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## Globalized Complexity and the Microbial Traffic of New and Emerging Infectious Disease Threats

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*Human-induced environmental shocks – overseas tourism, wetland destruction, a corporate 'Livestock Revolution', and a Third World urbanization with the attendant growth of mega slums – are responsible for turning influenza's extraordinary Darwinian mutability into one of the most dangerous biological forces on our besieged planet.*

Mike Davis (2005)

Over the relatively short span of a quarter of a century, the world appears to have witnessed the proliferation of an unusually large number of what are referred to as 'new and emerging diseases' – that is, infectious diseases that are newly appearing in a population or that have been known for some time but are rapidly increasing in incidence or in geographic range (Morse, 1995). Examples of these are numerous and include HIV-AIDS, SARS, *E. coli* 0157:H7, *Clostridium difficile*, West Nile virus, lyme disease, antibiotic-resistant tuberculosis, the ebola virus and avian influenza (Garrett, 1994; Drexler, 2003; Levy and Fischetti, 2003; Niki-foruk, 2006). In this chapter, using SARS and influenza A/H1N1 (Swine flu) as illustrative examples, I examine through the lens of complexity theory the question of how historically specific processes related to intensified globalization have influenced the emergence and spread of new diseases. As will be discussed, the complexity perspective offers a conceptual framework that is especially well-suited for the analysis of the multiple social and ecological aspects of globalization associated with the contemporary origins and responses to pandemics.

### Historical transitions and microbial traffic

A. J. McMichael (2001) has documented how significant changes in the relationship between human beings and the environment at particular junctures in history were accompanied by the concomitant rise of certain types of infectious diseases.

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The first such shift involved a change in settlement patterns 10,000 years ago as hunter-gatherers adapted to agrarian-village living based on herded food and agriculture. This shift created new ecological opportunities for the spread of disease as it enabled countless novel strains of bacteria/viruses to make the jump from domesticated herd animals and rodents to relatively stationary human beings. The origin of many diseases including smallpox, measles, tuberculosis, leprosy, influenza, the common cold, malaria, dengue and bubonic plague could be traced to this period (McMichael, 2001). During the time span of the past 1000 to 2500 years, increased trade, travel and military movement led to a new phase in disease emergence. Examples here include the spread of smallpox and measles from the Indian subcontinent to Europe via Roman Empire troops returning from settling unrest in Syria in AD 2; trade along the Silk Route that subsequently spread these diseases from Europe to China; and the introduction of the bubonic plague to 14th-century Europe as the caravans and armies of the Mongol Empire entered the continent through the Black Sea. The colonialist period spanning the 17th–19th centuries represented a third major shift in disease spread, particularly in relation to the transoceanic spread of disease via European ships. McMichael (2001) concludes by speculating that we may be entering a fourth transitional period defined by globalization, as evidenced through dramatic increases in the volume and speed of human mobility, changes in food production practices and newer medical techniques, all of which have implications for disease emergence.

It is readily apparent that changes in the flow of individuals and pathogens are key aspects of disease emergence no matter the epoch under consideration. This emphasis is captured by the notion of 'microbial traffic' proposed initially by Morse (1993) and refers to the mobility of a pathogen and how that will vary according to characteristics associated with cross-species transfer, pathogenic evolution (including changes in the structure and immunogenicity of earlier strains), spatial diffusion and changes in the human–environment relationship (Mayer, 2000). In what follows, using the lens of complexity theory, I will refer to the above-mentioned dimensions of microbial traffic to make the case that globalization may indeed represent another transformative epoch in the emergence of infectious disease.

Globalization and microbial traffic globalization is defined in various ways (Held et al, 2002) but a fundamental aspect of most definitions is that of time-space compression (Giddens, 1990; Harvey, 2005). Time-space compression refers to the idea that, largely because of modern technologies, there has been a dramatic increase in the speed at which the movement of people, money, images and information occurs, thus resulting in situational circumstances in which distance is not as insurmountable or as significant a barrier as it once was in the past. Time-space compression has some obvious implications for the spread of disease. Notably, the effects become evident when considering the time horizons associated with air travel and disease incubation (i.e. the period between infection

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and symptom onset). Thus, the 2–7 day incubation period of SARS and a similar incubation period for Influenza A/H1N1 (Picard, 2009c; Tuite 2009), has meant that those infected could easily complete a transcontinental flight before their symptoms developed, thereby increasing the potential for pandemic spread overall.

The enhanced and accelerated mobility of pathogens has also meant that a 'reterritorialization' of risk has occurred leading to the problematization of traditional territorially based strategies of disease control in which it was assumed that pathogens were biologically stationary targets that could be geographically sequestered (Garrett, 1996). This territorial notion of disease has immediate political and social implications for the manner in which disease spread is conceptualized by both the general public and the elites. It is in this context that King (2002) notes that the history of infectious disease control is very much influenced by the legacy of colonialism and territorialism in which the colonizers sought to protect themselves from disease through the creation of administratively cohesive and geographically bounded regimes. Yet, as we shall see, the rapid spread of SARS and Influenza A/H1N1 worldwide has dramatically demonstrated how the assumptions of territoriality no longer hold in an increasingly interconnected and globalizing world, despite response strategies that to some extent are still informed by territorializing assumptions. The highly mobile nature of new and emerging diseases, coupled with the advent of qualitatively different types of interactions between humans and animals have contributed to the emergence of pandemic as a unique and complex phenomenon distinct to our historical epoch – a distinctiveness which, as we shall see, is associated with changes in the scale and intensity of economic globalization. The analysis of contemporary pandemics therefore requires new tools, particularly those that emphasize the contingent and multifactorial causes of disease. In this light, the recent work in complexity theory may prove to be a useful starting point in the analysis of pandemics (Ali and Keil, 2007; Ali, 2008).

Complexity theory is a systems perspective that emphasizes the role of such features as: punctuated equilibrium, non-linearity, emergence, feedback loops and tipping points in the development of phenomena. It is of interest to us here because it enables a conceptualization of pandemic in terms of the interdependence of biophysical *and* sociopolitical factors, thus avoiding a tendency towards a narrowly defined essentialist stance that overemphasizes at either extreme the biological or the social. Furthermore, analysing pandemics through the complexity perspective may help us acquire a more critical position by directing analytical attention to the questions of how and why alterations in microbial traffic come about through human-induced (and therefore politically based) changes in society and the environment. For example, in considering the *longue durée*, we see that periods of social and economic stability are interrupted by changes in the relationship between human beings and the environment that dramatically alter the

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existent microbial traffic pattern. In this sense, the periods of stability interspersed with changes in microbial traffic patterns, some of which result in epidemics, may be thought of in terms of a series of punctuated equilibria. What is perhaps alarming is how, over the last few decades, the periods of relative calm and stability between the periodic changes in microbial traffic have shortened considerably. Thus, over the last decade alone we have faced a barrage of new and emerging diseases such as SARS, avian flu and influenza A/H1N1. Second, the extent to which the microbial traffic pattern now involves a global dimension is noteworthy.

To address the question of why in even greater detail than has been employed up until this point, it is useful to consider the notions of non-linearity and tipping points. Non-linearity refers to how small changes in a system may lead to sudden and dramatically disproportionate shifts, usually triggered by exceeding some critical parameter or tipping point. The tipping point represents the dramatic moment in an epidemic when everything can change all at once (Gladwell, 2002).<sup>1</sup> Often it is only a relatively minor change in the external environment that can have an unusually high and disproportionate impact on the way a biological and social system functions (Gladwell, 2002). In the case of SARS, for example, a tipping point in the pandemic spread occurred when an infected physician from Guangzhou stayed at the Metropole Hotel in Hong Kong, inadvertently initiating the simultaneous spread of the disease to different global cities across the world.<sup>2</sup> The suddenness of the unknown diseases' arrival meant that hospital staff in the various affected cities were unprepared to protect themselves. Consequently, during these early stages, a positive feedback loop was established in which those infected would lead to even more becoming infected – an increase defined as multiplicatively geometric rather than incremental linear/arithmetic.

Another tipping point to consider in relation to pandemics involves the point at which the virus has evolved to such an extent that it is able to survive within a human host and then be transmitted between human hosts. During times of stability, the viruses which affect humans tend to evolve relatively slowly in a process referred to as *antigenic drift*. This leads to the eventual development of new viral strains that require new vaccines on an annual basis. In contrast, occurring much more infrequently (every human generation or so), is a much more revolutionary shift where a bird or pig type of influenza A will exchange genes with a human type of influenza, thus enabling the virus to vault over the species barrier in a process known as *antigenic shift* – a shift that signals the beginnings of a pandemic (Davis, 2005, p11). As alluded to above, it appears that the frequency of tipping point initiations through antigenic shifts have increased dramatically over recent times. To understand why requires us to enquire how the nature of the relationships between animals and humans, as well as those between humans themselves, have changed during the recent past.

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One area of comparatively dramatic change is the increased global demand for meat and poultry, resulting in the imposition of immense stresses on the bio-physical environment and animals through the intensification of livestock operations (also referred to as factory farming). Many of these negative effects (or externalities) are hidden from urban dwellers who rely on such operations to maintain their meat-based diets, yet they have real consequences for altering microbial traffic patterns and inducing disease outbreaks and pandemics. For example, the development and spread of a lethal strain of *E. coli* could be traced to factory farming practices involving the international cattle trade (Ali, 2004). Similarly, the development of avian and swine flu strains is related to the factory farming of poultry and swine where opportunities for animal-to-human transmission (or vice versa) abound. The likelihood that a more virulent strain will develop under the conditions of globalized agroc capitalist operations is amplified in numerous ways, including an increased risk that animals will become more susceptible to infectious diseases due to the stresses endured in over-crowded factory farms or from the development of antibiotic resistance resulting from widespread administration of sub-therapeutic doses to promote weight gain.

Other global developments that can impinge on the microbial traffic of new and emerging diseases and the associated ecology of disease are those associated with intensified urbanization. Increasing poverty, particularly in the last 30 years, has driven exponentially more dispossessed people from rural areas to the peripheries of megacities across the developing world (Davis, 2005). If globalized factory farming contributes to the development of new and emerging pathogens, then mega-slums provide them with an environment in which they can flourish. Underserviced slum areas often lack proper sanitation and basic amenities and are overcrowded with a large pool of available susceptible human hosts – settings that are especially favourable to the spread of disease. This potential for epidemics to flourish is especially noteworthy given that 95 per cent of the world future population growth will be in the poorer cities of the Global South (Davis, 2005, p56) and that for the first time in history, more than half the world's population is now residing in urban areas (United Nations Population Fund, 2007). At the same time, it should be noted that the conditions conducive to disease spread are not necessarily found only in urban settings, but are common to those areas more generally characterized by poverty and lack of health-related amenities. In this light, certain non-urban areas are just as prone (if not more) to disease outbreaks as revealed by the extent to which influenza A/H1N1 has become widespread on some First Nations Reserves in Canada.

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## The SARS pandemic

In November 2002, the city of Foshan, Guangdong Province, China experienced an outbreak of a mysterious and highly contagious respiratory disease, then referred to as 'atypical pneumonia'. The disease spread quickly to other cities in the province including Heyang and Guangzhou, then subsequently to others in the country, most notably Beijing (Kaufman, 2006). Although the Chinese government initially took steps to keep knowledge of the outbreaks secret, by late February 2003 news about the outbreaks travelled through informal channels on text messaging and the internet – a notable development considering that in the past, such information could not be transmitted so readily across the country in such a short period and could thus be controlled by government to a greater extent (Heymann, 2005). Once confirmations of the informal rumours were received, the World Health Organization (WHO) coordinated a network of scientists from around the world to work together to characterize the disease agent, originally suspected to be a strain of influenza (Abraham, 2004). Much to the surprise of many infectious disease experts, however, the identification and subsequent characterization of the causative agent – completed in the unprecedented span of a few weeks – revealed it to be a strain of the Coronavirus, a variant of the virus associated with the common cold. Changes in the pathogenic structure and immunogenicity of this type of virus, from one that was relatively benign to a more lethal form, was not expected and the definitive mechanism for these changes has yet to be discovered.

The fact that over a third of the early cases of SARS occurred in food handlers – persons who handled, killed and sold food animals, or those who prepared and served food – led investigators to search the live animal markets of southern China for the animal reservoir that hosted the virus (Guan et al, 2003). At first it was thought that the viral crossover to humans had occurred from infected civet cats found in these markets. However, later studies revealed that the original viral reservoir may have been infected horseshoe bats, which subsequently infected the civet cat, where the virus evolved and multiplied in public markets until eventually evolving into a form that could spread to humans (Lau et al, 2005; Li et al, 2005; Normille, 2005). This was a plausible mechanism as bats were already known to serve as the natural reservoir for many human viruses such as the Ebola, Hendra and Nipah viruses (University of California Museum of Paleontology, 2006).

The evolution of the virulence of the SARS coronavirus highlights the contingent, multifactorial and emergent qualities of pandemic onset. In particular, the causal chain involved in the viral crossover alludes to other interconnected dimensions of disease emergence, namely changes in the human–environment relationship and spatial diffusion. The case of recent emerging diseases such as West Nile virus and Lyme disease, for instance, demonstrate how the expansion of human

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activities into previously untouched natural environs, particularly through intensified urbanization, have changed the nature and degree of human contact with wild animals. This in turn increases the potential for disease emergence in the human population. Thus, deforestation may have led to the release of mosquitoes carrying the West Nile virus into the urban population while also increasing the chance of human contact with the deer ticks that carry Lyme disease. In the case of SARS, it has been argued that increased wealth stemming from the development of the free market economy in China has triggered a change in culinary preferences; namely, as a traditional vegetable diet is increasingly replaced by a meat based one, interaction between human beings and animals in wet markets increases (Zhan, 2005; Jackson, 2008).

One of the major effects associated with contemporary globalization involves increased travel and changes in mobility patterns. Indeed, according to John Urry, air travel is an indispensable element of the emergent global order and 'Without the rapid development of the complex extended systems of mass air travel, what is now termed "globalization" would be utterly different, possibly non-existent' (2007, p149). SARS demonstrated how air travel was also central to the globalization of infectious disease, as it was the first pandemic of its kind in which airports and airlines were instrumental to such a degree in the spread of the disease in such a short period of time (Bowen and Laroc, 2006). Notably, the flow of SARS could be traced through the international airports of major global cities such as Beijing, Hong Kong, Toronto and Singapore and its subsequent diffusion through global city networks points to another dimension of globalization that is worthy of attention, namely the intensified and expansive interconnections among global cities through the flows of information, commodities, foodstuffs, ideas and capital (Knox and Taylor, 1995; Sassen, 2002), in addition to people and viruses (Ali and Keil, 2006; 2008). As the networked interconnections between the different types of flows increase with globalization, the potential also increases for the development of feedback loops, tipping points and non-linearity related to all kinds of complex emergent phenomena, including a pandemic. In light of the different types of interconnected flows between global cities that serve as the foundation for economic and cultural globalization, a deeper understanding of the basis of contemporary disease spread must go beyond mere mechanistic understandings of airline connections between airports to a broader analysis of the global political economic forces that channel these and the various other types of flows in certain directions, thereby ultimately influencing the flow of microbial traffic through particular sites such as cities.

The potential role that cities could play in converting a localized epidemic into a globalized pandemic has been recognized for a long time, as evidenced for centuries by the imposition of quarantines on incoming ships in port cities. What was noteworthy of the SARS pandemic was the speed at which the disease spread though the network of global cities – within a matter of days the disease spread

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from Hong Kong to Singapore, Vietnam, Taipei and Toronto (NACSPH, 2003). In part, the rapidity of disease diffusion in the case of SARS could be attributed to certain biological characteristics of the virus itself, including the fact that individuals were most infectious when they were the most ill and were therefore more likely to admit themselves to hospital at the point at which the transmission threat was greatest; hence the large degree to which SARS outbreaks were occurring within a hospital setting (i.e. nosocomial transmission).<sup>3</sup> At the same time, the diffusion of SARS was facilitated by the mechanism of 'superspread', that is, the tendency of certain individuals to infect an unusually high number of people, possibly because of the production of higher viral loads or a greater amount of respiratory secretions that linger in the surroundings for extended periods (Centers for Disease Control and Prevention, 2003). The biological characteristics of the virus also meant that the transmission of SARS could (and was) effectively prevented by adherence to traditional public health measures involving mechanisms of social distancing, including rapid case detection, case isolation, contact tracing and good infection control such as hand washing and the use of personal protective equipment (NACSPH, 2003). As a result of the particular biological characteristics of the SARS coronavirus, including its basic reproduction rate, public health officials needed only to block viral transmission in about half the infected cases to halt an outbreak.<sup>4</sup> Notably, this is very different from the case of pandemic flu, where an almost 100 per cent containment rate would be required for the effective disruption of viral flow (Davis, 2005, p79).

### The influenza A/H1N1 pandemic

Similar to the case of SARS, the emergence of influenza A/H1N1 involves the reterritorialization of risk through globalization and the complex changes in human-to-human and animal-to-human relationships. The earliest cases of Influenza A/H1N1 were identified in mid-March 2009 in the Mexican town of La Gloria, Veracruz state, in an area located near an intensified pig farming operation (Alphonso and Wingrove, 2009). The disease quickly spread to major cities and tourist areas in the country, including Mexico City which experienced a cluster of 120 cases (Ha and Laghi, 2009). International spread soon followed and within a month, influenza A/H1N1 cases had been reported in 17 countries across 5 continents (Picard, 2009a). By September 2009, the unfolding second wave of the pandemic had claimed more than 2800 lives worldwide (Boyle, 2009a).

The pathogenic evolution of the virus was a key concern from the start of the influenza A/H1N1 epidemic. Although most of the early cases appeared to be of a mild form, with the majority of those infected recovering through the use of antibiotics (Alphonso and Wingrove, 2009), concerns were raised that a second wave of the disease in the autumn could involve a more virulent strain of the virus



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(Ha and Laghi, 2009; Jimenez, 2009), exactly as occurred with the 1918 Spanish flu pandemic. Subsequent genetic analysis mitigated these fears somewhat as the current strain was not found to have any of the markers for virulence that characterized the 1918 strain (Galloway and Alphonso, 2009).<sup>5</sup> Other experts, however, contend that the virus was indeed exhibiting the potential to mutate into a more lethal form, as indicated by the case of human-to-swine transmission involving a Canadian farm worker returning from holidays in Mexico, who was subsequently believed to have infected pigs on a farm in Alberta (Picard, 2009b). The fear is that as the virus jumps from pigs to humans and back to pigs the likelihood increases that resulting genetic mutations will lead to a strain more dangerous to both species (Picard, 2009b) because the constant exchange of the virus' segment genes essentially enables the ever-evolving virus to genetically adapt so that it can more effectively evade the human immune system response and penetrate the human host cell (which a virus requires in order to reproduce itself). The enhanced ability to circumvent the immune system defence mechanisms through genetic adaptation in turn increases the virulence of the virus. Furthermore, the characterization of the genetic code of the influenza A/H1N1 virus revealed it to be a strange hybrid of North American swine influenza, North American avian influenza, human influenza and swine influenza typically found in Asia and Europe (Picard, 2009b), thus indicating a strong potential for rapid evolution into a more virulent form, as the enhanced genetic diversity of multiple strains offers greater genetic resources upon which the evolving virus can draw, thereby facilitating natural selection pressures to induce a viral strain that is more capable of evading the human immune response. Such indications added to the concern about the evolving virulence of the pathogen because swine flu had already been reported in parts of Asia where avian influenza was already present, and where it was thought that the pandemic strains could mix into a lethal cocktail transmissible to and between humans (Picard, 2009b). At the same time, the potential for increased virulence and transmissibility through mixing of the influenza A/H1N1 virus with existing northern hemisphere strains of the *seasonal* virus was ruled out on the basis of the genetic evidence – it was concluded that H1N1 would dominate other strains when flu season began in the northern hemisphere in the autumn (Smith, 2009).

Although sharing some similarities, the spatial diffusion of influenza A/H1N1 varied somewhat from that of SARS. It is clear, for example, that air travel played an integral role in both pandemics, particularly in relation to the rapid spread of the respective diseases. Nevertheless, differences are discernible when considering the localized nature of the outbreaks associated with each pandemic. With SARS, outbreaks occurred in major urban centres, many of which had a relatively high level of public health resources at their disposal. In contrast, increasing evidence gained from the Canadian experience revealed that influenza A/H1N1 was not a disease confined to nosocomial transmission within the hospitals of large urban

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centres, but, for as of yet unknown reasons, was taking hold in more rural areas. Notably, although these areas experienced a relatively greater degree of community spread, they had fewer available resources to address the impending pandemic. This is exemplified by the occurrence of influenza A/H1N1 outbreaks in First Nations reserves and summer camps. Particularly hard-hit were several remote fly-in reserves in Manitoba where dozens who became ill had to be flown over vast distances into major urban centres such as Winnipeg (White, 2009a). Furthermore, unlike the relatively mild cases experienced elsewhere, members of the First Nations communities were experiencing illnesses so severe that they required hospital and intensive care (Alphonso, 2009a); indeed about two-thirds of all flu victims on respirators in the province were of aboriginal descent (White, 2009b). The disturbing extent to which First Nations communities were affected by influenza A/H1N1 was not surprising given that the conditions on many reserves in Canada – limited availability of health-care resources, crowded living conditions and ongoing problems with water quality and sanitation (*Globe and Mail Editorial*, 2009) – make this group susceptible to infectious and respiratory diseases more generally.”

The community spread of influenza A/H1N1 was also in evidence in summer overnight camps in Ontario, as dozens of children in three such camps were found to have symptoms of swine flu (Alphonso, 2009b). These outbreaks, coupled with the tendency of influenza H1N1 to infect the young (Alphonso and Galloway, 2009) has led to increased concern over community outbreaks in schools and universities (Alphonso, 2009c). Such fears may have been warranted considering the fact that in September 2009, the pandemic strain was confirmed in at least four British Columbia schools (Boyle, 2009b).

## Conclusion

The emergence of new pathogens into human communities is not a new phenomenon. The increased frequency of the globalized spread of infectious diseases such as we have seen with SARS and now influenza A/H1N1 may, however, be indicative of a changing pattern of pathogen development and transmission. In this light, it has been argued that certain social and ecological developments associated with globalization (that we are only just beginning to understand) are playing a central role in increasing the potential for a pandemic. Notably, as reviewed in this chapter, these developments include the highly mobile nature of people and microbes today, as well as other macro-level developments such as the intensification of livestock operations and urbanization. Developments such as these have led to a complex array of social and ecological interconnections that are difficult to discern, disentangle and study through existing analytical perspectives. Indeed, Urry (2007, p244) notes that contemporary conditions make it less useful to

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conceptualize our world in terms of the traditional linear model of local, meso and global scales, as the world now seems to be made up of multiple systems with mobile connections. To deal with the types of analytical challenges that this fluidity poses with respect to contemporary infectious disease spread, I have suggested that complexity theory be used to focus in on how the dimensions of microbial traffic, including cross-species transfer, pathogenic evolution, spatial diffusion and human–environment relationships, are influenced by system properties and mechanisms, including punctuated equilibrium, non-linearity, emergence, feedback loops and tipping points.

I conclude here by noting that studying the relationships of human mobility, social organization and microbial traffic through the lens of complexity theory also promises to help us understand how historical factors influence the *response* to a pandemic. Pandemic responses have always been influenced by historically informed social, political and economic programmes from colonial imperatives to structural adjustment plans. In this light, what is perhaps worthy of future research is how the policies and programmes that define our globalized era – for example, globalized trade agreements, global public health initiatives and interventions to combat international terrorism – will influence pandemic response. In other words, globalization has not only had implications for the production and unfolding of pandemics but also for pandemic response. Certainly experiences with SARS and influenza A/H1N1 have raised many issues in this regard, including those related to sovereignty, surveillance and privacy, biosecurity, the social control of mobility, the distribution of vaccines and the role of international pharmaceutical companies. For example, David Fidler (2004) notes that with SARS, the domain of international public health entered a post-Westphalian era in which the WHO dared to violate for the first time, via the imposition of travel advisories, the long-held and diplomatically agreed upon norm that initiatives to manage infectious diseases should not interfere with the sovereign right of nation states to engage in trade and commerce. The WHO further intervened in matters of sovereignty by insisting that nation states adopt thermal screening and other initiatives in their major airports to help stop the spread of the disease. In fact, the WHO threatened that they would not lift the respective travel advisories unless their suggested actions were adopted. Notably, such imposed measures represent strategies through which mobility was socially controlled not by the sovereign state, but by an international agency.

However, in the case of influenza A/H1N1, the social control of mobility was overshadowed by concerns related to the shortage of vaccine doses required by the population. Public controversies around this led to the raising of such issues as the ethics behind the prioritization of certain groups to receive the vaccine first, as well as increasing awareness of the significant influence that the monopoly of a few vaccine manufacturers (many of which are owned by huge pharmaceutical companies) may have during a pandemic. It is also clear that advanced

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information and communications technology (i.e. internet-based technologies) have played a key role in recent pandemic responses. Important questions remain as to how these political and technological interventions and factors will influence future patterns of microbial traffic and the effects they will have in either deterring or inadvertently amplifying the potential for pandemics in an era characterized by increasing complexity and the unintended consequences of emergent phenomena resulting from the economic, cultural and environmental forces brought forth through globalization.

### Notes

1. John Urry (2007) gives other examples of tipping points in the modern era, that is, where apparent long-term stabilities unpredictably flip towards their opposite. These include the overnight 'collapse' of the Soviet Union and the astonishing growth of the Internet from no users to 1 billion users, the spread of mobile phones and the overnight emergence of global terrorism after 11 September 2001.
2. In late February 2003, this physician travelled to Hong Kong to attend a relative's wedding and stayed at the Metropole Hotel. Here the virus spread to 11 hotel guests who continued their respective travels to various cities around the world, including Toronto, Singapore, Taipei, Hanoi and to other parts of Hong Kong (Abraham, 2005). The exact mode of transmission in the hotel has not been conclusively determined as some of the guests who became infected may not have had direct contact with the index case. The prevailing theories propose that the virus contaminated an elevator or travelled through the ventilation system (NACSPH, 2003).
3. There were, however, two significant community outbreaks of SARS – in the Amoy Gardens apartment complex in Hong Kong (Ng, 2008) and the Pasir Panjang Wholesale Market in Singapore (Teo et al, 2008).
4. The basic reproductive rate refers to the average number of people a disease carrier infects, for SARS this was 2–5 and for Influenza A/H1N1 it was 1.5–2. By comparison, this rate is 1.5–3 for seasonal influenza; 5–7 for polio; and 12–18 for measles (Picard, 2009a).
5. Specifically, influenza A/H1N1 lacks several genes that code for certain proteins (i.e. PB1-F2 and NS-1) that increase the virus' lethality. All pandemic flues of the past, including Spanish, Hong Kong, Asian flues and H5N5 (avian flu) contained these specific genes (Galloway and Alphonso, 2009).
6. It is also for these reasons that the First Nations communities have very high rates of tuberculosis (Public Health Agency of Canada, 2007). Furthermore, such conditions have persisted over the duration, and fatality rates among the First Nations of Canada during past pandemics has been between 5 and 10 per cent, while entire First Nations towns succumbed to the Spanish flu in 1918 (White, 2009a).

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