situation, the Committee recognised that the spread of H1N1 seemed largely to have 'run its course' and would likely continue to circulate for some years to come, taking on the behaviour of a seasonal influenza virus. As a result, it

[113]CDC, '2009 H1N1 Pandemic Timeline' (2019), available at: {https://www.cdc.gov/flu/pandemic-resources/2009-pandemic-timeline.html} accessed 16 December 2022.

[114]Elke Starick, Elke Lange, Sasan Fereidouni, Claudia Bunzenthal, Robert Höveler, Annette Kuczka, Elisabeth Grosse Beilage, Hans-Peter Hamann, Irene Klingelhöfer, and Dirk Steinhauer, 'Reassorted pandemic (H1N1) 2009 influenza: A virus discovered from pigs in Germany', *Journal of General Virology*, 92 (2011), p. 1184.

[115]WHO, *Strengthening Response to Pandemics*, p. 31.

[116]WHO, *International Health Regulations*, pp. 40–6.

[117]CDC, 'Types of Influenza Viruses' (2022), available at: {https://www.cdc.gov/flu/about/viruses/types.htm} accessed 16 December 2022.

[118]Sullivan et al., '2009 H1N1 influenza', p. 66.

[119]WHO, *Strengthening Response to Pandemics*, p. 29; Michael T. Osterholm and Mark Olshaker, *Deadliest Enemy* (London, UK: John Murray, 2020), p. 287.

[120]WHO, *Strengthening Response to Pandemics*, p. 31.

[121]Ibid., p. 32.

[122]David P. Fidler, 'H1N1 after action review: Learning from the unexpected, the success and the fear', *Future Microbiology*, 4:7 (2009), p. 768.

[123]WHO, *Strengthening Response to Pandemics*, p. 40.

was agreed that the global influenza situation no longer represented an extraordinary event requiring immediate emergency action on an international scale.[124] The Committee advised the Director-General that the PHEIC should be ended and that the temporary recommendations adopted in response should be terminated.

The failure both of the virus to mutate into a more lethal form and for widespread resistance to the antiviral oseltamivir/Tamiflu to develop, in addition to the creation of an effective and safe vaccine, created the fortunate conditions out of which a very mild pandemic was realised.[125] This was, though, an infectious disease outbreak that was securitised in coordination with scientific evidence that categorised and objectified the virus in relation to its unique and untypable nature. This scientific evidence was made visible and intelligible via the detailed sequencing of its genome. As we will see now, another molecular technology in the form of RT-PCR tests would also play an essential role in providing evidence for the securitisation of an outbreak of Ebola a mere five years later.

RT-PCR tests and the securitisation of Ebola

On the 8 August 2014, the WHO declared the Ebola virus disease (EVD) outbreak in West Africa a PHEIC, stressing the need for international attention and collaboration to control and mitigate its effects.[126] A month later on the 18 September, the UN Security Council declared that this outbreak constituted a threat to international peace and security and called on Member States to respond urgently to the crisis, and to refrain from isolating the affected countries. This outbreak primarily affected the countries of Guinea, Liberia, and Sierra Leone and would result in the most widespread occurrence of this disease in history. The virological investigation identified and categorised Ebola Zaire as the particular species and strain of Ebolavirus responsible for this outbreak.[127]

Following the declaration of a PHEIC, the WHO put forward temporary recommendations emphasising the travel restriction of all EVD cases and contacts but stated that there should be no general ban on international travel or trade. All states were advised to be prepared to detect, investigate, and manage EVD cases. Unfortunately, dozens of countries implemented measures in response to this crisis that neither followed the WHO's recommendations, nor had a scientific and public health justification, such as travel bans or restrictions on persons travelling from West Africa.[128] Many countries also failed to inform the WHO when implementing these measures or justify them when asked to, signifying for David P. Fidler a further violation of the international legal obligations prescribed in the IHRs.[129] It has also been noted that the international political motivation to intervene in West Africa only arose in July 2014 after the first case of Ebola was diagnosed outside of Africa.[130]

As with many other viral haemorrhagic fevers, Ebola can be difficult to diagnose, and requires laboratory diagnostics in order to confirm or rule out infection with confidence.[131] As a result, rapid and reliable laboratory testing for the diagnosis of suspected Ebola cases is essential in making the spread of this virus visible and intelligible as an object of knowledge. This information is

[124]Ibid., p. 42.
[125]Ibid.
[126]Goeijenbier et al., 'Ebola virus disease', p. 442.
[127]M. Barry, F. A. Traoré, F. B. Sako, D. O. Kpamy, E. I. Bah, M. Poncin, S. Keita, M. Cisse, and A. Touré, 'Ebola outbreak in Conakry, Guinea: Epidemiological, clinical, and outcome features', *Médecine et maladies infectieuses*, 44 (2014), p. 492.
[128]David P. Fidler, 'Epic failure of Ebola and global health security', *The Brown Journal of World Affairs*, 21:2 (2015), p. 189.
[129]Ibid.
[130]Jolie Kaner and Sarah Schaack, 'Understanding Ebola: The 2014 epidemic', *Globalization and Health*, 12:53 (2016), p. 5.
[131]Sealy et al., 'Laboratory response to Ebola', p. 44.

also vital to the control of the virus via the initiation of contact tracing.[132] During this outbreak, the WHO organised laboratory response activities as part of the Emerging and Dangerous Pathogens Laboratory Network (EDPLN) and GOARN. The WHO in coordination with the EDPLN, which includes WHO CCs, set up a global laboratory database that centrally compiled data in order to understand global disease trends and guide public health interventions.[133]

From March 2014 onward, WHO EDPLN, together with GOARN and partners, deployed 32 laboratories into the three most affected countries and Nigeria to provide safe and high-quality laboratory diagnostic services.[134] Their efforts were also focused on providing clinical care, the identification of new cases and the monitoring of survivors. They also ensured that all districts, counties, and prefectures in the affected countries had access to laboratory testing capacity within 24 hours.[135] The EDPLN network was instrumental in providing a fixed platform for the laboratory analysis of RT-PCR tests to not only confirm cases of EVD but to also direct patients to treatment centres. Confirmed cases of the disease using this test were also used in contact tracing efforts.[136] The information provided proved essential in making visible and intelligible the reality of the regional epidemiological situation, including the increased spread and growth in cases.

In April 2015, the database was made up of 86,154 samples taken from approximately 1,600 unique spreadsheets from 32 laboratories located in the three countries.[137] The number of laboratories involved would grow to 47 by the end of the outbreak and 256,343 specimens would eventually be tested from March 2014 through to August 2016.[138] At the core of this data collation was the collection and analysis of specimens from patients presenting at hospitals, treatment centres, and clinics with symptoms of EVD. All specimens were transported to the laboratories for subsequent real-time qualitative RT-PCR testing.[139]

As testing ramped up from March 2014 onward a positivity rate of around 50 per cent was revealed from June up until the declaration of the PHEIC by the WHO in early August.[140] Across the three countries the number of cases and deaths rose from 86/59 on the 25 March to 1617/886 on the 4 August,[141] a massive increase of 1780/1401 per cent respectively. The WHO Emergency Committee, following a meeting on the 6 and 7 August, unanimously decided that the conditions for a PHEIC had been met. On the 8 August, 2014, the WHO declared a PHEIC stating that this outbreak constituted an 'extraordinary event' and a public health risk to other States.[142] This was a result of 'the intensive community and health facility transmission patterns', the virulence of the virus, and the weak health systems in the countries affected.[143] The nature and spread of this disease outbreak, these transmission patterns and rates of infection across the population groups tested were made visible and intelligible via the utilisation of RT-PCR tests.

[132]Ibid.

[133]Kara N. Durski, Shalini Singaravelu, Junxiong Teo, Dhamari Naidoo, Luke Bawo, Amara Jambai, Sakoba Keita, Ali Ahmed Yahaya, and Beatrice Muraguri, 'Development, use, and impact of a global laboratory database during the 2014 Ebola outbreak in West Africa', *The Journal of Infectious Diseases*, 215 (2017), p. 1799.

[134]Dhamari Naidoo, Kara Durski, and Pierre Formenty, 'Laboratory response to the West African Ebola outbreak 2014–2015', *Weekly Epidemiological Record*, 32 (2015), p. 393.

[135]Ibid., p. 394.

[136]WHO, *Contact Tracing During an Outbreak of Ebola Virus Disease* (Brazzaville: WHO, 2014), p. 3, 13.

[137]Naidoo, Durski, and Formenty, 'Laboratory response to the West', p. 394.

[138]Durski et al., 'Development, use, and impact of', pp. 1799–800.

[139]Ibid., p. 1800.

[140]See Naidoo, Durski, and Formenty, 'Laboratory response to the West', p. 395.

[141]CDC, 'Case Counts' (2020), available at: {https://www.cdc.gov/vhf/ebola/history/2014-2016-outbreak/case-counts.html} accessed 16 December 2022.

[142]Maev Kennedy, 'WHO declares Ebola outbreak an international public health emergency', *The Guardian*, available at: {https://www.theguardian.com/society/2014/aug/08/who-ebola-outbreak-international-public-health-emergency} accessed 16 December 2022.

[143]Ibid.

These tests made visible and intelligible the increasing spread and threat that Ebola posed in this region forming it into an object to be securitised. As a result, a call was issued for a coordinated international response to stop and reverse its international spread. The PHEIC was lifted on the 29 March 2016, following 28,616 confirmed, probable and suspected cases with 11,310 deaths.[144] As we will see now, a combination of the genetic technologies discussed so far was utilised in our understanding of the novel nature of the SARS-CoV-2 virus and its securitisation.

Genome sequence data, RT-PCR tests, and the securitisation of COVID-19

On the 30 January 2020, following the recommendations of the Emergency Committee, the WHO Director-General declared that the outbreak of COVID-19 constituted a PHEIC.[145] This declaration followed the discovery and objectivation of the threat of this novel virus using a combination of PCR, RT-PCR tests, and genome sequencing and its rapid spread across the globe and serious public health impact.[146] In response, countries around the world were advised to prepare for containment, including active surveillance, early detection, isolation and case management, contact tracing, and the prevention of onward spread of infection.[147]

By the end of January 2020, the virus had travelled from China to 18 other countries with only seven of these cases having no history of travel in China. Human-to-human transmission was also recorded in three countries outside China. Following this, the virus proceeded to move across the globe leaving few places unaffected. In response, countries around the world implemented a range of restrictive travel and trade measures, particularly against China, acting in violation of their obligations under the IHRs and the advice of the WHO at the time.[148] As of the 16 December 2022, there have been 647,972,911 confirmed cases of COVID-19, resulting in 6,642,832 deaths, reported to the WHO.[149]

The novel nature of this coronavirus was determined using a combination of PCR, RT-PCR tests, and genome sequencing technology. PCR and RT-PCR tests analysed samples for the presence of 22 different pathogens, 18 viruses, and 4 bacteria to eliminate the presence of known microbes.[150] In combination with these tests, high-throughput genetic sequencing[151] and metagenomics next-generation sequencing[152] were utilised to objectify and make visible the whole genome of the virus, discover microbial sequences not identifiable by the PCR and RT-PCR tests and make intelligible the novel characteristics of this pathogen and the threat that it posed to the global population.

[144]WHO, *Situation Report Ebola Virus Disease 10 June 2016* (Geneva: WHO, 2016), p. 1.

[145]WHO, *COVID 19 Public Health Emergency of International Concern (PHEIC)* (WHO: Geneva, 2020), p. 2.

[146]WHO, 'Statement on the Second Meeting of the International Health Regulations (2005) Emergency Committee Regarding the Outbreak of Novel Coronavirus (2019-nCoV)', available at: {https://www.who.int/news/item/30-01-2020-statement-on-the-second-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-outbreak-of-novel-coronavirus-(2019-ncov)} accessed 16 December 2022.

[147]Ibid.

[148]Sara E. Davies and Clare Wenham, 'Why the COVID-19 response needs International Relations', *International Affairs*, 96:5 (2020), p. 1231; Samantha Kiernan and Madeleine DeVita, 'Travel restrictions on China due to COVID-19', *Think Global Health*, available at: {https://www.thinkglobalhealth.org/article/travel-restrictions-china-due-covid-19} accessed 16 December 2022.

[149]WHO, 'WHO Coronavirus (COVID-19) Dashboard', available at: {https://covid19.who.int/} accessed 16 December 2022.

[150]Na Zhu, Dingyu Zhang, Wenling Wang, Xingwang Li, Bo Yang, Jingdong Song, Xiang Zhao, Baoying Huang, Weifeng Shi, Roujian Lu, Peihua Niu, Faxian Zhan, Xuejun Ma, Dayan Wang, Wenbo Xu, Guizhen Wu, George F. Gao, and Wenjie Tan, 'A novel coronavirus from patients with pneumonia in China, 2019', *The New England Journal of Medicine*, 382:8 (2020), p. 728.

[151]Ibid.

[152]WHO, *Genomic Sequencing of SARS-CoV-2: A Guide to Implementation for Maximum Impact on Public Health* (Geneva: World Health Organization, 2021), pp. 2, 15.

This novel coronavirus[153] was first sequenced by the National Institute of Viral Disease Control and Prevention,[154] part of the Chinese WHO CC in Beijing, identified above. The sharing of the complete genetic sequence of this virus online in early January 2020 was fundamental to its characterisation, enabling the rapid development of diagnostics and the development of therapies and vaccines.[155] Complete sequences uploaded to GISAID supported the phylogenetic or evolutionary analysis of the virus that would reveal its relationship with different organisms. While this virus shared around 86 per cent of its genetic material with SARS from 2003, it poses much more of a public health threat because of its higher reproductive rate and high proportion of asymptomatic infections that amplify the outbreak through silent spread.[156]

In response, a range of surveillance efforts around the world were sparked to develop RT-PCR tests that could confirm suspected cases of COVID-19. Consensus or conserved regions of the virus's genetic code were used to design RT-PCR tests[157] and the primers used in the designation of these tests were shared with the WHO to aid surveillance and detection activities in China and around the world. The WHO quickly developed guidance for countries on how to implement surveillance systems that could not only monitor the spread of the virus within populations but also measure the changing characteristics of the viral genome itself as has been revealed with the identification of novel variants to date labelled Alpha, Beta, Gamma, Delta, and Omicron.[158] This surveillance would utilise both RT-PCR and genomic sequencing technologies.

In order to facilitate the range of sequencing needed to maintain surveillance the WHO set up a COVID-19 Reference Laboratory Network to provide confirmatory testing.[159] In coordination with this network, the WHO also set up the SARS-CoV-2 Evolution Working Group focused on providing timely information on the identification and evaluation of potentially relevant mutations, as well as advice for risk mitigation.[160] The WHO has also leveraged and utilised NICs and the range of other laboratories within GISRS to facilitate genomic surveillance of SARS-CoV-2 and monitor genetic variants.[161]

As of the 16 of December 2022, the WHO Director-General determined that the COVID-19 pandemic continues to constitute a PHEIC.[162]

Conclusion

This article has investigated the WHO's declaration of a PHEIC and the securitisation of three infectious disease outbreaks in the form of H1N1, Ebola, and COVID-19. It has argued that the securitisation of these outbreaks was dependent upon global surveillance networks that

[153]WHO, 'Statement on the Second'.

[154]Wenjie Tan, Xiang Zhao, Xuejun Ma, Wenling Wang, Peihua Niu, Wenbo Xu, George F. Gao, and Guizhen Wu, 'A novel coronavirus genome identified in a cluster of pneumonia cases: Wuhan, China 2019−2020', *China CDC Weekly*, 2:4 (2020), p. 61.

[155]WHO, *SARS-CoV-2 Genomic Sequencing for Public Health Goals* (Geneva: WHO, 2021), p. 7; WHO, *Genomic Sequencing of SARS-CoV-2*, p. 19.

[156]Annelies Wilder-Smith and Sarah Osman, 'Public health emergencies of international concern: A historic overview', *Journal of Travel Medicine*, 27:8 (2020), p. 8.

[157]Zhu et al, 'A novel coronavirus from', p. 728.

[158]See WHO, 'Tracking SARS-CoV-2 Variants', available at: {https://www.who.int/en/activities/tracking-SARS-CoV-2-variants/} accessed 16 December 2022.

[159]WHO, *Terms of Reference for WHO Reference Laboratories Providing Confirmatory Testing for COVID-19* (Geneva: WHO, 2020), p. 1.

[160]WHO, *SARS-CoV-2 Genomic Sequencing*, p. 9.

[161]WHO, *Operational Considerations to Expedite Genomic Sequencing Component of GISRS Surveillance of SARS-CoV-2* (Geneva: WHO, 2021), pp. 1–2.

[162]WHO, 'Statement on the Thirteenth Meeting of the International Health Regulations (2005) Emergency Committee Regarding the Coronavirus Disease (COVID-19) Pandemic', available at: {https://www.who.int/news/item/18-10-2022-statement-on-the-thirteenth-meeting-of-the-international-health-regulations-(2005)-emergency-committee-regarding-the-coronavirus-disease-(covid-19)-pandemic} accessed 16 December 2022.

utilised genetic technologies to visualise and categorise the molecular characteristics and spread of the pathogen in question. These instances of securitisation give us new insight into the role that visual evidence in the form of genetic data on pathogens plays in this process. In the case of H1N1 the unique genetic sequence data of the virus was an important driving factor in the WHO's decision to declare a PHEIC. In the case of Ebola, too, the widespread re-emergence of this well-known virus within the West African population, made intelligible via the use of RT-PCR tests, was a vital factor in the declaration of the PHEIC. The case of COVID-19 also revealed the key role that genomic sequencing and RT-PCR tests played in revealing the unique nature of the SARS-CoV-2 virus and its spread around the world in the declaration of the PHEIC.

Drawing from the literature focused on the role of science in securitisation efforts this article identified two key dynamics through which genetic technologies were able to play such a vital role in the declaration of PHEIC in these cases. Firstly, in relation to H1N1, Ebola and SARS-CoV-2, these technologies revealed the novel molecular characteristics and prevalence of these viruses within populations that literally created them as objects of knowledge. This process of *objectification* led to their categorisation and securitisation in terms of the threat that they posed to the health of the international community. Secondly, the evidence in all three cases was mobilised by the WHO Director-General and the Emergency Committee to support their securitisation agenda and the declaration of a PHEIC. In combination with the surveillance networks that facilitate them, scientific evidence provided by genetic technologies is now playing a necessary and essential role in the process through which the WHO securitises infectious disease outbreaks via the declaration of PHEIC. As a result, the securitisation of infectious disease outbreaks is now reliant upon the evidence made intelligible by genetic technologies.

Of course, the securitisation of infectious disease is still subject to political dynamics and prejudices and the evidence provided by genetic technologies on the nature and spread of infectious pathogens alone is not sufficient in determining the declaration of a PHEIC. This case though demonstrates the extremely influential and now *necessary* role that evidence on the genetic data of pathogens plays in this process. To date, this element has been overlooked by thinkers working in this area. Commentators have noted that the process of securitising health threats is frequently shaped by non-medical considerations[163] and that relevant evidence cannot, in itself, account for the belief of a community in a security phenomenon.[164] While this article has argued that indeed, genetic technologies alone cannot generate the securitisation of infectious disease outbreaks, we must now come to understand their increasing power to make intelligible the nature of disease causing pathogens and the way that these understandings influence our political and security practices. If as Alison Howell notes, health and medicine has always been imbricated within security and military efforts,[165] we are now seeing the ways in which particular genetic technologies now play a *necessary* role in the securitisation of infectious disease outbreaks.

One wider implication of this contribution relates to the way in which the analysis of the role of genetic technologies can give us insight into the securitisation of infectious disease outbreaks around the world and outside the bounds of the states of the Global North. As Claire Wilkinson has argued, securitisation theory universalises a political system that predominantly reflects European and North American understandings of society and the state in terms of political continuity, stability, and cohesion that, in contrast, is not present in many developing countries, if indeed it is present in Western countries at all.[166] The result is a civilisationist dynamic in which Western societies and states are positioned as more 'advanced' than their underdeveloped others.[167]

[163]Lo Yuk-Ping and Thomas, 'How is health', p. 448.

[164]Balzacq, Léonard, and Ruzicka, '"Securitization" revisited: Theory and cases', p. 519.

[165]Howell, 'The global politics of', p. 973.

[166]Claire Wilkinson, 'The Copenhagen School on tour in Kyrgyzstan: Is securitization theory useable outside Europe?', *Security Dialogue*, 38:1 (2007), pp. 5, 10.

[167]Howell and Richter-Montpetit, 'Is securitization theory', p. 7.

One of the effects of the recent COVID-19 pandemic has been the increasingly widespread use of genomic sequencing to guide public health responses in near-real time. For the WHO this has represented nothing less than a revolution in viral genomic investigations.[168] While there are very severe and widespread inequalities that surround and structure the architecture of global health security, not least in the economic, racial, and epistemic realms, Low and Middle Income Countries are in the process of developing their own biomedical capabilities.[169] These capabilities will build on and extend the increasingly global landscape of genomic surveillance that has emerged through efforts to combat the SARS-CoV-2 virus and its variants.[170] The result is an opening up of the horizon through which we can understand the ways in which infectious disease outbreaks are securitised around the world in the development of nuanced conclusions that can engage more sensitively with local conditions.

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[168]WHO, *Genomic Sequencing of SARS-CoV-2*, p. 1.

[169]Stefan Elbe, 'Who owns a deadly virus? Viral sovereignty, global health emergencies, and the matrix of the international', *International Political Sociology*, 16 (2022), pp. 7, 12.

[170]See Zhiyuan Chen, Andrew S. Azman, Xinhua Chen, Junyi Zou, Yuyang Tian, Ruijia Sun, Xiangyanyu Xu, Yani Wu, Wanying Lu, Shijia Ge, Zeyao Zhao, Juan Yang, Daniel T. Leung, Daryl B. Domman, and Hongjie Yu, 'Global landscape of SARS-CoV-2 genomic surveillance and data sharing', *Nature Genetics*, 54 (2022), pp. 499–507.

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