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Perspective Essay

A landscape planning agenda for global health security: Learning from the history of HIV/AIDS and pandemic influenza

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HIGHLIGHTS

• Defines the general issue of Emerging Infectious Diseases in the context of landscape planning.
• Proposes a “global urban ecosystem” (GUE) conceptual framework to best understand how pandemics occur.
• Outlines pandemic HIV/AIDS and pandemic influenza as the result of the global urban ecosystem.

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ABSTRACT

This paper considers the role of landscape planning and design in the context of a growing need for research and policy recommendations associated with Emerging Infectious Diseases (EIDs), of which COVID-19 is the most recent. Beginning with a definition of EIDs and their origins within the context of landscape planning, the paper then argues that planning and design scholars and practitioners should begin by seeing the importance of a “global urban ecosystem” (GUE) comprised of rapidly transforming metropolitan and regional “patches” connected through “corridors” of relatively unregulated global transportation and mobility networks. It then revisits the history of the two prior global pandemics of HIV/AIDS and pandemic influenza to establish the importance of a landscape planning perspective at the intersection of wildlife, livestock, and globally connected human communities. The essay concludes by arguing that this GUE concept can facilitate creative planning and design by adapting concepts established in other patch and corridor networks like urban transit systems to the ongoing risk of future pandemic EIDs.

1. Introduction

Where did the COVID-19 virus come from? More specifically, how did this regional epidemic become a global pandemic? In this paper I use the conventional distinction that an “epidemic” is an unexpected rise in cases of any disease within a community, while a “pandemic” is an epidemic that crosses national and/or global borders, generally creating new epidemics in distant places. It is essential to answer origin questions about pandemics – and not just epidemics – in ways that lead towards policies for prevention and management of future pandemics.

Since COVID-19 is the latest and most widespread of many recent zoonotic diseases, it is important to ask about its origin not simply to clarify responsibility for the current problems, but as a more pro-active starting point for understanding what can be done to mitigate the risk of future pandemics. In this paper, I argue that landscape and urban planning should be an area of study at the forefront of answering the question, and outline a theoretical perspective on why the biotic and built landscapes, as well as the human behaviors happening within them are so important. Moreover, I assert that this landscape and urban planning perspective must be complemented by an understanding of how distant landscapes are connected through global networks of landscape patches. Future pandemic mitigation strategies need to go well beyond the current range of policy alternatives that have emphasized medical and biological interventions, and this theoretical framework I describe below can help guide these strategies.

Even before the advent of COVID-19, public health agencies worldwide had become very concerned with how infectious disease outbreaks take hold in the world’s most vulnerable areas – often times in countries with few health and other resources needed to stem the tide of infection locally before it becomes a global threat (CDC, 2017). Pandemics have become a growing security concern for many countries, and even three years prior to COVID-19, the CDC wrote that the United States’ national
security at risk within 36 h of a pathogen outbreak in any remote area of the world (CDC, 2017). As COVID-19 has shown very clearly, compounding the dire health threats are economic impacts imposed by potential slowdowns of global trade and movements enabled by today’s extensive global connectivity of people and goods. With large numbers of passengers traveling by air each year, and many of them crossing national borders, EID’s have long posed a significant health and economic threat that came to light in late 2019 (CDC, 2020b). This planetary mobility of people has been mirrored by an equally expansive growth in trade and container shipping of goods (Cudahy, 2006), which also should push us to think about the origins of pandemics clearly and thoughtfully.

This global impact points towards mitigation strategies based on what I call (Spencer, 2014) the global urban ecosystem (GUE) comprised of dense mixing-bowl-like patches of physical, tangible, built and biotic landscapes managed by local communities, and connected to one another by planetary corridors of travel and transportation. The importance of this network of landscape patches and corridors of the GUE should be underlain by an understanding of the category of diseases that become pandemics. Emerging Infectious Diseases (EIDs) comprise a category of illnesses that pose the greatest threat of pandemics because—by definition—so little is understood about identifying, treating, and preventing them.

2. Emerging Infectious Diseases: what are they and what is known about them?

A growing literature describes the outbreaks of EIDs in remote areas of the globe as the result of several convergent conditions: 1) infectious zoonotic pathogens “spilling over” from animals to humans; 2) unplanned and rapid urbanization; 3) agricultural intensification; 4) the development of antimicrobial resistance; and 5) weak public health infrastructures (Wilcox and Colwell, 2005; Kapan et al., 2006; Neiderud, 2015; Boyce, Katz, & Standley, 2019; Wu et al., 2017; Daszak, Eisen, Gaunt, Morse, & Woolhouse, 2009). The first three of these five drivers of EIDs center on landscape-level trends. Such studies argue and document that intensive farming practices and dense urban populations create perfect “mixing bowl” environments for the evolution of new human viruses. Others have also detailed and summarized for planners the specific hypothesized mechanisms for virus evolution into new pathogens, and proposed some preliminary thoughts for controlling them at their source at low financial and political cost (Spencer, Marasco, & Eichinger, 2021). This practical planning orientation aligns with current developments in public health practice.

Recently, public health practitioners have highlighted the importance of understanding the landscape patches where human and animals interact intimately, extensively, and regularly. The “one health” approach promoted by the CDC and supported by over 20 national governments across the developing and developed world (e.g. CDC, 2020a, CDC, 2020b) recognizes that a shared physical environment between humans and animals means that the protection of human health depends on the protection of animal health. According to these professionals, regular animal contact with humans and with one another necessitates that we understand the health status of both wild and domesticated animals, their relationships with one another, and with the humans they live next to. In these mixing bowls, pathogens move seamlessly across species boundaries because landscapes of development and rapid change are where humans and animals come into dense proximity without mitigating plans and designs. Thus, identifying landscapes of new and dense human and animal interactions is an important gap that planning and design scholars are positioned to fill.

For these reasons, landscape scholars are well versed in the dynamics of the kinds of biotic, built, and social landscape patches that result in new and pathogenic viruses.

However, since pandemics include ecological disturbances, whereby an EID is introduced to a new and non-proximal place, a socio-ecological landscape perspective is not helpful unless it envisions how one local landscape is connected to other local landscapes, a framework underlying the field of ecology. In other words, a policy relevant theoretical framework must be more refined than simply recommending universally closed borders, and account for precisely how a regional and localized epidemic becomes a global pandemic. It should provide a more comprehensive framework for charting the upstream and downstream sequences of events, and where they occur. Developing this conceptual framework, with an eye towards developing interventions to mitigate the risk of future pandemics is crucial because the stakes are so high in human and economic costs.

COVID-19 has shown in stark terms the catastrophic impact that an EID can have on national and global supply chains, employment, and savings, to say nothing of the death toll and health impact. While these comprehensive impacts have yet to be tallied for the current pandemic, in 2017 the CDC estimated that global pandemics were likely to cost over $6 trillion over the next century, with an annualized expected loss of more than $60 billion for potential pandemics. However, investing $4.5 billion per year in building global capacities, it argued, could avert these catastrophic costs. Additionally, the Institute of Medicine (US) Forum on Microbial Threats (2009) and others suggested that some success had resulted from building platforms for improved virtual surveillance such as monitoring global news and health reports through artificial intelligence at the global scale. These policy approaches are, by definition, limited to once a pandemic has broken out and had time to affect large numbers of people, so they must be complemented by new tools for prediction and planning (e.g. Rubin et al., 2013; Kilpatrick & Randolph, 2016). Studies focused in this realm, however, have been scarce even though prediction and planning can help solve some of the difficult financial and political barriers to EID risk reduction by recommending evidence-based, and realistic prevention strategies (Spencer et al., 2021).

While the phenomenon of EIDs may be new to planning scholars, it is important to note that zoonotic disease transmission has occurred throughout history, and microbiologists, medical doctors, and virologists have long sought to identify their origins based on the methodological tools of their disciplines. Increasingly, however, experts from these fields with conceptual and empirical tools centered on microbes, individual humans, and other a-spatial units of analysis have called for wider, landscape-level studies (e.g. Wilcox and Colwell, 2005; Neiderud, 2015). Here, I suggest that a planning and design research agenda for combining landscape analysis with global connectivity is needed to understand current and future pandemic outbreaks such as COVID-19, and thereby develop appropriate new policy tools.

Murugesa (2020) has documented the growing interest of urban planners in the issue of EIDs, and Spencer et al. (2021) have provided a planning-oriented outline of how zoonoses—the phenomenon of animal viruses jumping from animal to humans—is at the center of EID origins. Preliminary empirical work has shown that large agglomerations of settlement and economic activity may be sources of these EIDs (e.g Spencer, 2013; Saksena et al., 2015), especially as they experience rapid urbanization and peri-urbanization. If this is indeed true, then with rapid urbanization of large parts of the developing world, especially the peri-urban regions of Asia and Africa, the risk conditions for the development of new pathogens such as Highly Pathogenic Avian Influenza, Ebola, and others, have been elevated (e.g. Institute of Medicine (US) Forum on Microbial Threats, 2009; Kontgis et al., 2014; Alirol, Getaz, Stoll, van Empelus, & Lounis, 2011; Alkendig et al., 2015).

Beyond these place-based investigations, a fewer number of scholars have emphasized global connectivity factors that connect distant communities as key drivers turning regional epidemics into global pandemics (e.g. Martin & Boland, 2018; Gendreau & DeJohn, 2002; Ryan, Wilson, & Cain, 2002). This dearth of studies of the origins of EIDs that usefully lead to new policy alternatives, therefore, requires an understanding of the upstream and downstream relationships from point A, where a zoonotic event of virus reassortment (Spencer et al., 2021) in a
limited number of individuals living close to one another, to point Z, whereby hundreds of millions are infected globally. It is only a framework that integrates complex local landscape interactions and maps of planetary routes that connect these landscapes that can answer the simple question posed above.

EIDs have been part of human populations for thousands of years, and there are surely many new zoonotic diseases that never become epidemics, let alone global pandemics. These new infectious disease outbreaks have generally been limited in geographic scope due to the new pathogens’ transmission through local populations until these host human groups were no longer viable hosts for the virus due to high mortality rates. Pandemics, however, disrupt these dynamics with relatively low short-term mortality rates, which allows low- and asymptomatic carriers to cross over vast distances undetected. Thus, newly sick individuals from these endemic landscapes where the pathogen has gradually arisen interact in new – non-proximal – landscapes where protection (both immunologic and social) has not had a chance to build up defenses. Pandemic EIDs are a function not just of dense local ecologies, but also the connectivity of these diverse ecologies across extensive distances that can introduce EID viruses into new landscape patches that have not been gradually exposed to these virus strains as they have developed over time.

3. The global urban ecosystem: revisiting the HIV/AIDS and pandemic influenza EIDs

In prior work, I have extensively described a “global urban ecosystem” that characterizes the contemporary movement goods, people, ideas, and even viral micro-organisms as a global network of urban regions connected for both economic and cultural reasons (Spencer, 2014). This conceptual framework rests on the idea that global connectivity is comprised of interacting cities and regions (Spencer, 2014, pp. 7-38) is premised on ecological thinking that defines both “patches” and “corridors” (e.g. Henein and Merriam, 1990; Taylor, Fahrig, Henein, & Merriam, 1993), and associated principles of punctuated equilibrium (e.g. Grime, 1973; Connell, 1978). I argue here that EIDs are generated in specific types of landscape patches, and are transmitted globally through unregulated transportation corridors that “teleconnect” (Seto et al., 2012) geographically discontinuous landscape patches. It is through this GUE of landscape patches and teleconnecting transportation corridors that historic EIDs have turned regional epidemics into global pandemics.

This framing of the GUE consolidates empirical work on the ecology and science of cities and regions (e.g. Bettencourt, 2013; Corning, 2002) and that of teleconnections that documents the direct cause and effect relationships of specific events in distant locales (e.g. Seto et al., 2012; Baird & Fox 2015; Baird, Noseworthy, Tuyen, Ha, & Fox, 2019) into a shared conceptual framework.

In sum, dense biotic and built landscapes gradually evolve and transform based on the human and animal individuals and communities that occupy them. This gradual evolution and transformation is periodically shaken by “disturbance” events that bring new, non-gradual human and animal individuals and communities into close proximity. As with periodic ecological disturbance events like wildfires and invasive species, viral disturbances can have devastating impact that result in deadly epidemics that transform local communities.

Thus, while microscopic zoonotic transmission is necessary, it is not sufficient for creating a pandemic. Rather, pandemics are the result of these frequent and locally-rooted zoonotic transmission events, combined with networks that can disseminate them rapidly across the planet. A scientifically-informed narrative of the two most recent pandemics at the same scale as COVID-19 – Human Immunodeficiency Virus/Acquired Immunodeficiency Syndrome (HIV/AIDS) and pandemic influenza – can illustrate how the GUE operates.

Before illustrating how it operates, however, it is important to recognize that even a preliminary and incomplete theory of how pandemics evolve can be essential for identifying ways to mitigate disaster. Taking a landscape-level approach to explaining such complex phenomena as global pandemics, even decades later, can provide only circumstantial evidence. Even the most commonly understood explanations cannot be definitively proven. Nevertheless, useful perspectives based on scientifically-informed narratives can change current and future policy even though evidence may remain largely circumstantial (Vance, 2019). Thus, a GUE level analysis of the HIV/AIDS and pandemic influenza crises may provide useful circumstantial evidence resulting in broad planning and policy guidelines that are simply good things to do, even though the “scientific answers might still be open.” Following Vance (2019), I argue here, there is enough “uncertainty in our (current) narratives” of EIDs to warrant a detailed and wide-ranging exploration of HIV/AIDS and pandemic influenza from the landscape perspective.

4. HIV/AIDS

Given that the HIV/AIDS crisis became a pandemic over 40 years ago, it is remarkable how little planning research has engaged with the subject (Takahashi & Snutny, 2001; Takahashi, 1997), even though studies of HIV (Talman, Bolton, and Watson, 2013) have argued forcefully that urbanization and other landscape-level processes gave rise to it.

From the public health perspective, Talman, Bolton, and Watson (2013) have posited what they call a “syndemic” framework to explain the evolution of HIV as a global pandemic. In sum, HIV/AIDS is the result of regularized human-simian interactions, regional EID spread through urbanization, transportation and unprotected sex; and global spread through travel, tourism and international aid. Today, 40 years after HIV/AIDS became known as a global pandemic, it is generally accepted that the disease has geographic origins in central Africa and biological origins in apes’ Simian Immunodeficiency Virus (SIV). After decades of ambiguity on the precise origins of the disease and numerous possible explanations of how it arose, today there is general consensus that the regional origins of the HIV pandemic center around Kinshasa, based on virologic studies establishing its presence in the region over 80 years ago (Fehervari, 2018).

Specifically, David Ho discovered the first plasma sample to contain the HIV virus in the Central African region dating from 1959 (as cited in Fehervari, 2018), thereby definitively establishing evidence that HIV was present in humans in and around Kinshasa, Zaire as early as the 1950s. Beatrice Hahn studied wild chimpanzees in the region, finding that by around the year 2000 they served as hosts for an SIV virus almost identical to HIV. Related studies confirmed (Sharp & Hahn, 2011; Sharp et al., 2001) that the biological origin of the HIV virus was certainly among the SIV of the pan troglodyte subspecies of chimpanzee common in southern Cameroon, and that the jump from this group to humans occurred before 1940.

Genetic analysis suggests that the first case of the HIV in Kinshasa may have been even earlier, between 1909 and 1930 (Gryseels et al., 2020; Faria et al., 2014). These studies of specific landscapes appear to tell a consistent story regarding the geographic origins of the primary strain of HIV that went global, a story that begins with the patterns of human/animal interactions surrounding Kinshasa, Zaire in the first half of the 20th Century.

This historic virologic analysis among animals and humans in a single regional landscape in central Africa aligns with what has been found regarding the global distribution of HIV strain diversity. HIV is categorized into several subtypes, and each arose from independent cross-species infection events (Sharp & Hahn, 2011). In other words, HIV/AIDs does not originate in a single chance event; instead, numerous related but diverse viruses arose independent of one another in a shared geographic “landscape patch” (Hemelaar et al., 2019). Their proximity was the result of common regional environmental and human behavioral conditions, leading to a critical mass of events and exposures.
among humans. Because of this regularity, the studies suggest, it is clear that the HIV class of EIDs arose from complex regional dynamics rather than as the result of a single unique event.

Hemelaar et al. (2019) reviewed empirical findings reported from 1990 to 2015, and mapped the drastic reduction in genetic variety of HIV strains outside of central Africa, arguing that it is smaller-n events that spread the disease rather than widespread community infection of the wide range of virus subtypes. Specifically, they argue that the HIV-C strain is almost exclusive in its dominance in South Africa, Ethiopia and India, and that HIV-B is almost as exclusively dominant in Western and Central Europe, North America, the Caribbean, and Central and South America. Thus, a landscape patch and transportation corridor approach strongly suggests a corridor connecting the local and regional landscape patch of central Africa in directions south and east, and a separate corridor connecting it west to Europe and the Americas led to two geographically distinct pandemics of the same virus. Again, while difficult to prove definitively, this compelling narrative outline can usefully shed light on the question of where HIV/AIDS came from by defining one pathway east and a different one west.

The scientific evidence suggesting that HIV was endemic to the region surrounding Kinshasa is clear. To understand how this epidemic became a pandemic, however, it is then important to understand the level of connectivity between Kinshasa and other regional and global points. Epidemiologists suggest that diamond mine workers from Kenya, Zimbabwe, Uganda and Tanzania were significant vectors carrying the particular HIV strain back to their home countries by the 1970s (e.g. Faria et al., 2014; Dalai et al., 2009; Tully & Wood, 2010). From there, viral genetic evidence suggests, that the 1980s and 1990s saw the HIV-C strain (the most common version in South Africa and India) introduced into South Africa from these and other neighboring countries; moreover, given that South Africa was simultaneously a major destination for regional workers, as well as connected globally to economies outside of Africa, the conditions for turning an epidemic of central Africa into a global pandemic was enabled by a country with modern transportation infrastructure and global partnerships (Wilkinson et al., 2016).

At the same time, HIV-B, which is the dominant strain in the Americas, is seen to have taken a different pathway that connects the central African region to global populations along a different transportation corridor of movement. Worobey Cox & Gill (2019) analyzed numerous cases of HIV samples and compared them with 117 from other parts of the world, estimating that it is 99% likely that Haiti served as the entry point for HIV in the United States. Moreover, the fact that Haiti shows the widest variety of HIV-B subtype of anywhere in the Americas, also suggests that it served as a node connecting central Africa to North and South America (Gilbert et al., 2007). Some outline the important role that the United Nations Organization in the Congo from 1960 – 1964 (ONUC) played in recruiting French-speaking professionals (doctors, engineers, and others) from Haiti to replace the departing Belgian colonial administrators (Jackson, 2014). Serving in this role for up to four years provided an adequate opportunity for Haitian professionals to intermingle in large numbers and over relatively long periods of time with native Congolese, thereby serving as unwitting points of entry for HIV to the Americas upon their return home to Haiti. Thus, these professionals facilitating decolonization in Africa may have been a key vector that allowed the HIV regional epidemic to connect the central African region to a non-proximal, global node. By 1966, HIV-B was established in Haiti and subsequently spread to the United States by around 1969, although it did not become a commonly understood disease until much later.

In sum, over 90 percent of HIV cases in South Africa, India, and Ethiopia are subtype C, whereas nowhere else in Africa does a single subtype comprise greater than 50 percent, and subtype B makes up well over 75% of the cases throughout the Americas and Australia/New Zealand (Gartner, Rochea, Churchill, Gorry, & Flynn, 2020). This evidence of distinct eastern and western teleconnecting transportation corridors originating from a shared patch in central Africa clearly suggest the importance of global corridors connecting regional and local socio-ecological landscapes.

This story of landscape patches and teleconnecting transportation corridors is based on circumstantial evidence, pieced together through numerous empirical studies of the natural and health sciences, describes the key aspects of dynamic locality-based transformations in “mixing-bowl” like conditions at the animal/human interface, combined with growing regional and global network connections. Earlier, I posed the question “where did COVID-19 come from?” This is a question that remains imprecise even today for the HIV/AIDS pandemic. Yes, the virus itself did originate in the patch of central Africa, along with numerous other related viruses. But why did the type C virus dominate in India and type B in the Americas? These are the implied questions that cannot be answered by a single geographic identifier, but lie at the heart of preparing for a next pandemic.

Part of the difficulty of developing policy alternatives for rare events like pandemics is the dearth of case studies. With the cases of recorded and well documented pandemics in the single digits, what kinds of lessons can be drawn from HIV/AIDS? So far, I have asserted that the GUE perspective of interconnected landscape patches and teleconnecting transportation corridors is a useful framework for shedding light on the origins of EIDs that can usefully lead to new policy alternatives and provided a narrative history of one known and studied pandemic to illustrate the case. This circumstantial evidence can be significantly strengthened by investigating the science and theories regarding the origins of pandemic influenza. Unlike the HIV/AIDS pandemic, the influenza pandemic of 1918 has been exhaustively summarized in book-length, science-based narratives that already point towards the importance of the GUE, but without naming it as such (e.g. Barry, 2005; Kolata, 1999).

5. Pandemic human influenza

As an EID that has occupied the attention of health policy makers and researchers for over 40 years, especially in a time of advanced research methods and support, there is a rather large body of empirical research and evidence on the origins and dissemination of HIV/AIDS. However, the prior global pandemic of flu in the early part of the 20th Century occurred not only before exponential growth in the capacities of the biomedical and social sciences, but also during a period of tremendous global turmoil that surely limited virtually every nation’s capacity to focus on the disease. Nevertheless, a retrospective examination of the origins, dissemination, and likely causes of the 1918 “Spanish” Flu can pinpoint some very likely truths about the disease and pandemic that also illustrate the power of thinking in landscape terms that focus simultaneously on complex human-ecological patches connected globally by transportation networks enabling immediate interaction over non-proximal spaces.

In his 2004 book The Great Influenza: The story of the deadliest pandemic in history, historian John Barry traces the evolution of the influenza virus through the global turmoil of World War I and its worldwide impact as it killed over 50 million individuals in the course of two years, 675,000 in the United States alone (CDC, 2020).

As a scientifically informed, popularly oriented narrative, Barry’s work weaves stories of key individuals into the disjointed facts that are known about the virology of the influenza virus and its impacts. For my purposes of illustrating the importance of regional design and planning through the lens of dynamic multidisciplinary models, the tropes of human and animal interactions and teleconnecting transportation corridors placing non-proximal landscapes into immediate and direct contact, his description of the origins of the 1918 Influenza pandemic disease is interesting. His summary of what is known about the origins and spread of the disease fits neatly with the argument presented here:

Epidemiological evidence suggests that a new influenza virus originated in Haskell County, Kansas, early in 1918. Evidence further...
suggests that this virus traveled east across the state to a huge army base, and from there to Europe. Later, it began its sweep through North America, through Europe, through South America, through Asia and Africa, through isolated islands in the Pacific, through all the wide world (p. 92).

Using the metaphors of “swarms” and “tinderboxes”, Barry goes on to describe the mixing bowl characteristics of central Kansas at the turn of the 19th Century. At this time, the United States was undergoing a rapid industrialization of its economy, and the exponential growth of urban centers associated with it. In 1870, he points out, the United States’ population of 40 million people lived predominantly – almost 75% – in small towns or on farms; by 1914, the population had reached 105 million and several years later more than 50% of them lived in urban areas (p. 122). Naturally, the growth of cities at the time required increased agricultural productivity, and an explosion of industrial agriculture helped fuel urban growth during this period. Barry describes Haskell County as a place where “...land, crops and livestock were everything, and the smell of manure meant civilization. Farmers lived in close proximity to hogs and fowl, with cattle, pigs and poultry everywhere.” (p. 91). This history aligns with contemporary theories on today’s deadly avian influenza is the result of these “mixing bowl” landscapes characterized by the dense interactions of humans and animals – and their viruses – without much attention from planning and design.

Reading Barry’s scientifically informed narrative of the geography of Haskell County and the argument that it is the origin of the 1918 pandemic, it is difficult not to imagine the contemporary urbanization and agricultural intensification dynamics of regions in the 21st Century such as China, Viet Nam, Thailand, Indonesia and elsewhere (as described in Spencer, Finucane, Fox, Sakse, & Sultana, 2020; Wilcox & Colwell, 2005; Kapan et al., 2006). As the evidence of HIV/AIDS origins suggested, however, the creation of new viruses through zoonotic transmission, while a health threat locally, does not constitute a pandemic on its own. Rather, the connections across wide distances that position infected humans in close proximity with others who have a very different profile of immunity is what Barry calls the “tinderbox.” In 1918 these local virus dynamics combined with the exponential growth of global military enlistment and travel associated with World War I to disseminate a locally generated zoonotic disease across the globe. Farmers and their sons from Haskell County enlisted at nearby Camp Funston near Manhattan KS, joining thousands of other young men in cramped, often unsanitary living conditions – conditions replicated at US and other military camps around the world – thereby creating the perfect conditions for the 1918 Influenza to spread globally.

This macro-level understanding of the origins and spread of the 1918 Influenza is not simply historical speculation informed by a limited body of biological and public health evidence. Rather, evolutionary biologists have also begun to reconsider the 1918 Influenza in the context of rapidly changing landscapes of urbanization and farming. Worobey, Cox and Gill (2019) have critically evaluated Barry’s claim as to the origins in Haskell County, in the context of two other origin possibilities in France and China, finding some contradictory evidence of simultaneous infection in New York City. They conclude, however, that Barry’s story has a stronger evidentiary basis than the other two origin stories, whether or not Haskell County can be definitively shown to be the origins. It appears fruitful, therefore, to developing a planning-relevant understanding of EIDs from this urbanization perspective.

On this point, Worobey’s research is clearer. According to Worobey, “[w]hat we’re seeing is maybe our domesticated animals like ducks and chickens, they might be this huge pool of vulnerable hosts that viruses can get into and amplify and then you can have spillover from domestic into the wild” (as recounted by Barchfield, 2014). His research finds that there were major outbreaks of horse influenza and avian influenza in Haskell County during the years immediately preceding the 1918 flu, suggesting that influenza had long found receptive hosts in large-scale domesticated animals, and that the 1918 Influenza did not simply appear from nowhere as the result of a one-off event. Instead, this history of prior circulation among animal stock – as opposed to wild species, as was the case for HIV/AIDS – suggests to Worobey and his colleagues that the human-livestock interface is the most likely origins of the 1918 human influenza. Moreover, he argues, it suggests a more logical origin story than antigenic drift within humans, which is sometimes used to explain the origins of pandemic influenza and other EIDs. In other words, the implications of Worobey’s genetic analysis broadly concur with Barry’s “most-likely” explanation that it was the intensification of farming practices and the dense proximity of humans and livestock that likely led to the 1918 pandemic, whether the specific case happened in Haskell County or not. Once developed in these dense patches of rapid socio-economic, cultural, and ecological transition, it is not hard to see how the influenza virus quickly transmitted across the military camps and communities that operated at a global scale during this advanced stage of World War I. Thus, just as colonialism/decolonization and growing global trade links to Central Africa served as an unwitting corridor for pandemic, World War I also helped create a pandemic out of a regional epidemic.

Since 1918, the human influenza virus has been an annual infection spreading widely among human populations without anywhere near the deadly impacts of 1918. Mostly, it has been a nuisance dealt with through vaccination, masks, and isolation. Periodically, however, a new virulent strain of influenza originates in a livestock and jumps to humans with deadly consequences. In the 2000s, for example, Highly Pathogenic Avian Influenza (HPAI) threatened to lead to major epidemics and possibly a pandemic due in large part to urbanization and agricultural practices (Saksena et al., 2015; Finucane et al., 2014).

During the 2004–05 outbreak of avian influenza in Viet Nam, for example, 119 people were infected with the H5N1 virus, and 59 died—an alarming mortality rate of nearly 50 percent. Nearly all of these infections were the result of direct contact with diseased chickens or ducks, and the virus did not have time to evolve into a strain able to transmit easily between humans. Had the virus spread more widely within the human population, public health officials estimate that thousands more would have died. Fortunately, this epidemic EID strain failed to evolve into a pandemic.

Empirical analyses of this more recent strain of influenza do show, however, that the zoonotic influenza occurred in the kinds of rapidly urbanizing and agriculturally intensifying landscapes that Barry describes in Haskell County (Saksena et al., 2015; Spencer et al., 2020; Finucane et al., 2014; Spencer, 2013). Clearly the landscape conditions that facilitated the evolution of the original HIV/AIDS and influenza viruses remain throughout large portions of the world. In today’s connected world, these regional dynamics are certainly connected to global networks that might transform regional epidemics into pandemics even after COVID-19 has subsided.

6. Planning for global pandemics requires outlining the global landscape: a research and practice strategy for EIDs

This condensed history of the origins and dissemination of HIV/AIDS and pandemic influenza outlined above, while admittedly circumstantial based on limited empirical evidence, does clearly point to critical sequences of events that happened in transitional, developing areas at the interface of animals (both wild and domesticated) and people. Moreover, the regional and global links that allowed individuals – some of whom were symptomatic and asymptomatic carriers of EIDs – across both moderately and extremely distant spaces without any systematic surveillance or regulation turned epidemics into pandemics. What can we learn from HIV/AIDS and pandemic influenza by asserting the narrative of the GUE? The circumstantial evidence described above should give planners and designers the confidence to believe they can chart the most likely patches of zoonotic EIDs and their corridors of likely spread. An empirically informed GUE map, thus, would provide
guidance for the most effective places to look for and mitigate these developing regional EIDs before they become pandemics.

7. What is the landscape where pandemic planning should happen? the global urban ecosystem

It is in this realm of developing risk mitigation strategies for future pandemics that the metaphor of a GUE can be useful, even if the science cannot be definitively proven. Because there will always be uncertainty in a narrative explanation of a problem on such a global scale, looking to other managed systems of patches and corridors can be useful for policy and planning design.

The Global Urban Ecosystem described earlier is best understood as a kind of global version of an urban subway system (Spencer, 2014, pp. 29–30), whereby non-proximal “neighborhoods” are connected through a standardized system of linear pathways that make travel to unknown areas predictable and navigable. However, unlike a formal transportation infrastructure such as a metro system or a flight network, the Global Urban Ecosystem is governed by a diffuse and disjointed set of global regulations on the mobility of people, goods and services, combined with numerous cultural and linguistic norms that allow it to function. While more complex than a unilaterally constructed and managed system, understanding the dynamics and learning patterns inherent to this type of global system of connected landscapes – each of which serves as a complex mixing bowl of human and animal viruses – is essential for tackling the human-driven challenges of EIDs.

Fortunately, the metaphor of a metropolitan transportation system provides more than just a conceptual framework for scholars; as a human developed and managed system, it provides a set of policy and planning alternatives for practicing planners and designers to consider, evaluate, and adapt. Above, I have described a global system of regional and local landscape patches connected by global transportation corridors, and the importance of understanding this system as it relates to EIDs. This defined system, however, is not governed by any planning institution and thus requires further specification related to what kinds of actions might be possible to limit exposure to new EIDs. A metropolitan transportation system is a small version of how intergovernmental entities create and manage a system of neighborhood patches with regional teleconnecting corridors. This managed system not only achieves transportation goals, but also mitigates a range of risks and contextual factors that facilitate its safe and effective operations.

Managing transportation systems requires surveillance, stations, a trained security and workforce, and a coordinated schedule and emergency management plan. If a disturbance breaks out at one station, for example, numerous mathematical algorithms chart new connection routes to minimize passengers transiting through that station, while suspending routes that have that station as their destination. Similarly, most modern transit systems have some form of ticket tracking for knowing the prices, locations, and durations of millions of individual trips each day, consistently analyzing them for the purposes of deploying resources where they are most needed to optimize the system for cost efficiency, time efficiency, or some other goal. Moreover, a core function of the system is to define and incentivize appropriate behavior through signs and checkpoints not only in the system itself, but in the neighborhoods it serves – a standardized system of linear pathways that make travel to unknown areas predictable and navigable.

These simple illustrations show that thinking of the GUE’s role in pandemics may be useful for developing future plans and designs to mitigate the risk of EIDs. Health experts have, of course, made recommendations to manage the growing risk of EIDs, such as creating surveillance systems to rapidly detect and report cases, developing an international laboratory network to accurately identify local causes of illness, training a workforce to identify, track, and contain outbreaks at their sources, and coordinating emergency management systems to mount effective responses. Placing these isolated recommendations into a more systematic institutional framework defined by the landscape patches and teleconnecting corridors inherent to the GUE, I argue, would allow these isolated efforts to be targeted more efficiently and sustainably. Clearly the GUE is much more complex than a metropolitan transit system. Nevertheless, our planning and design experience with such connected systems of landscape patches can provide much needed organizational framework to usefully define policy responses to the growth and consequences of EIDs.

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