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Article (Accepted Version)

Long, Christopher (2019) Challenging contingency: viruses and the nature of molecular life. Security Dialogue. ISSN 0967-0106

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Challenging contingency: Viruses and the nature of molecular life

Forthcoming in *Security Dialogue*

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This is the author-accepted version, accepted 2 September 2019.
Please cite the publisher's version of record, once it becomes available.

Abstract

Understandings of the nature or inherent workings of molecular life in the field of biopolitical security studies have today been characterized predominantly in terms of contingency. This article challenges this characterization. It does so by identifying a particular logic of operation that organizes political action and intervention at both the level of the population and the molecular in response to the threats of smallpox, Ebola and pandemic influenza. It argues that, in fact, rather than securing by instantiating a general economy of the contingent (Dillon and Lobo-Guerrero, 2008: 284), governing practices rely upon the characterization of the nature of molecular life in terms of its constant biological dynamics. Governments around the world, and the US government in particular, have reacted to the increased likelihood of the emergence of disease through the stockpiling of new pharmaceuticals, including the antivirals ST-246, ZMapp and Tamiflu. Antivirals represent a pharmaceutical tool stockpiled by governments to ensure that they can respond to the emergence of novel biological threats. The characterization of the nature of molecular life in terms of its constant biological dynamics is so important, then, as it is this that underpins political programmes of preparedness that utilize antivirals in the prevention of disease.

Keywords

Antivirals, biopolitical security studies, governmentality, molecular life, nature, viruses

Nature is something that runs under, through, and in the exercise of governmentality. It is, if you like, its indispensable hypodermis.

Foucault, 2010: 16.

Introduction

Scientific understandings of the way that life works have recently undergone a significant shift as a result of molecular and digital revolutions. In response, governments around the world have become ever more attuned to the potential of molecular life, such as bacteria and the influenza virus to randomly evolve into new forms of disease. The political response to this threat has predominantly focused on the development and stockpiling of a range of new pharmaceutical defences, including antivirals and vaccines. Such pharmaceuticals support and make possible political programmes of preparedness. In the field of biopolitical security studies, a particular conception of the nature or inherent workings of life at the molecular level in terms of its randomness or contingency has been identified as a driver behind these processes (see Braun, 2007; Cooper, 2006; Dillon and Lobo-Guerrero, 2008, 2009; Dillon and Reid, 2000, 2001; Diprose et al., 2008; Elbe, 2014; Elbe et al., 2014; King, 2002; Kittelsen, 2009; Lakoff, 2008; Roberts and Elbe, 2017). As a consequence, other understandings of the nature of molecular life in this field have been overlooked. This article challenges this conception through an investigation into the antiviral stockpiles of governments and international organizations to combat the threats of smallpox, Ebola and pandemic influenza. It argues that, in fact, central to the development of these antivirals is a characterization of the nature of molecular life in terms of its constant biological dynamics. This is of particular significance as this characterization has made possible the development of these pharmaceutical defences, so underpinning the preparedness and response activities of governments in the face of these threats.

Scientific developments, particularly in the field of molecular biology, have led to a new scale at which we understand the workings of life. Termed the molecular vision of life, these new understandings have allowed us to visualize and intervene in life at the molecular level (see Rose, 2007). The complexity sciences have been one of the most significant influences on the characterization of the nature of molecular life, and indeed theoretical biologist Stuart Kauffman has identified it in terms of complexity. The search within this field is for a deep theory of biological order that gives rise to contingent and unpredictable life (Kauffman, 1995: 18–19). To be emphasized are the nonlinear forms of change through which systems evolve and order is reproduced (Dillon and Reid, 2001: 42–43). As understood by the complexity sciences, molecular life is ‘not more certain life. It is differently contingent life’ (Dillon and Lobo-Guerrero, 2009: 16). It has been argued that one of the important consequences of this shift is that

security practices informed by understandings of living matter as a function of force fields of morphogenesis are not prophylactic practices. Regeneration rather than protection is more their condition of operation. Transformation rather than preservation is their object. They become preoccupied instead with securing (which now means engendering and manipulating) the contingent correlation of the events through which life-forms morph and change (Dillon and Lobo-Guerrero, 2008: 288).

This characterization of security practices in light of the contingent nature of molecular life is challenged here through an investigation into the antiviral stockpiles created by governments to combat the random emergence of smallpox, Ebola and pandemic influenza. Such efforts represent mass prophylaxis caches (Ryan and Glarum, 2008: 260) designed to prepare for and respond to the emergence of novel viruses. Further, their goal is the prevention of illness and the preservation and maintenance of a bodily state free from disease. Crucially, the development of these antivirals depends upon the characterization of molecular life in terms of its constant biological dynamics.¹

This article then challenges the excessive determination of the nature or inherent workings of molecular life in terms of contingency and the security practices it is argued this instigates. In order to do this, it analyses the governance of smallpox at both the level of the population and the molecular. Drawing on Michel Foucault, an analysis of the governance of smallpox at the level of the population in *Security, Territory, Population* is conducted in relation to the production of three antivirals – ST-246, ZMapp and Tamiflu. An investigation into the governmental and operational logics (Dillon and Lobo-Guerrero, 2008: 272) employed to deal with the threat of disease at these two scales reveals one not of radical shift but of continuity. Despite the change in technologies used to shape smallpox as an object of knowledge at the molecular level and that of the population, governing practices at both these scales rely upon the characterization of the nature of disease in terms of its constant biological dynamics through and on which to act. It is only by utilizing this under-appreciated concept of nature (see Foucault, 2004, 2009, 2010) that we can discern the governing practices across these two scales. Natural regularities that manifest as constant biological dynamics provide the basis through which such practices in the form of vaccination programmes and antiviral drugs can be developed and implemented to address biological threats, including that of smallpox, Ebola and pandemic influenza.

This argument is developed in three sections. The first section demonstrates the way that a particular conception of the nature of molecular life in terms of contingency has come to

¹ The term ‘constant’ is used here deliberately to emphasize the biological characteristics that governing practices depend upon that predominate over a particular period of time. Crucially, this incorporates the possibility for change and represents a distinct understanding of the nature of molecular life in contrast to those seen as inherently random or contingent on the one hand or those that are permanent or fixed on the other.

predominate in the work of security studies in this area. Such work has developed in relation to research on the political response to the evolutionary potential of the influenza virus and bacteria. The wide-ranging political implications of this have further been captured in the 'emerging disease world-view'. The significance of this for the field of security studies has also been set out in the work on 'recombinant biopolitics'. The second section, drawing on particular aspects of Foucault's work, identifies key factors in the governance of smallpox at the level of the population. This includes the way that statistics revealed certain regularities and probabilities, such as the rates of smallpox from year to year, that made its governance possible. Importantly, the *constancy* of biological dynamics such as this form one dimension of the population's inherent naturalness. The third section details the way that governments and international bodies such as the World Health Organization (WHO) have responded to the threats of smallpox, Ebola and pandemic influenza through the mass stockpiling of antivirals. Such preparedness efforts could only be put in place once advances in the molecular sciences were capitalized upon. These advances have revealed the constant dynamics through which the variola, Ebolavirus and influenza virus exit, enter and move between human cells, respectively. This section demonstrates the way in which these constant biological dynamics are targeted by the antivirals ST-246, ZMapp and Tamiflu in the prevention of disease. The article concludes with the implications of this analysis for studies on biopolitical security practices.

Contingent molecular life

As noted in the introduction, advances in the life sciences in general and the molecularization of biology in particular have revealed a new scale at which life reorganizes itself. Various technologies, such as x-ray crystallography and gene mapping, have made intelligible the precise genetic complement of human genes in addition to those of viruses and bacteria. In response, a particular field of security studies has emerged to analyse the political implications of such epistemological advances. This section of the article will argue that this field has come to conceptualize and categorize the nature or inherent workings of molecular life in terms of its contingent or random nature. One of the most prominent threats characterized in these terms has been that of the influenza virus.

Random viral mutation

A significant concern for governments today is the emergence of a novel influenza virus that has the potential to cause a new flu pandemic. In the National Security Strategies of the United Kingdom, pandemic threats are ranked as a (top) Tier 1 threat on a par with terrorism (Elbe et al., 2014: 449). Such concern has arisen as a result of the massive scale of casualties to emerge from previous pandemics, including that of 1918, which claimed the lives of 50 million people worldwide, and the

processes of 'globalization' that intensify and encourage the circulation of dangerous new diseases (Collier and Lakoff, 2008: 16). Molecular immunology has analysed and made visible the constituent elements of viruses responsible for causing flu and the way in which their genetic complement can either change subtly into seasonal varieties of influenza or dramatically into more lethal pandemic versions. Subtle or dramatic changes have been termed genetic 'drift' and 'shift', respectively (Braun, 2007: 16; Elbe et al., 2014: 451; Lakoff, 2008: 405). Unpredictable changes to the viral genome impact the make-up and function of proteins, including hemagglutinin and neuraminidase, that enable viruses to enter and exit human cells (Braun, 2007: 15). The genetic composition of these proteins in turn reflect how widely the virus can spread and how lethal it will be (Braun, 2007: 16). As we will see later, the constant workings of these proteins, the neuraminidase in particular, provides the foundation for the development of the antiviral Tamiflu.

For Braun the impact of such knowledge on the molecular workings of viruses has recoded molecular life as 'inherently unpredictable, as always, in a sense, "uncanny"' (2007: 17). As a consequence, human beings are plunged into a 'molecular world of chaotic change' (Braun, 2007: 17) with its corporeality 'radically open to the world, thrown into the flux of an inherently mutable molecular life where reassortment is not what we control, but what we fear' (Braun, 2007: 17). Such molecular unpredictability exacts a toll in terms of subjective vulnerability and the fear of biomolecular manipulation (see Kittelsen, 2009). Virtuality best captures this threat in the potential mutations that could occur, its unpredictable spatio-temporalities and the political focus on surveillance and pharmaceutical solutions that seek to preempt its emergence (Braun, 2007: 18–21).

The stockpiling of pharmaceuticals to combat the constantly and continuously mutating, changing and evolving (Elbe et al., 2014: 450; Elbe, 2014: 929) nature of influenza viruses (see also Diprose et al., 2008: 282) has also been noted in response to the specific threat of H5N1 or 'bird flu' in 2005. In this case governments across Europe stockpiled antiviral medications such as Oseltamivir, also known as Tamiflu, in order to facilitate a preparedness response. Algorithmic-enhanced syndromic surveillance systems have also been deployed to rapidly detect the random emergence of new influenza viruses with pandemic potential (see Roberts and Elbe, 2017). Viral mutation and change have further been categorized as facts of nature and, as a result, novel pathogen emergence is an inevitability with human health and survival to be challenged ad infinitum (Henderson, 1993: 283). Viruses, though, are not the only biological agent whose nature has been characterized in terms of contingency.

Bacterial evolution and the emerging infectious diseases world-view

The influenza virus represents to some degree the paradigmatic example of the contingent nature of molecular life. Governments are, however, also coming to recognize the disturbing societal implications resulting from the ability of bacteria to genetically morph into new complements with resistance to vital antibiotics. Microbiology has demonstrated the way that bacteria are able to share and exchange DNA between themselves through various processes, including horizontal gene transfer (Cooper, 2006: 115–116). This has led to a new conceptualization of the bacterial genome as dynamic, flexible and subject to both small and large changes in the course of its development (Ho, 1998: 104). As a result of this capacity, the continuing evolution of infectious disease becomes inevitable (Cooper, 2006: 115–116). Emergence comes to capture the contingent nature of bacterial evolution. Infectious disease is defined ‘as *emerging* and *emergent* – not incidentally, but in *essence*’ (Cooper, 2006: 118). The random and unforeseen nature of bacterial evolution becomes public health’s greatest enemy. In response, the US government’s Defense Advanced Research Projects Agency (DARPA) has engaged in pathogen and pharmaceutical development to preempt ‘infectious diseases *that have not yet even emerged*’ (Cooper, 2006: 126).

Such a view of infectious disease shaped governmental policy discourse in the late 20th century. Organizations including the Institute of Medicine and the National Intelligence Council emphasized the threat posed by the evolutionary potential of microbes to overcome defences such as vaccines through selective mutations (Lederberg et al., 1992: preface v) and the threat that the constant evolution of infectious disease microbes posed to US and global security (National Intelligence Council, 2000: 23). The events of this time would be collected into an ‘emerging disease world-view’ consolidating the unpredictable nature of molecular life to evolve and mutate into new pathogenic forms threatening US national security, international development and global health (see King, 2002). Work in security studies would see far-ranging implications arising from such conceptions of the nature of life at the molecular level.

Recombinant biopolitics

For the commentators Michael Dillon, Julian Reid and Luis Lobo-Guerrero, the digital and molecular revolutions, in tandem with the complexity sciences, have not only fundamentally reshaped how we understand life and its workings but, more importantly, also reshaped the way that security practices now function in response. Life has become informationalized and classified in terms of digital and molecular code (Dillon and Lobo-Guerrero, 2009: 8). Species life following the evolutionary insights of Darwin is understood to be emergent and radically contingent (Dillon and Lobo-Guerrero, 2009: 14). The digital and molecular revolutions have not only entrenched this

account of species-being but also extended it (Dillon and Lobo-Guerrero, 2009: 15). The molecular universe is

comprised of bodies in continuous formation. These consist of shifting ensembles and assemblages whose very relationality ensures unpredictable nonlinear mutation, transformation, and change since information is said to be transferred not only by words but also by particles (of DNA) and each in the same way (Dillon and Reid, 2000: 138).

Molecularized life is then ‘not more certain life. It is differently contingent life’ (Dillon and Lobo-Guerrero, 2009: 16). Further, when security processes take molecular life as their referent object, ‘a recombinant biopolitics of security emerges oriented towards becoming an experimental scientific art of design’ (Dillon and Lobo-Guerrero, 2008: 289). As set out in the introduction, security now changes fundamentally and is no longer based on prophylactic practices. Its focus now becomes regeneration and transformation rather than protection and preservation. It seeks to incite, manipulate and act through the very (random) ways in which life develops (Dillon and Lobo-Guerrero, 2008: 288). This article challenges these conclusions, arguing that while contingent understandings of molecular life have certainly shaped perceptions of insecurity surrounding infectious disease, this is only half the story. An altogether different conception of the nature of molecular life and operational logic is at the root of efforts to deal with the random emergence and spread of disease through antiviral development. In doing so it draws on Michel Foucault and in particular his to-date-unexplored work on the role of natures in governmental efforts to deal with the threat of diseases to the population. His focus is on one of the most notorious viruses and diseases known to man: smallpox.

Governing smallpox at the level of the population

Smallpox, caused by the variola virus, has been described as the most feared disease in history, blighting human society until its eradication in 1977. Foucault’s analysis of the governance of smallpox in 18th century Europe is situated within his work on the emergence of liberal governmentality that took the condition, longevity and health of the population as one of its prime concerns (Foucault, 2009: 105). This section identifies a distinct operational logic to the management of smallpox at the level of the population; one based upon the identification of constant biological dynamics that form part of the population’s inherent naturalness.

Processes of capitalist development and urbanization encapsulated in the emergence of ‘the town’ famously posed new problems regarding the circulation of people, goods and diseases. Smallpox had the potential to realize itself in very sudden and intense epidemic outbursts (Foucault, 2009: 58). Practices such as variolation or inoculation with smallpox and later cowpox were utilized to contain its spread. As Foucault notes, the effects of these processes were ‘a pure matter of fact,

of the most naked empiricism' (2009: 58). The classical methods of biology, demonstrated here, relied upon the phenotype or physical changes in the body to signify a deeper molecular shift in immunity (Hanley, 2011: 637). As we will see with the analysis of the smallpox antiviral ST-246, molecular biology has opened up a new range of techniques with which to decipher and directly edit the molecular make-up of a virus. As a result, the virus is formed as an object of knowledge in relation to the genetic basis of its reproduction and spread. For Foucault, a crucial tool in the management of this disease was the use of statistics.

The statistical analysis of the occurrence of smallpox within a population revealed certain regularities and probabilities, such as the number of cases that occurred within a particular age group and the risk they faced of catching the disease versus the risk of its occurring as a result of vaccination or variolization (Foucault, 2009: 59–61). The differential levels of risk faced by different age groups identified those who were in greater danger of death. For Foucault the endgame of this calculation was to bring those more unfavourable calculations of risk and mortality in line with the more favourable, to normalize (Foucault, 2009: 62–63). As Lakoff notes, the statistical analysis of disease rates 'revealed that while the future was contingent, there were nonetheless certain regularities according to which governments could rationally plan' (2015: 43). The case of smallpox and the attendant attempts to manage the disease within the population revealed the crucial biological dynamics, in this case the rates of disease in particular age groups that must be taken into consideration when promoting the health of the population. The management of smallpox within the population was for Foucault tied directly to its naturalness.

The inherent naturalness of the population

The population emerged as a new political personage as a result of the need to position the modern town within open circuits of exchange. Thus, the fundamental principle of economic government in the Physiocrats' and François Quesnay's thought was the freedom of commerce and the circulation of grain (Foucault, 2009: 50 note 5). A physiocratic conception of economic productivity dependent upon circulation necessitates that the population be considered 'as a set of processes to be managed at the level and on the basis of what is natural in these processes' (Foucault, 2009: 70). As a result, the population under the physiocrats is reframed as a technical–political object of management and government, the naturalness of which is conceived of in three ways.

In one way, it is a datum that depending upon a series of variables, such as the climate and legal regulations, whose effect can be understood through reflection and analysis, removes it from the direct control of the sovereign (Foucault, 2009: 70–72). The naturalness of the population also appears, in a second way, with its desire that given the freedom to express itself will act in the

collective interest (Foucault, 2009: 73). A third aspect of the naturalness of the population, and most importantly for us here, is demonstrated in the *constancy* of certain phenomena (Foucault, 2009: 74). Statistical analysis of the population revealed the constancy of events such as suicides and accidents. The constant nature of phenomena only becomes pertinent in their political and economic effects when the population is analysed as a collective (Foucault, 2004: 245–246). The seemingly contingent behavioural characteristics of a population could be mapped and calculated through the use of statistics (Dillon and Lobo-Guerrero, 2008: 279). Through such reflective technologies, a population is revealed to have certain inherent regularities. We can then draw out two key characteristics of the population that made the spread of smallpox amenable to liberal governance – its biological dynamics, such as the rates of disease across a population, and the constancy of these dynamics that in recurring year to year can be understood to have a particular naturalness and inherent regularity.

For Foucault the political technology of statistics shaped the population as a subject and object of knowledge constituted by ‘living beings, traversed, commanded, ruled by processes and biological laws’ (Foucault, [1981] 2007: 161). Such biological laws or constants demonstrated an inherent naturalness to the population. Nature is no longer an original and reserved region on which the exercise of sovereign power should not impinge (Foucault, 2010: 15). Not only is there a certain naturalness specific to the practice of government itself, but the objects of governmental action are also conceived of as having a specific nature (Foucault, 2010: 15). ‘Nature is something that runs under, through, and in the exercise of governmentality. It is, if you like, its indispensable hypodermis’ (Foucault, 2010: 16). As a consequence, governmental practice must observe and inductively analyse patterns of circulation in order to understand and respect the naturalness specific to the objects of its concern that are revealed through this freedom. The statistical regularities of the natural occurrence of smallpox within the population must be respected (Foucault, 2010: 16), shaped, worked within and around so as to normalize and make more acceptable. A core operational logic runs through the governmental management of smallpox at the level of the population, one that identifies the nature of the phenomenon in terms of its constant biological dynamics.

As the next section will demonstrate, despite the shift to the molecular scale in the way that we can now visualize and manipulate life, this operational logic can also be found at work in the management of smallpox, Ebola and pandemic influenza via the development and stockpiling of particular antivirals, specifically ST-246, ZMapp and Tamiflu. Each one intervenes at a specific molecular site, yet it does so in relation to the constant biological dynamics of the virus. These dynamics shape each virus as an object of knowledge with inherent natural characteristics capable

of manipulation. They also form the basis for the production and stockpiling of antiviral medications essential to the preparedness efforts of governments in response to these threats.

Antivirals, stockpiling and constant biological dynamics

This section investigates government efforts to combat the disease threats of smallpox, Ebola and pandemic flu through the stockpiling of antivirals. The US government in particular, but also governments more widely around the world have developed and stockpiled ST-246, ZMapp and Tamiflu to combat these threats. Each antiviral targets and intervenes in a constant biological dynamic that has been identified within each of the three viruses responsible. This includes the way that the variola virus exits human cells, the Ebolavirus's entry into human cells and the influenza virus's movement between human cells. As will be argued and in contrast to the conclusions of those commentators detailed above, security practices informed by contingent understandings of molecular life remain focused on prophylaxis measures, in this case the widespread development and stockpiling of antivirals. In this way, the characterization of the nature of molecular life in terms of its constant biological dynamics underpins preparedness efforts to combat the spread of disease.

The widespread stockpiling of antivirals and their underpinning

The development of mass prophylaxis caches, otherwise known as pharmaceutical stockpiles, has been noted as a core exercise in the facilitation of preparedness to combat biological threats (Ryan and Glarum, 2008: 260). Mass prophylaxis refers to the medical care provided to populations to prevent and protect them from disease (Ryan and Glarum, 2008: 260). The first US government effort to develop mass prophylaxis caches to protect the population took the form of the National Pharmaceutical Stockpile (NPS), set up in 1999 to distribute essential medical materiel during an emergency within 12 hours of a federal decision to deploy (Prior, 2004: 1). Following the attacks on 11 September 2001 and the anthrax letters that followed soon after, the Strategic National Stockpile (SNS) was established to extend and replace the NPS.

The SNS is not just made up of antivirals including ST-246, ZMapp and Tamiflu, but it is also the nation's repository of antibiotics, chemical antidotes, antitoxins, vaccines and other medical materiel designed to supplement and resupply state and local public health agencies in the event of an emergency (National Academies of Sciences, Engineering, and Medicine, 2016: 1). These pharmaceuticals are combined into 'push packages' that at various points have consisted of 124 cargo containers, weighing 94,424 pounds and taking up 5,000 square feet of floor space (Prior, 2004: 7). The SNS currently holds approximately \$7 billion in products distributed across six large secret facilities in different locations throughout the United States (National Academies of Sciences, Engineering, and Medicine, 2016: 3).

The United States is not the only country that has invested significant efforts into the development of stockpiles. As Elbe has noted (2014: 925), a number of other countries and intergovernmental organizations have stockpiled pharmaceuticals. This includes the European Union's establishment of a legal basis for the coordination of vaccine procurement, the Australian government's National Medical Stockpile containing essential vaccines, antibiotics, antiviral drugs as well as chemical and radiological antidotes, the Canadian government's National Emergency Stockpile System and also the United Kingdom's Reserve National Stock for Major Incidents that contains nerve agent antidotes, antitoxins, antibiotics and other post-exposure medications. Pharmaceutical stockpiling is then a widespread government practice employed to combat biological threats. As will be detailed below, ST-246 and ZMapp have been extensively acquired and placed by the US government into the SNS.

Tamiflu is perhaps the most widely stockpiled antiviral, with billions of doses of this and similar antivirals stockpiled around the world to combat the pandemic potential of bird and swine flu in 2005 and 2009 respectively (see Reddy, 2010). The case of Tamiflu also represents the value of antivirals for international bodies such as the WHO. In preparation for bird flu, in January 2006 the WHO set up an international antiviral stockpile of five million treatment courses for rapid deployment to anywhere in the world (Elbe, 2014: 926–927). Antivirals have thus become essential to the national and international response to emerging biological threats. Underlying this government and organizational turn to pharmaceuticals is a key principle in the way that modern medicines are developed.

The germ theory of disease first identified and categorized contagious agents as necessary causes of disease (Caduff, 2015: 30–31). The molecularization of biology has intensified this process of classification and causation. A general principle in the production of modern medicines, from the development of antibiotics to cancer treatments is the identification of compounds that can selectively bind to and inhibit the receptors and tissues of particular parasites and rogue cells (Drews, 1999: 64–65). Target identification of specific molecular sites is a prerequisite for drug discovery and development. The molecularization of biology has supported an understanding of disease processes at the genetic level and the determination of the optimal molecular targets for drug intervention (Drews, 2000: 1962). In 2000, drug development focused on 500 molecular targets; a greater understanding of the disease-causing properties of genes has increased the number of potential molecular drug targets to between 5,000 and 10,000 (Drews, 2000: 1962). As will be demonstrated below, each of the three antivirals discussed target particular molecular sites on the relevant virus, interfering in a constant biological dynamic responsible for the replication of

the virus and the spread of disease. This section will now detail why antivirals represent such a valuable political tool for governments.

Viral natures and the political turn to antivirals

While there is debate surrounding the status of viruses as living entities, it cannot be denied that in their many different forms and types, viruses have exacted a considerable toll on human existence in terms of illness and death. The variola, Ebolavirus and influenza viruses, like all viruses, cannot replicate on their own and so must enter the host cell, hijack its genetic machinery to replicate and then exit the host cell and spread to others in order to effectively survive and cause disease (Caduff, 2015: 138). As we shall see, this essential factor in the nature of viral reproduction also provides a range of constant biological processes through and on which the antivirals discussed in this article can work. Yet, these three viruses all differ in relation to the way in which they reproduce in the wider environment. While the variola virus responsible for smallpox existed exclusively in human beings, the influenza virus exists widely amongst other animal reservoirs, including wild birds, domesticated chickens, horses and pigs (Zimmer, 2015: 22). When two different influenza viruses meet in a host, they potentially swap genes, creating new strains against which human beings have little defence.

For example, the genes of the H1N1 influenza virus responsible for the 'swine flu' outbreak of 2009 have been sequenced to reveal a combination of four separate strains that jumped from pigs to birds and back to pigs before finally moving to humans (Zimmer, 2015: 23). The Ebolavirus also circulates often harmlessly in some animals, such as bats, and lethally in others, including gorillas and chimpanzees, before spilling over into humans, generating outbreaks such as that which occurred in West Africa between 2013 and 2016 (Zimmer, 2015: 82) and that which is currently occurring in the Democratic Republic of Congo. To date, four different species of Ebolavirus have been identified as lethal to humans. Vaccines are developed to target particular strains. The circulation of viruses amongst different animal species increases genetic diversity and results in novel forms and outbreaks making the development of effective vaccines extremely difficult. To combat a novel influenza virus of pandemic potential, at least six to nine months is necessary to mass-produce a new vaccine (Elbe, 2018: 39). One key advantage of antivirals, particularly those developed to combat the influenza virus, is that they can target functions shared by different viral strains (De Clercq, 2004: 715). One such function and constant biological dynamic is the working of the neuraminidase protein that, as we will see below, is the target of Tamiflu.

In addition to the long lead-time necessary to mass-produce a vaccine, they also take time to stimulate the host immune response, generating a window of vulnerability (Yang et al., 2005:

13139). Antivirals can fill this window and complement vaccination as they reduce viral load quickly, regardless of immune status, and can also lower transmission rates by diminishing the amount of the virus circulating in a patient's body (Yang et al., 2005: 13139). It is no surprise then that governments have turned to this particular pharmaceutical defence to combat the emergence of disease. This section will now turn to the antiviral ST-246, developed and stockpiled to combat the threat of smallpox, which acts on the variola virus's constant process through which it exits human cells.

ST-246, smallpox and the viral exiting of human cells

Following the events of 11 September 2001, and the anthrax letters that followed soon after, the US government significantly enhanced its efforts to deal with the deliberate release of biological threats. Smallpox was a prime concern as following its worldwide eradication in 1977, vaccination was halted. As a result, if an attack were to occur, virtually the entire population of the United States, and indeed the globe, would be susceptible to this highly contagious virus (Institute of Medicine, 2005: 47). The Centers for Disease Control and Prevention (CDC) quickly moved to stockpile enough smallpox vaccine to protect the entire US population (Tucker, 2001: 245–246). Antivirals were also actively developed and stockpiled to complement the use of vaccines and address their limitations. To support these efforts the US government set up a range of new laws and institutions, including Project BioShield in 2004, and the Biomedical Advanced Research and Development Authority (BARDA) in 2006. They would provide technical and financial support to private companies via public–private partnerships to develop new pharmaceuticals known as medical countermeasures essential to preparedness efforts. Such measures would lead to considerable government adaptation and the emergence of novel bio-economies (see Long, 2019).

SIGA Technologies, the parent company of ST-246 (also known as Tecovirimat, Arestvyr and Tpoxx), partnered with the US government and received financial and technical development support under Project BioShield and through BARDA. This primarily came in the form of a five-year contract worth US\$ 433 million in 2011 that supported the advanced development of ST-246 and procured 1.7 million treatment courses into the SNS (HHS News, 2011). Approval from the US Food and Drug Administration followed in July 2018 (SIGA, 2018a). In September of that same year, BARDA awarded SIGA a multi-year contract valued at up to \$629 million to maintain the stockpile of 1.7 million courses of ST-246 (SIGA, 2018b). Yet, the integration of ST-246 into the preparedness armamentarium of the US government would only be carried out following the discovery that it could effectively prevent smallpox. Crucially, ST-246 does this by intervening in a constant biological dynamic through which the variola virus travels through the human body, specifically in this case its ability to exit human cells in its attempt to spread to others.

The first sighting of the variola virus came in 1947 with the use of the electron microscope (Koplow, 2003: 33). This was the first sighting of any virus with this tool and it supported research that up to this day has tried to understand the different ways in which the virus reproduces, spreads through the body and infects other cells. Once the variola virus has infected a human cell, like all viruses it uses the genetic machinery of the host to replicate. Replication results in two different forms. One form of the virus, unlike the other, acquires an extra membrane allowing it to exit the cell under its own agency, further spreading the disease. This particular form of the virus plays a more critical role in cell-to-cell spread within the body than those that do not have this feature (Jahrling et al., 2005: 818; Koplow, 2003: 34).

Armed with this knowledge, ST-246 prevents the production of virus particles that have this extra membrane and that have been implicated in the long-range spread of the virus within the body (Grosenbach et al., 2011: 657). In the absence of this membrane the virus disseminates poorly from the site of original inoculation (Grosenbach et al., 2011: 657). In addition to poor dissemination, the lack of this membrane also reduces the virulence of the virus, making it less capable of causing disease (Grosenbach et al., 2011: 657). ST-246 intervenes, therefore, in the variola virus's constant pathway of infection and replication so as to prevent the occurrence of disease. It does so via the interference with a key gene responsible for the formation of this extra membrane.

Through the use of various molecular biological techniques it was discovered that ST-246 inhibits the workings of a particular protein, p37, that is responsible for the formation of the variola virus with this extra membrane. P37 is a protein that makes up the genetic complement of all viruses within the genus – orthopoxviruses – that includes the variola and for which there is no common equivalent gene in mammals (Grosenbach et al., 2011: 659). This is a key factor and overcomes the problematic fact that viruses replicate inside human cells, noted above. ST-246 can be administered without the fear that it will harm human cells. Using gene mapping and through a comparison with those viruses resistant to ST-246, the specific gene which codes for the p37 protein was revealed as the target of this antiviral (Yang et al., 2005: 13146). This gene, responsible for the formation of an extra membrane, is further responsible for the spread of the virus within the body.

The molecularization of biology and the categorization of DNA into proteins and genes have allowed us to intervene in a constant biological dynamic of the variola virus, specifically, in this case, the working of a particular gene responsible for the exit of the virus from human cells and its spread and replication within the body. Following its eradication, smallpox drew government concern as a result of the fear of its deliberate release in an act of bioterrorism. Ebola was also originally viewed as a potential bioterrorist agent. Its perception as a public health threat more generally, along with

significant efforts to develop new vaccines and antivirals such as ZMapp, would emerge following the sustained outbreak in West Africa that began in 2013.

ZMapp, Ebola and the viral entry of human cells

Ebola virus disease, Ebola hemorrhagic fever or simply Ebola, is caused by the Ebolavirus that forms part of the Filoviridae family of viruses. It first emerged in Zaire in 1976, terrifying patients and doctors alike with its symptoms and lethality (Zimmer, 2015: 80). Subsequent outbreaks have been sporadic, occurring at various times in the recent past, particularly in Central and Western Africa, until December 2013 when by far the largest outbreak occurred. This epidemic across West Africa drew global attention to the threat of this disease and spurred the search for new vaccines and antivirals.

Antiviral development to combat the threat of Ebola had stalled before the outbreak in 2013 (Espeland et al., 2018: 1). This lack of investment resulted from a number of factors. Previous Ebola outbreaks had been rare and sporadic, occurring in developing regions making the clinical evaluation of potential therapeutics complicated (Byrd et al., 2013: 537). The development of any new antiviral was also inhibited by the lack of an established commercial market to spur private investment. Ebola was also primarily categorized as a bioterrorist and security threat. This meant that following the outbreak in West Africa in 2013, responsibility for the development of a new antiviral within the arms of the US government would fall under the auspices of BARDA. BARDA quickly moved to support the development and stockpiling of a new antiviral – ZMapp.

ZMapp, developed by Mapp Biopharmaceutical, Inc., is a therapy made up of three different monoclonal antibodies developed in mice and originally produced in tobacco plants. BARDA's support in the development of ZMapp began in 2014 with a \$24.9 million, 18-month contract providing funding as well as access to subject matter expertise or seasoned veterans in pharmaceutical development and technical support for manufacturing, regulatory and non-clinical activities (Global Biodefense, 2014). In September 2017, a \$44.7 million contract was awarded using Project BioShield funds that supported late-stage development and procurement of ZMapp into the SNS and its place in the US government's preparedness armamentarium (HHS, 2017).

During the 2013–2016 Ebola epidemic, ZMapp was used to treat 36 patients and continues to be available through an expanded access protocol in the United States and West Africa (HHS, 2017). It is now widely considered to be a component of standard of care, was part of the response to the emergence of cases in Guinea in March 2016 and was also available for use in the May 2017 outbreak in the Democratic Republic of the Congo (Espeland et al., 2018: 2). ZMapp neutralizes the

Ebolavirus by binding to certain proteins, so decreasing the amount of the virus in the body that the patient's immune system has to fight (HHS, 2017). As will now be demonstrated, this is done through the identification of a constant biological dynamic that again is found within the Ebolavirus's pathway of infection in the human body. In this case, ZMapp targets the constant process through which the Ebolavirus binds to and then enters human cells.

The specific proteins that are the target of ZMapp's monoclonal antibodies are the Ebolavirus's glycoprotein (Espeland et al., 2018: 2). This protein, the only one that is expressed on the surface of the virus, is critical in its life cycle as it is solely responsible for attachment to, fusion with and entry into target cells (Lee and Saphire, 2009a: 623). As viruses replicate using the machinery of living cells, an antibody preventing the entry of the virus's genetic material into human cells would also prevent the spread of the virus and consequent illness. While there is much that is not understood about the process through which the glycoprotein facilitates entry of the virus into human cells, its essential function is the reason why it is the target of neutralizing antibodies (Lee and Saphire, 2009a: 621). Using the techniques of molecular biology, including x-ray crystallography, the molecular architecture of the glycoprotein and its role in viral entry and membrane fusion has been discovered (Lee and Saphire, 2009a: 621). It has been revealed to have two structurally attached yet functionally distinct parts – GP1 and GP2. GP1 is responsible for attaching the virus and binding it to the outside of the human cell (Lee and Saphire, 2009b: 409). GP2, on the other hand, is responsible for fusing the viral and host cell membranes that allow for the safe passage of genetic material into the human cell and further replication of the virus and the spread of disease (Lee and Saphire, 2009b: 409).

The visualization of the molecular structure of the cocktail of antibodies that make-up ZMapp have allowed us to identify the particular regions targeted on the Ebolavirus's glycoprotein. Two particular antibodies (c2G4 and c4G7) target the side/base of glycoprotein at the GP1–GP2 interface, overlapping extensively, and differing mainly in their angle of approach to their binding sites (Murin et al., 2014: 17185). It has been recognized that a combination of two or more antibodies binding to similar sites may confer protection via complementary mechanisms (Murin et al., 2014: 17182). Further, the targeting of the glycoprotein base, or GP2, is a shared feature of multiple antibodies that neutralize Ebolaviruses (Murin et al., 2014: 17185).

The third antibody in the cocktail (c13C6) has been confirmed as binding within the glycan cap, a functionally important region of GP1 (Murin et al., 2014: 17185; Lee and Saphire, 2009b: 409). ZMapp, by targeting these three sites, one antibody against the top of the glycoprotein plus two against the glycoprotein base, offers superior protection compared to other antivirals (Murin et al.,

2014: 17186). As a result, the GP1–GP2 interface at the base of the glycoprotein has been recognized as a major site of vulnerability for the purposes of combatting the Ebolavirus (Murin et al., 2014: 17186). The three antibodies that make-up ZMapp bind to key sites on the glycoprotein, inhibiting the constant process through which the Ebolavirus binds to and then enters and infects human cells, a process that is responsible for the virus’s reproduction and ability to spread disease. As we shall see next in the case of the antiviral Tamiflu, another constant biological dynamic is targeted, this time the influenza virus’s process through which it moves from one human cell to another. This realization would stimulate government stockpiling efforts on the largest scale seen to date to combat the pandemic potential of bird and swine influenza.

Tamiflu, influenza and the viral movement between human cells

Pandemic influenza is perhaps the most pressing biological threat facing governments today. The influenza virus, much like the Ebolavirus, also circulates widely in a number of animal reservoirs, particularly birds and pigs. It is known to replicate rapidly but also inaccurately. The random errors that occur in the process of its replication aids the virus in its spread and survival, allowing it to adapt, adjust and escape the immunological memory and defences of the host (Caduff, 2015: 100). Yet, unlike smallpox and Ebola, the influenza virus exists in significantly fewer lethal varieties, specifically its seasonal form. Following the genetic ‘drift’ of its genome (Braun, 2007: 16), the virus is transmitted via droplets in the air allowing it to spread widely amongst susceptible populations. A consequence of this leads to a further distinction from the cases discussed previously. Seasonal flu represents a viable commercial market for private companies to capitalize upon without the need for government support that, as we saw above, was essential to the development of ST-246 and ZMapp. Tamiflu was developed with a commercial eye on the lucrative seasonal flu market (Elbe, 2018: 54). It was this commercial market that spurred early-stage development by the small biotechnology company Gilead Sciences and its licensing for further commercial development to the much larger and more established pharmaceutical company, Roche (Elbe, 2018: 54–55).

Although Tamiflu was developed and approved for the treatment of seasonal influenza in adults in 1999, its action against potentially pandemic strains of influenza would attract the attention of governments and lead to its widespread stockpiling. The emergence of two novel influenza viruses – H5N1 ‘bird flu’ and H1N1 ‘swine flu’ – in 2005 and 2009 respectively, stoked fears that these viral genomes had undergone a dramatic ‘shift’ resulting in heightened transmissibility and virulence among human populations (Braun, 2007: 16). In response, governments across Europe scrambled to create sizeable stockpiles of antiviral medications, particularly Tamiflu, in anticipation of an imminent threat (Elbe et al., 2014: 443). By 2007, many countries in Europe and around the

world had stockpiled enough antivirals to cover as much as 20 to 30% of their population (Trakatellis, 2007: 23; cited in Elbe et al., 2014: 443). Between 2004 and 2009 alone, around 350 million treatment courses, or 3.5 billion doses, of Tamiflu were supplied to governments worldwide (Reddy, 2010: 37). Underpinning this preparedness response is an operational logic that again relies upon the identification of the workings of the influenza virus in terms of its constant biological dynamics, this time intervening upon the influenza virus's ability to release itself from the surface of human cells before spreading to others.

As was discussed above, two proteins are expressed on the surface of the influenza virus – hemagglutinin and neuraminidase. Hemagglutinin allows the virus to enter cells while neuraminidase cuts newly formed viruses loose from an infected cell, influencing how efficiently the virus can spread (Taubenberger et al., 2005: 66). As the newly formed viruses attempt to exit human cells, they are coated with sialic acid. To prevent viruses from binding to each other and to the surface of the host cell, the bond formed by the sialic acid must be broken. The neuraminidase protein carries out exactly this task, clipping the sialic acid, freeing the virus to infect other cells (Taubenberger et al., 2005: 66).

It has been recognized that without the active functioning of the neuraminidase protein, new virus particles would remain 'stuck' on the surface of the host cell and so would not be able to circulate, penetrate other cells and spread infection (Elbe, 2014: 930). Tamiflu, designated as a neuraminidase inhibitor, intervenes in this constant biological process through which the neuraminidase acts and frees the virus. Following the crystallization of neuraminidase and its examination using x-rays, the molecular structure of this protein was discovered (Elbe, 2018: 43). Such information revealed several structural features common among all influenza neuraminidase proteins, specifically that the active molecular site contains several large well-defined binding pockets (Lew et al., 2000: 663). By binding to the particular pockets within this molecular site, Tamiflu is able to inhibit the role of the neuraminidase protein and its ability to free the influenza virus from the surface of the human cell, so preventing its movement to other cells and further infection (Mendel et al., 1998: 644). As a result, Tamiflu, by targeting the key molecular sites on the neuraminidase protein, is able to inhibit the constant process through which the influenza virus frees itself from one cell allowing it to spread to another. Along with Tamiflu, this section has identified two other antivirals in the form of ST-246 and ZMapp that also capitalize on the constant ways in which the smallpox and Ebola viruses exit and enter human cells. The result has been the widespread stockpiling of these antivirals by governments and international organizations in an attempt to prevent disease and preserve the health of populations.

Conclusion

This article has investigated the efforts of governments and international organizations in the face of biological threats. A core activity is the stockpiling of particular pharmaceuticals, including antivirals that facilitate preparedness and response mechanisms. Such efforts are driven by the fear that molecular life will randomly evolve and emerge into new and pandemic forms of disease. Yet, undergirding the development of ST-246, ZMapp and Tamiflu lies an altogether different conception of the nature of molecular life, one focused on identifying and intervening in its constant biological dynamics in the prevention of disease. This article, in challenging a predominant conception of the nature of molecular life in terms of contingency, has identified a core operational logic that guides the management of disease at both the level of the population and the molecular. Security practices, in this case informed by contingent understandings of molecular life, remain focused on prophylactic measures, particularly the stockpiling of antivirals in the facilitation of preparedness.

Biopolitical security practices today are profoundly shaped by the policies and technologies driving advances in the molecular sciences. This article has conducted an in-depth analysis of the way in which governments have responded to the potentially random emergence of novel biological threats through the development and stockpiling of particular antivirals. Central to this has been the role of technologies in shaping molecular life as an object of knowledge with a particular nature made up of constant biological functions and processes. Rather than engendering a recombinant art of design, the security practices identified here rely upon the identification of a specific molecular site essential to the reproduction and spread of the virus within the human body. The results are prophylactic antiviral treatments designed to respond to a potential infection. To fully address biopolitical security practices that utilize novel biotechnologies we must remain attuned to their empirical workings, object constructions and conceptual implications.

Commentators today have argued that contingency is one of modern society's defining attributes (see Luhmann, 1998). We have seen here that it is a significant driver of government concern regarding the emergence of biological threats. This though is only half the story. Scientific tools and technologies have often been inextricably tied to the unveiling of the world and its workings in new and fascinating forms of order and linearity (see Bousquet, 2009). The molecularization of biology has intensified the classification of contagious agents as necessary causes of disease, identifying the constant and precise molecular sites through which viruses replicate and spread. Such identifications of the nature of molecular life run through and make possible the development and stockpiling of new antivirals, so underpinning governmental programmes of preparedness. In the end, our very survival in the face of viral threats may depend upon them.

Acknowledgements

I would like to thank Stefan Elbe and Demet Dinler for their comments on drafts of this paper as well as the editors of *Security Dialogue* and the anonymous reviewers.

Funding

The author received no financial support for the research, authorship, and/or publication of this article.

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References

- Bousquet A (2009) *The scientific way of warfare*. London: Hurst & Company.
- Braun B (2007) Biopolitics and the molecularization of life. *Cultural Geographies* 14(1): 6–28.
- Byrd CM, Grosenbach DW and Hruby DE (2013) Antiviral options for biodefense. *Current Opinion in Virology* 3: 537–541.
- Caduff C (2015) *The pandemic perhaps*. Oakland: University of California Press.
- Collier S and Lakoff A (2008) The problem of securing health. In: Collier S and Lakoff A (eds) *Biosecurity Interventions*. New York: Columbia University Press, 7–32.
- Cooper M (2006) Pre-empting emergence: The biological turn in the war on terror. *Theory, Culture & Society* 23(4): 113–135.
- De Clercq E (2004) Antivirals and antiviral strategies. *Nature Reviews | Microbiology* 2: 704–720.
- Dillon M and Lobo-Guerrero L (2008) Biopolitics of security in the 21st century: An introduction. *Review of International Studies* 34: 265–292.
- Dillon M and Lobo-Guerrero L (2009) The biopolitical imaginary of species-being. *Theory, Culture and Society* 26(1): 1–23.
- Dillon M and Reid J (2000) Global governance, liberal peace, and complex emergency. *Alternatives* 25: 117–143.
- Dillon M and Reid J (2001) Global liberal governance: Biopolitics, security and war. *Millennium – Journal of International Studies* 30(41): 41–66.
- Diprose R, Stephenson N, Mills C, Race K and Hawkins G (2008) Governing the future: The paradigm of prudence in political technologies of risk management. *Security Dialogue* 39(2–3): 267–288.
- Drews J (1999) *In quest of tomorrow's medicines*. Translated by D Kramer. New York: Springer-Verlag.
- Drews J (2000) Drug Discovery: A historical perspective. *Science* 287(5460): 1960–1964.

Elbe S (2014) The pharmaceuticalisation of security: Molecular biomedicine, antiviral stockpiles, and global health security. *Review of International Studies* 40(5): 919–938.

Elbe S (2018) *Pandemics, pills and politics*. Baltimore: Johns Hopkins Press.

Elbe S, Roemer-Mahler A and Long C (2014) Securing circulation pharmaceutically: Antiviral stockpiling and pandemic preparedness in the European Union. *Security Dialogue* 45(5): 440–457.

Espeland EM, Tsai C-W, Larsen J and Disbrow GL (2018) Safeguarding against Ebola: Vaccines and therapeutics to be stockpiled for future outbreaks. *PLoS Neglected Tropical Diseases* 12(4): 1–4.

Foucault M ([1981] 2007) The meshes of power. In: Crampton J and Elden S (eds), translated by G Moore, *Space, knowledge and power: Foucault and geography*. Aldershot: Ashgate, 153–162.

Foucault M (2004) *Society must be defended: Lecture at the Collège de France 1975–1976*. Translated by D Macey. London: Penguin.

Foucault M (2009) *Security, territory, population: Lectures at the Collège de France 1977–1978*. Translated by G Burchell. New York: Palgrave Macmillan.

Foucault M (2010) *The birth of biopolitics: Lectures at the Collège de France, 1978–1979*. Translated by G Burchell. Basingstoke: Palgrave Macmillan.

Global Biodefense (2014) BARDA to rapidly accelerate ZMapp Ebola drug. Available at: <https://globalbiodefense.com/2014/09/04/barda-rapidly-accelerate-zmapp-ebola-drug/> (accessed 25 July 2019).

Grosenbach DW, Jordan R and Hruby DE (2011) Development of the small-molecule antiviral ST-246® as a smallpox therapeutic. *Future Virology* 6(5): 653–671.

Hanley KA (2011) The double-edged sword: How evolution can make or break a live-attenuated virus vaccine. *Evolution* 4(4): 635–643.

Henderson DA (1993) Surveillance systems and intergovernmental cooperation. In: Morse SS (ed.) *Emerging viruses*. Oxford: Oxford University Press, 283–289.

HHS (2017) HHS accelerates development of first Ebola vaccines and drugs. Available at: <https://www.hhs.gov/about/news/2017/09/29/hhs-accelerates-development-first-ebola-vaccines-and-drugs.html> (accessed 25 July 2019).

HHS News (2011) BARDA supports first Project BioShield contract for smallpox drug, contract funds late-stage development, future acquisition of antiviral drug to treat smallpox. Available at: <https://www.phe.gov/Preparedness/news/Pages/smallpox-antiviral-110513.aspx> (accessed 25 July 2019).

Ho M-W (1998) *Genetic engineering: Dream or nightmare?* Bath: Gateway.

Institute of Medicine (2005) *The smallpox vaccination program: Public health in an age of terrorism*. Washington, DC: The National Academies Press.

Jahrling PB, Fritz EA and Hensley LE (2005) Countermeasures to the bioterrorist threat of smallpox. *Current Molecular Medicine* 5: 817–826.

Kauffman S (1995) *At home in the universe*. Oxford: Oxford University Press.

- King NB (2002) Security, disease, commerce: Ideologies of postcolonial global health. *Social Studies of Science* 32(5–6) (October–December): 763–789.
- Kittelsen S (2009) Conceptualising biorisk: Dread risk and the threat of bioterrorism in Europe. *Security Dialogue* 40(51): 51–71.
- Koplow DA (2003) *Smallpox: The fight to eradicate a global scourge*. London: University of California Press.
- Lakoff A (2008) The generic biothreat, or, how we became unprepared. *Cultural Anthropology* 23(3): 399–428.
- Lakoff A (2015) Real-time biopolitics: The actuary and the sentinel in global public health. *Economy and Society* 44(1): 40–59.
- Lederberg L, Shope RE and Oaks SC (1992) *Emerging infections: Microbial threats to health in the United States*. Washington DC: National Academy Press.
- Lee JE and Saphire EO (2009a) Ebolavirus glycoprotein structure and mechanism of entry. *Future Virology* 4(6): 621–635.
- Lee JE and Saphire EO (2009b) Neutralizing Ebolavirus: Structural insights into the envelope glycoprotein and antibodies targeted against it. *Current Opinion in Structural Biology* 19: 408–417.
- Lew W, Chen X and Kim CU (2000) Discovery and development of GS 4104 (oseltamivir): An orally active influenza neuraminidase inhibitor. *Current Medicinal Chemistry* 7: 663–672.
- Long C (2019) Resilience as molecular enhancement: Bio-economies and medical countermeasures in the United States. *Critical Studies on Security* 7(1): 51–67.
- Luhmann N (1998) *Observations on modernity*. Stanford: Stanford University Press.
- Mendel DB, Tai CY, Escarpe PA, Li W, Sidwell RW, Huffman JH, Sweet C, Jakeman KJ, Merson J, Lacy SA, Lew W, Williams MA, Zhang L, Chen MS, Bischofberger N and Kim CU (1998) Oral administration of a prodrug of the influenza virus neuraminidase inhibitor GS 4071 protects mice and ferrets against influenza infection. *Antimicrobial Agents and Chemotherapy* 42(3): 640–646.
- Murin CD, Fusco ML, Bornholdt ZA, Qiuc X, Olinger GG, Zeitlin L, Kobinger GP, Warda AB and Saphire EO (2014) Structures of protective antibodies reveal sites of vulnerability on Ebola virus. *PNAS* 111(48): 17182–17187.
- National Academies of Sciences, Engineering, and Medicine (2016) *The nation's medical countermeasure stockpile: Opportunities to improve the efficiency, effectiveness, and sustainability of the CDC Strategic National Stockpile: Workshop summary*. Washington, DC: The National Academies Press.
- National Intelligence Council (2000) *The global infectious disease threat and its implications for the United States*. Washington, DC: National Intelligence Council.
- Prior SD (2004) *Who you gonna call? Responding to a medical emergency with the Strategic National Stockpile*. National Defence University: Center for Technology and National Security Policy. Available at: <https://apps.dtic.mil/dtic/tr/fulltext/u2/a476356.pdf> (accessed 25 July 2019).
- Reddy D (2010) Responding to pandemic (H1N1) 2009 influenza: The role of oseltamivir. *Journal of Antimicrobial Chemotherapy* 65(Suppl 2: ii): 35–40.

Roberts S and Elbe S (2017) Catching the flu: Syndromic surveillance, algorithmic governmentality and global health security. *Security Dialogue* 48(1): 46–62.

Rose N (2007) *The politics of life itself: Biomedicine, power, and subjectivity in the twenty-first century*. Princeton, NJ: Princeton University Press.

Ryan JR and Glarum JF (2008) *Biosecurity and bioterrorism*. Oxford: Butterworth-Heinemann.

SIGA (2018a) US Food and Drug Administration approves SIGA Technologies' TPOXX® (tecovirimat) for the treatment of smallpox. Available at: <https://investor.siga.com/news-releases/news-release-details/usfood-and-drug-administration-approves-siga-technologies> (accessed 25 July 2019).

SIGA (2018b) SIGA Technologies awarded BARDA contract for TPOXX®. Available at: <https://investor.siga.com/news-releases/news-release-details/siga-technologies-awarded-barda-contract-tpoxxr> (accessed 25 July 2019).

Taubenberger JK, Reid AH and Fanning TG (2005) Capturing a killer flu virus. *Scientific American* 292(1): 62–71.

Trakatellis A (2007) *Pandemic influenza in the EU: Are we sufficiently prepared?* Report on a high-level policy debate, Brussels, European Parliament, 12 June.

Tucker JB (2001) *Scourge: The once and future threat of smallpox*. New York: Grove Press.

Yang G, Pevear DC, Davies MH, Collett MS, Bailey T, Rippen S, Barone L, Burns C, Rhodes G, Tohan S, Huggins JW, Baker RO, Buller RLM, Touchette E, Waller K, Schriewer J, Neyts J, DeClercq E, Jones K, Hruby D and Jordan R (2005) An orally bioavailable antipoxvirus compound (ST-246) inhibits extracellular virus formation and protects mice from lethal orthopoxvirus challenge. *Journal of Virology* 79(20): 13139–13149.

Zimmer C (2015) *A planet of viruses*. Chicago: Chicago University Press.