

**Viral Myths and Biopolitical  
Disruptions Amidst the Emergence of  
a Novel Coronavirus**

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**Abstract:**

*The 21st century has seen the emergence and re-emergence of novel infectious diseases. Following in the footsteps of its communicable predecessors, the recent emergence in Saudi Arabia of a SARS-like novel coronavirus, or Middle East respiratory syndrome (MERS-CoV), since 2012 has weaved narratives of globally interdependent economic, political, and social intimacies. I will examine the contrasting narratives that reflect investigations and responses to this novel threat from Middle Eastern, European, and North American media networks, the WHO, the global biomedical community, and the Saudi Arabian Ministry of Health through several intersecting discourses: intellectual property rights and viral sovereignty; the deliberation on the taxonomy of the novel coronavirus; and geopolitical differences in information sharing and biosecurity in the context of emergent 21st century epidemics. Using Priscilla Wald's concept of outbreak narratives and the imaginative hold of myths as a framework, I will explore how the stories on the global effort to investigate and respond to the MERS outbreaks continue to be revealed, repackaged, and transformed as experts around the world scramble to uncover its epidemiological pathways. I argue that the consideration of these counter-narratives are critical for rethinking underlying, potentially harmful, factors beyond dominant epidemiological and biomedical discourses surrounding the MERS epidemics. Such considerations may serve as a microcosm for biopolitical barriers in the response to past, present, and future emergent diseases. These counter-narratives should be regarded in light of uncertainties that still cloud the etiology and transmission of the virus, which has since infected over 500 people and claimed over 150 lives in eighteen countries in Europe, the Middle East, Southeast Asia, and North America.*

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Since 2012, the emergence of a novel respiratory virus among countries in the Middle East, Western Europe, and North Africa, has rapidly escalated to a global public health threat. This new disease, aptly named the Middle East Respiratory Syndrome Coronavirus (MERS-CoV), draws close connections to the coronavirus that caused the SARS (Severely Acute Respiratory Syndrome) pandemic in 2003 and has sparked intense research into understanding its epidemiology—its origins, ecological interfaces, transmission routes—and its molecular biology to develop diagnostics and treatments. In the advent of emergent and re-emergent infectious diseases in the 21<sup>st</sup> century, the intersecting relations between microbe, human, and animal seen with MERS outbreaks are not unlike the events that the global community has experienced with SARS, Influenza (H1N1, H5N1, H7N9), Cholera, and Nipah virus, to name a few. Disease experts fly across the world searching for etiological pathways, scientists probe for microbial weaknesses in hopes for a cure, countries deliberate on travel precautions, and families at home receive breaking news of the next disease threat. These scientific, journalistic, and fictional discourses encapsulate a landscape of epidemiological stories that form what is collectively known as the “outbreak narrative” (Wald, 2008)<sup>31</sup>.

This research paper will explore the MERS-CoV outbreak narrative and its current circulating news in the context of global policies and advancements that followed the aftermath of past communicable diseases to capture the precarious intersections of disease emergence and human connections beyond biological susceptibility. The globalized world we live in today is constantly transforming and improving its capacity to better prepare for novel and re-emerging disease threats. After the SARS pandemic in 2003, which infected 8098 people and claimed 774 lives (CDC, 2012)<sup>7</sup>, the World Health Organization developed the Outbreak Communication Guidelines in 2005 to address key outbreak risk communication components through five principles: Trust, Transparency, Announcing Early, Listening, and Planning (WHO, 2005)<sup>37</sup>. These

guidelines emphasizes effective outbreak communication among Member States and the public as a means to “minimize the damage to a nation’s national standing, its economy, and its public health infrastructure.”

The WHO Outbreak Communication Guidelines plays a crucial role in the social and political transformations of global modernity. Combined with advances in biomedical and genomic sequencing, as well as open-sourced monitoring and information sharing tools like ProMED and HealthMap, the modernization of outbreak response promotes a sense of optimism in combatting novel diseases. However, in the same vein as SARS, the MERS outbreak narrative represents “the latest reminder of how powerful [these new global] connections can be”—often allowing “these accounts to offer modernization as a promised solution to, rather than part of the problem of, emerging infections.”(Wald, p.8, 2008). As we will see, the ecological interfaces between the MERS coronavirus—or any infectious microbe—and humans are inextricably tied to political and economic forces that often work to mitigate or even propagate the spread of the outbreak.

The pragmatic nature of biomedical research to contain a potential pandemic creates an urgent hold on both authority and fascination through the development of diagnostics, drugs, and vaccines. Similarly, epidemiology seeks to systematically anticipate and respond to outbreaks—“each case must be described exactly the same way each time in order to standardize disease investigations...they must be described and diagnosed consistently from case to case, using the same diagnostic criteria” (Timmreck, p. 17, 2002)<sup>30</sup>. Viruses like MERS-CoV create a centralized space in which biomedical science and epidemiology can directly intervene upon. In doing so, these forces cast an authoritative hold on an outbreak narrative through both scientific predictability and validity to create *the* narrative. While they are certainly necessary tools for

alleviating disease outbreaks, a “sanguine reliance on science” often emerges, which simultaneously obscures social and political responsibility to health (Wald, p.268, 2008).

Drawing upon Bruce Lincoln’s definition of myths as “a small class of stories that possess both credibility and authority” (Wald, p.10, 2008), I will examine the authoritative persistence of myths throughout the MERS outbreak narratives. An analysis of several intersecting narratives involving stakeholders in media, policy-making agencies, and scientific communities will reflect how certain constructs of biopolitics reveals more than just etiological pathways and susceptibility. From the deliberation on the precariously named Middle East Respiratory Syndrome, and the shifts in biopower exemplified by intellectual property rights and viral sovereignty, to the potential dangers of the Hajj pilgrimage on international biosecurity—these narratives work to reveal and perhaps obscure the scientific, social, and political responsibilities to global public health. In light of uncertainties that still cloud the epidemiology of MERS-CoV, I will place this coronavirus within the context of an ontologically mobile body beyond its molecular biology: A precarious microbe that is able to transform and be transformed by a shifting set of human relations rather than a fixed, well-bounded form (Lavau, p.3 2012)<sup>19</sup>.

## **Virology of MERS-CoV**

The virus behind Middle East Respiratory Syndrome belongs to the genus *Betacoronavirus* in the family *Coronaviridae*. Different species of betacoronaviruses are all of zoonotic origin, mutating and reasserting its genetic material within animals such as bats. While both MERS and SARS share the same genus and present similar symptoms, the former belongs in clade 2c, which is genetically unique from SARS. Coronaviruses derive their name from the Latin word *corona*, a reference to the crown-like glycoprotein spikes on the surface specific to certain receptors on its

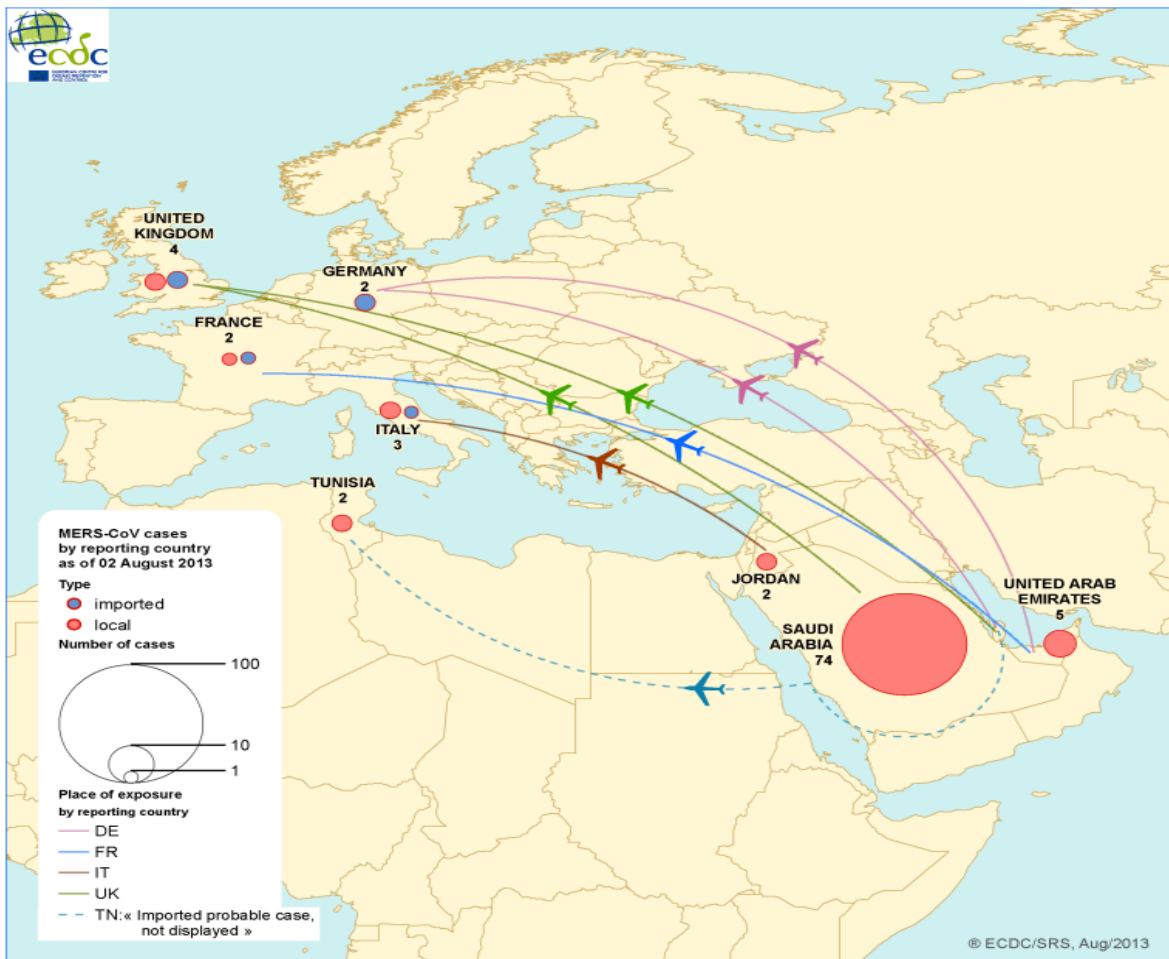
host cell. A study on the pathogenesis of MERS shows a strong tropism, or preference, towards epithelium cell receptors found in the respiratory tract and kidneys of human hosts (Raj et al., 2013)<sup>24</sup>.

While coronaviruses usually cause mild common cold-like illnesses, MERS-CoV have revealed itself to be a particularly severe, often fatal, respiratory disease. Similar to other SARIs (Severely Acute Respiratory Infections), those infected by MERS experience fever, cough, and shortness of breath that quickly progress to acute pneumonia within a week. Atypical symptoms include kidney damage and diarrhea, and the combination of pneumonia and acute renal failure often creates a fatal result (WHO, 2013)<sup>37</sup>. There are currently no MERS-specific vaccines and antivirals to prevent or treat these severe symptoms—the only option being supportive ICU care for acute respiratory distress and septic shock, which usually only occur near the devastating end stages of a MERS infection (WHO, 2013)<sup>38</sup>.

In a cluster of hospital outbreaks in Al-Hasa, involving 23 hospital patients and providers, a demographic report showed that among those infected, most were male, above the age of 50, and were immunocompromised from underlying illnesses (Assiri et al., 2013)<sup>1</sup>. In the absence of specific treatment, 15 of the 23 patients died. This demographic seems to hold true as reflected in the total number of cases worldwide<sup>i</sup>. As of August 16, 2013, there have been a total of 94 MERS-CoV cases and 46 deaths—a mortality rate of 49%. While 74 of the 94 cases originate in Saudi Arabia, there has been imported and nosocomial (hospital-acquired) cases in France, UK, Italy, Tunisia, Jordan, Qatar, and United Arab Emirates (CDC, 2013)<sup>6</sup>.

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<sup>i</sup> As of July 2013, the median age is 51 and 62% of all cases are male patients.



**Figure 1. Distribution of confirmed cases of MERS-CoV by place of reporting as of August 2013 (ECDC, June 18, 2013)<sup>10</sup>**

The etiology, reservoir, and transmission routes of MERS-CoV are still speculative at best. Human-to-human transmission has occurred only in close family or healthcare provider contact, possibly through aerosolized droplets, fomites, or body fluids. Another speculation is that since bats were the reservoir species for harboring the SARS virus, they are strongly suspected for MERS; however, the limited interaction between human and bats also leads to a suspected intermediate animal species, akin to Chinese civet cats connecting the transmission of SARS from bats to humans. Current epidemiological studies have begun tying MERS human-animal

connections to camels, particularly in Oman<sup>i</sup>, and have identified a closely related bat coronavirus as a possible ancestral origin in South Africa (Stoffberg et al., 2013)<sup>29</sup>.

The lack of sufficient epidemiological and scientific understanding of MERS-CoV comes into conflict with the pragmatic nature of these outbreak narratives. Fundamental uncertainties in transmission patterns, drug development, and etiology also create a space of vulnerability that disrupts the normally systematic outbreak narratives. As we orient the discourse towards disease naming as well as political and commercial agendas in global public health, the MERS virus, far from being ontologically fixed, continues to move through a path of instability—eroding human relations along the way.

### **Naming the Virus is Naming the Problem**

The world of microbial taxonomy and nomenclature exists within the context of biology, genetics, established conventions, logic, and politics. The transformative naming process from novel coronavirus to Middle East Respiratory Syndrome is no exception. The role of viral classification in the overall outbreak narrative not only intensifies the social and geopolitical mobility of the virus, but also potentially obscures its unique agency beyond human-made borders.

When Dr. Ali Mohamed Zaki, a virologist in Jeddah, Saudi Arabia, tested the sputum sample from an elderly man with severe pneumonia and renal failure in June 2012, a range of lab tests came back negative for possible viruses, including the coronavirus that caused SARS. Only once a reference laboratory at Erasmus Medical Center genetically sequenced that sample did the global scientific community realize what they were dealing with: an entirely novel species of

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<sup>i</sup> All fifty Omani camels tested were found to harbor protein-specific antibodies against MERS-CoV, though not the actual isolated virus (Reusken et al., 2013)<sup>25</sup>.

coronavirus. Since Erasmus named it Human Coronavirus-Erasmus Medical Center (HCoV-EMC), the coronavirus began gaining notoriety through names like Human Coronavirus England 1 and Jordan N-3—after the location of obtained samples—and England-Qatar—after the travel pattern of an infected Qatari man. Colloquially, the coronavirus was also called Saudi SARS in circulating media and message boards online because of a concentration of cases in Saudi Arabia (Avian Flu Talk, 2013)<sup>2</sup>. Due to its uncertain etiology and the absence of a unifying name, the prevailing vernacular used by the WHO, CDC, and other agencies remained as Novel Coronavirus or simply SARS-like virus, before the name MERS-CoV was given.

On May 2013, the Coronavirus Study Group of the International Committee on Taxonomy of Viruses, which comprised of leading virologists and consultants from the WHO and the Saudi Ministry of Health, announced Middle East Respiratory Syndrome Coronavirus as the official name of the novel coronavirus. The name was given to reference its suspected geographical origin, the nature of symptoms, and the genus of the virus. The naming process reflected an effort to address a “lack of uniformity in virus nomenclature [which] complicates communication both in the research field and with health care authorities, governments, and the general public” (De Groot et al., 2013)<sup>9</sup>. The WHO later issued a contradictory and obfuscatory statement stating that while the organization “generally prefers that virus names do not refer to the region or place of the initial detection of the virus... given the experience in previous international public health events” (WHO, 2013)<sup>40</sup>, they nevertheless “strongly urged the use of this name in scientific and media communications”(WHO, 2013)<sup>39</sup>.

In contrast, the Saudi Ministry of Health has thus far avoided using the name “MERS” on their website and media statements and has opted for Novel Coronavirus instead (Saudi MOH, 2013)<sup>26</sup>. It is within this space of contrasting vernaculars that a dialogue of geographical blame, discrimination, and obscurity begins to emerge. As we follow along the evolution of the novel

coronavirus's taxonomy and its epidemiological discoveries, this ontologically mobile virus exposes a heterogeneous framework of disease naming, its past inadequacies, and the potential geopolitical anxieties that follow.

The culmination of the SARS pandemic in 2003 revealed its etiology through horseshoe bats native to China and in civet cats as the intermediate transmission species likely originating from the Guangdong Province (Wang et al., 2006)<sup>33</sup>. Despite strong connections to Chinese origins, SARS (Severely Acute Respiratory Syndrome) reflected a geographical neutral message in its taxonomy, with reference only to its symptoms. However, MERS-CoV, a distant cousin of SARS, not only harbors life-threatening symptoms towards its host, but also equally serious geopolitical implications for entire populations. Furthermore, the geographical specificity in its taxonomy does not truly reflect the geographical distribution of human cases: The Middle East encompasses the majority of Western Asia, from Egypt to Iran, yet the majority of cases (seventy four out of ninety four) occurred in Saudi Arabia alone, with the remaining twenty cases spread across Western Europe, North Africa, and Saudi Arabia's neighboring countries, Jordan and UAE. With institutionalized thoughts of terrorism, military conflicts, and capitalist interests distorting the modern Western perception of the Middle East, the global public health threat that MERS harbors can potentially serve as a catalyst for more geopolitical unrest, exacerbating existing conflicts along the way.

Thus, the taxonomy of MERS-CoV may become a tool for a geography of blame—albeit latent only because there is currently little impact of MERS outbreaks in Western, First World countries, including the United States. Similarly, one can see the perpetuation of geography of blame in past influenza outbreaks.

The association of the 2009 H1N1 outbreaks with its more colloquially known names such as the “Mexican Flu” and “Swine Flu”, highlighted a key chink in the epidemiological armor: A

distorted lens of underlying human relations to disease outbreaks and the disproportionate burden of blame placed on Mexican citizens and factory farm pigs as potential carriers of the flu that ensued (Sparke, Anguelov, 2012)<sup>28</sup>. The economic inequities of NAFTA (North American Free Trade Agreement) between the US and Mexico, coupled with racial anxieties on disease-carrying Mexicans, created a perfect storm of irrational fears amidst popular media around the world. In a compilation of videos put together by Media Matters titled “Pandemic Paranoia: ‘Swine Flu’ Fear and Loathing in the Conservative Media”(Linkins, 2011)<sup>20</sup>, the derogatory use “Swine” and “Mexican” flu not only perpetuated a distinct geography of blame on undocumented Mexican immigrants as disease carriers, but also obscured the economic and political relations in the underlying H1N1 outbreak narrative.

As we peel away the obscuring layers of dominant, often distorted, epidemiological causalities, we also begin to reveal the omnipresence of underlying, and indeed very human, geopolitical and economical relations of a precarious virus.

Pigs have very little to do with how influenza emerges. They didn’t organize themselves into cities of thousands of immune-compromised pigs. They didn’t artificially select out the genetic variation that could have helped reduce the transmission rates at which the most virulent influenza strains spread. They weren’t organized into livestock ghettos alongside thousands of industrial poultry. They don’t ship themselves thousands of miles by truck, train or air. Pigs do not naturally fly. (Wallace, 2009)<sup>32</sup>

When the emergence of a vaccine-resistant strain of H5N1 swept across Southern China in 2006, “Fujian-like” virus was used in media reports and statements ranging from the Daily Mail, SCMP (South China Morning Post), and CIDRAP (Center for Infectious Disease Research and Policy). Consequently, government officials of the Fujian

province expressed anxieties over the geographical association to the virus as more cases popped up in Laos, Myanmar, and Vietnam (Butler, 2008)<sup>5</sup> These patterns of geographical discrimination are not only harmful to political structures, but also fails to acknowledge the agency of communicable disease beyond human-made political borders. Rob Wallace, an evolutionary ecologist at UCI, highlights the inadequacy of geographical specificity by noting that “there’s nothing more frustrating and useless to a phylogeographer than a perfectly sequenced isolate labeled ‘China’”<sup>5</sup>. In response, the WHO completely revised the classification process of H5N1 nomenclature in 2008 from an ad-hoc system to a numbering system to avoid the “stigmatizing labeling of clades by geographical reference”<sup>5</sup>. Instead of geographical references, new strains of H5N1 would be systematically classified into distinct phylogenetic clades based on their unique haemagglutinin genetic sequences. The strain of “Fujian-like” viruses became Clade 2.3.4 and H5N1 viral strains commonly found in Indonesia became Clade 2.1.

While both the ICTV Coronavirus Study Group on MERS and the 2008 WHO classification reform of H5N1 share commonalities in addressing the lack of uniformity in communicating disease names, the former harbors remnants of an ad-hoc system not unlike that of the “Fujian-like” virus. The latter, however, holds greater biological relevance, complimenting additional spatial data on land use, climate, and trade relations instead of obscuring them. While the 2008 WHO reform was intended to amend nomenclature for H5N1, the geographies of blame perpetuated by the nomenclature of other viruses are no different in the potential political and economical ramifications.

A recent study on *Pipistrellus* bats in South Africa and Europe revealed its close phylogenetic relationship with MERS-CoV—a difference of about 0.3% amino acid sequence in African *Pipistrellus* bats and 1.8% in European bats (Stoffberg et al., 2013)<sup>29</sup>. Reflecting on an outbreak of Rift Valley fever virus in 2000 in Saudi Arabia, which followed an importation of

livestock from East Africa, researchers suggested that a reservoir host of possible African or European origin might have been a potential source for the emergence of MERS-CoV.

In the aforementioned WHO document on the naming of the novel coronavirus, officials followed their preference for non-discriminatory nomenclature by stating that “this approach [aimed] at minimizing unnecessary geographical discrimination that could be based on coincidental detection rather than on the true area of emergence of a virus”<sup>37</sup>. Yet, the naming of MERS harbors these unnecessary geographical discriminations despite a clear lack of knowledge on its biological and geographical etiologies. The phylogenetic research indicates that the well-bounded geographical specificity of MERS does not serve well in elucidating its true origin of transmission routes—in fact it may serve to further obfuscate its etiologies. Additionally, the implication of geographical blame, which surfaced during the H1N1 and H5N1 outbreaks, reflect the ontological mobility of the MERS virus to encompass the risks of other communicable diseases. In doing so, the MERS virus is able to embody the viral cloud conceptualized in Celia Lowe’s article on H5N1: “Uncertainty about what influenza was and what it could become, disrupted existing arrangements among species, peoples, institutions, and nations—remaking biological and political relations along the way” (Lowe, p. 626, 2010)<sup>21</sup>.

### **In the Name of (Commodified) Health**

Michel Foucault defines the beginning of an era of bio-power as achieving the subjugation of bodies and control of populations through optimizing forces and aptitudes in improving and maintaining the health of a population (Foucault, p. 262, 1988)<sup>13</sup>. As “an indispensable element in the development of capitalism”<sup>13</sup>, bio-power as we see today has slowly displaced the juridical existence of sovereign power that once controlled the right to life over a population. This concept

of bio-power manifests itself in the discourse of the politicization of biomedical research and the MERS virus itself. However, bio-power surrounding scientific research today goes beyond the contrast between the power to *make live, let die* and the sovereign right to *take life, let live*. Biotechnological advances, spurred by the molecularized threat of unknown microbes, are able to transform and be transformed by social identities, new forms of political association, and new circuits of capital (Braun, 2007)<sup>4</sup>.

The concepts of intellectual property rights, patents, and viral sovereignty (wherein a nation claims sovereign possession over a virus found within its border) exposes a deep rift among stakeholders of bio-power surrounding the MERS-CoV outbreak narratives: A power struggle between deregulated neoliberal biomedical research and sovereign autonomy of nations over the benefits of sharing virus samples. In claiming service to public health as moral justification, both these forms of power perpetuate a contrast of myths that exposes the political and economic mobility of MERS and makes visible the obstacles to a global responsibility to pandemic preparedness.

We will revisit Erasmus Medical Center's involvement in being the first to isolate and bring to attention the MERS virus, then named HCoV-EMC, that was sent by Ali Mohamed Zaki—but this time in the context of political and commercial ties to scientific research and sample sharing. When Zaki became increasingly puzzled over inconclusive tests on his patient's mysterious respiratory infection, he sent a sample to Ron Fouchier, a colleague virologist at Erasmus, for analysis. Fouchier's lab was able to isolate and identify the genetic sequence of the novel coronavirus. In September, Zaki posted a ProMED notice<sup>i</sup> revealing the news and shortly afterwards in November, an article titled "Isolation of a Novel Coronavirus from a Man with Pneumonia in Saudi Arabia" was published and co-authored by Zaki and scientists in Fouchier's

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<sup>i</sup> Novel Coronavirus – Saudi Arabia: Human Isolate, published on September 20, 2012  
<http://www.promedmail.org/direct.php?id=20120920.1302733>

lab (Zaki et al., 2012)<sup>42</sup>. Although Zaki claims that he had sent samples to the Saudi Ministry of Health— which reportedly came back with inconclusive tests—the Saudi Arabian government were not aware of the discovery of MERS until Zaki’s bilateral collaborations went public and accused him of sending the sample out of the country without their permission (Aljazeera, 2013)<sup>22</sup>.

By the time the Saudi Arabian government began to take notice of Zaki’s actions, Erasmus had already “patented” and filed for a MTA (Material Transfer Agreement) for the virus— specifically on its genetic sequence and host receptor data (Garrett, 2013)<sup>14</sup>. This incident has since sparked intense international debate over the politicization and precariousness of MTAs and with it, the commercial side of biomedical research.

The Material Transfer Agreement, or MTA, is a widely used contract for the bilateral transfer of tangible research materials between two entities—most often between research laboratories. MTA defines the rights of both the provider and the recipient with respect to the research materials, its derivatives, and innovations associated with them (Berkeley, 2013)<sup>23</sup>. The concern with MTAs most often lies within the types of MTAs that have for-profit and industry-related ties. The language and legal implications of these types of MTAs differ from simplified material transfers between non-profit academia in that they politicize, complicate, and often restrict the research process for recipients.

As claimed by Erasmus Medical Center and their MTA on MERS-CoV, restrictions in open sample sharing of biological materials exists to ensure that recipients have the capability to safely work with it and to prevent the possibility of bioterrorism. As long as laboratories comply with safety criteria, recipients are allowed unrestricted access (Erasmus MC, 2013)<sup>11</sup>. What is not being discussed and what often lies at the heart of impeded research progress is that MTA restrictions and legalities also exist to ensure provider benefits in the form of patents and

intellectual property rights. Highly negotiated contracts often involve reserving commercial gains solely for the provider and the ability to seek intellectual property rights on any innovations such as diagnostics, medications, and vaccines derived from the original research materials.

Such negotiations not only slow the process of material transfer due to complicated legal contracts, but also serve to discourage scientists at recipient laboratories or institutions from developing scientific innovations and placing them under the risk of patent infringement. Ian Lipkin, Director of the Center for Infection & Immunity at Columbia University, who has also been working with MERS stated that “infectious agents that have implications for public health should be shared freely with any and all qualified investigators who are committed to working safely with those agents and are equipped to do so” (Garrett, 2013)<sup>14</sup>. Despite the public health urgency of MERS, the MTA contract also extends to restricting recipient laboratories from sharing samples with third parties. The National Microbiology Laboratory in Winnipeg, Canada, which played a crucial role in identifying the SARS virus in 2003, had received a MERS sample from EMC only after a prolonged negotiation of tight regulations, paperwork, and lawyers. Even then, they were unable to distribute any samples to other labs for further analysis and collaboration (Crowe, 2013)<sup>8</sup>.

In defense against allegations of impeding research progress on MERS, Albert Osterhaus, head of the Institute of Virology at EMC, argued that MTAs and patents were necessary incentives for companies to invest in developing diagnostics, treatments, and vaccines. In an interview on Aljazeera, Osterhaus defended the use of MTAs on the grounds that it was “moral” and “fast” and that “if vaccines need to be made at the end of the day, private companies need to be incentivized to study the virus via patents” (Aljazeera, 2013)<sup>22</sup>. Additionally, MTAs were justified as being simply a “fairly standard agreement”, and that patent rights were standard for drug and vaccine development companies.

The rhetoric around the justification of patent rights and MTAs amidst the looming threat of MERS perpetuates an authoritative narrative present in the highly capable and advanced scientific knowledge and capacity of Westernized research communities. World-renowned and seasoned disease experts from developed countries become crucial stakeholders in inherently advocating for free-market, non-conditional virus sharing and in doing so, become known as “medical sleuths” or “disease detectives” in circulating media (Grady, 2013)<sup>16</sup>. In a timely article from *The Star*, virus hunting experts like Albert Osterhaus and Ron Fouchier at Erasmus, Maria Zambon in the UK, and Christian Drosten from Germany—whose team quickly developed MERS-CoV diagnostic tests in September 2012—reignited the “old SARS club”, in which “teams of experts [were] collaborating once again across borders and have been deployed to the Middle East to aggressively investigate the virus and its origins” (Yang, 2012)<sup>41</sup>. The Saudi government’s response to the MTA dispute has been nothing short of hostile, given the lack of prior knowledge when Zaki sent the sputum sample without their permission. The WHO had also expressed support against patents at the annual World Health Assembly where Director-General Margaret Chan exhorted that “making deals between scientists because they want to take intellectual property [or] because they want to be the world’s first to publish in scientific journals...are issues we need to address. No IP will stand in the way of public health actions” (Garrett, 2013)<sup>15</sup> She also assured Ziad Memish, the Saudi Deputy Health Minister, that she would “look at the legal implications together with the Kingdom of Saudi Arabia,” and that “No IP should stand in the way of you [Ziad Memish], the countries of the world, to protect your people.”<sup>15</sup>

Perhaps hidden underneath WHO’s politically charged agenda for equitable collaboration is a cautionary tone reminiscent of the H5N1 sample sharing conflict involving Indonesia’s claim of “viral sovereignty”. In 2007, Indonesia’s Minister of Health, Siti Fadilah Supari, halted the sharing of bird flu samples to the WHO on the grounds that for-profit drug companies were

exploiting the poor for profitable business. News of an Australian pharmaceutical company's plan to develop a vaccine against H5N1 using a strain sample that Indonesia had strictly given bilaterally to the WHO further catalyzed Indonesia's mistrust of the global sample sharing system (Sedyaningsih, 2008)<sup>27</sup>. Despite the public health urgency and potential global health risk of deadly new H5N1 outbreaks in Indonesia<sup>i</sup>, the government was adamant on claiming rights of autonomy over the virus itself—likely in fear that new vaccines and treatments developed out of their control by foreign companies would in turn be unaffordable to citizen in developing countries like Indonesia. This ultimately led to an adoption of the Pandemic Influenza Preparedness Framework in 2011 that guaranteed equitable benefits in access and distribution of affordable treatment for developing countries that share influenza virus samples (WHO, 2011)<sup>34</sup>.

While emerging diseases has historically brought nations and scientific communities together in solidarity against increasingly globalized public health threats, it can also deepen the rift between developed and developing countries in their perception of responsible global public health. The dichotomy of bio-power amidst the MERS outbreak narratives, from those involved with deregulated patents to viral sovereignty, may eventually find solidarity through the promise of benefits and autonomy in exchange for sample sharing. However, highly politicized and incentivized motives may threaten to disrupt and obscure arrangements of global public health capacities and accountable systems of sample sharing. In particular, I will examined a public health implication for a potential pandemic spread through an outbreak narrative of susceptibility using this framework of obscuring pandemic preparedness.

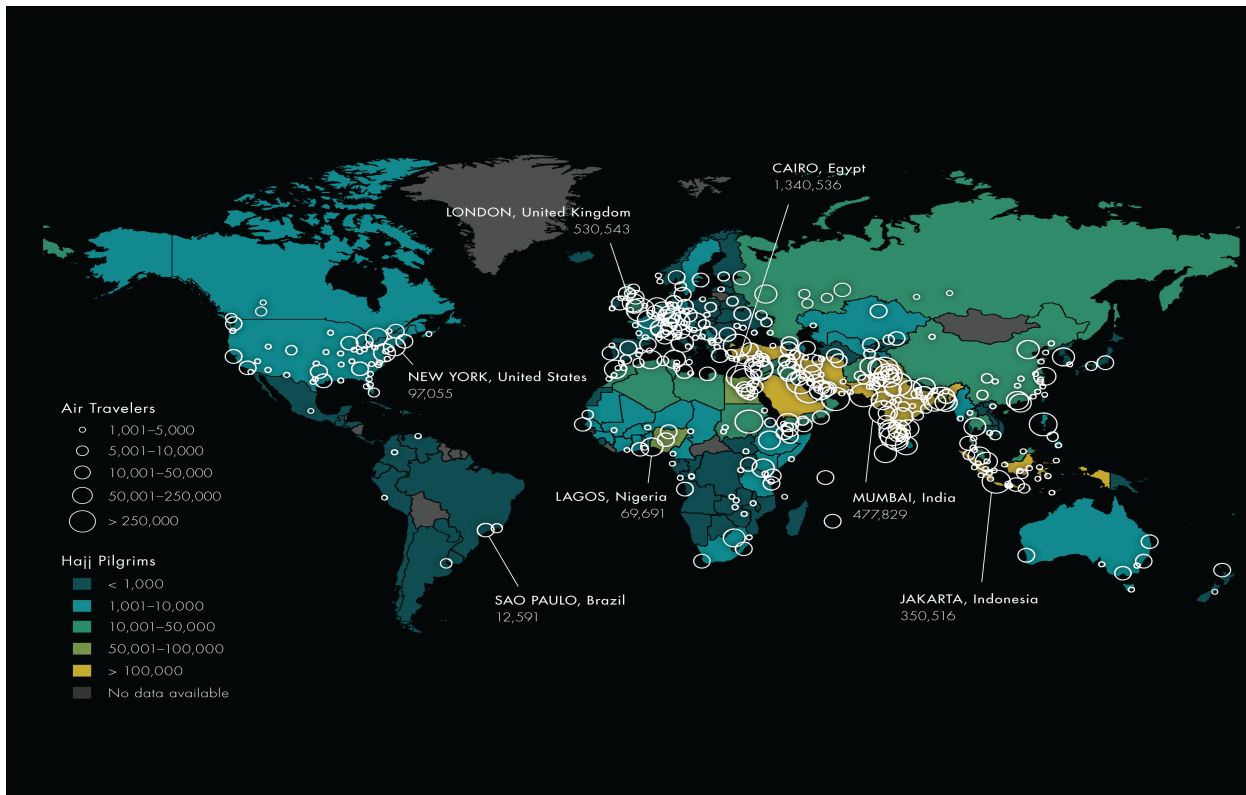
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<sup>i</sup> A cluster of H5N1 outbreaks erupted in Indonesia on May 2006 with an 88% case fatality rate, killing seven out of eight patients.

## **Future Public Health Implications**

One of the main concerns in assessing the potential pandemic threat of MERS-CoV is the massive annual Hajj pilgrimage to Mecca, Saudi Arabia in October. The Hajj plays a pivotal part in the Islamic religion as an obligatory journey of spiritual enlightenment for Muslims at least once in their lives. Every year, over two million pilgrims travel from all corners of the world to Mecca to perform the rituals that the Prophet Muhammad had once done. Thus, the Hajj pilgrimage not only has deep cultural and religious ties, but is also a monumental task that the Saudi government must take up to establish accommodating facilities and services for the pilgrims. Close proximity and contact with both people and animals (over 600,000 animals are sacrificed for food donations) embodies the behavioral, social, and biosecurity risks that may potentially catalyze further international spread of MERS.

An article titled “Potential for the International Spread of Middle East Respiratory Syndrome in Associations with Mass Gatherings in Saudi Arabia” articulates the potential vulnerabilities of the pilgrimages by identifying probable pathways for the further spread of MERS-CoV (Kahn et al., 2013)<sup>15</sup>. Researchers compiled both commercial flight itinerary data and the geographical distribution of both domestic and foreign Hajj pilgrims in 2012 into a GIS (Geographical Information System), which showed that of estimated three million pilgrims, 55% of them were from foreign countries. In addition, of these foreign pilgrims, 65.1% of them originate from low and lower-middle income countries. These results exposed concerns with the biosecurity of resource poor countries with significant travel connections to Saudi Arabia. The spread of MERS-CoV to high-risk countries like Bangladesh, Afghanistan, India, or Pakistan poses a serious global health burden because of a lack of strong public health surveillance infrastructure and health care resources to respond to imported outbreaks.



**Fig 2. City-level Destinations of Air Travelers Departing MERS-CoV Source Countries and Origins of Hajj Pilgrims (Khan et al., 2013)<sup>17</sup>**

The risk for further global spread of MERS through the pilgrimages becomes more apparent in light of the past impact of SARS on developed countries alone. A Singapore newspaper reported that it “took only a few dry coughs in Hong Kong to spread the deadly SARS virus to seven people...and it took only a few air passengers for the illness to reach about twenty countries in Asia, North America, and Europe” (Wald, p.18, 2008). Even a singular event like the Hajj pilgrimage, in addition to Ramadan or Umrah, can have profoundly detrimental health burdens on resource-limited countries if supporting their diagnostic and outbreak response capacity is left unaddressed.

## Moving Beyond Viral Myths

The authoritative persistence of narratives around MTAs and viral sovereignty clearly digresses from the urgency to support pandemic preparedness in resource-limited countries. Geographies of blame present in the ad-hoc rhetoric of viral nomenclature, which are also obscured by speculative etiologies and transmission routes, work to divert focus away from a global solidarity in building effective disease response. Together, these discourses become a microcosm for a collection of viral myths of past, present, and future outbreaks that disrupt the current landscape of dominant epidemiological stories.

On July 17<sup>th</sup>, the International Health Regulations Emergency Committee, including the WHO Director-General, convened to determine the global threat of MERS-CoV using a risk-assessment approach (WHO, 2013)<sup>36</sup>. Conclusively, the Committee did not declare the MERS threat a Public Health Emergency of International Concern, which will institutionally minimize its priority on the political and public health agendas of countries around the world. A modeling study of the pandemic potential of MERS estimated the basic reproduction number of infections to be 0.69, which is lower than that of SARS in the pre-pandemic stages, causing researchers to conclude that, “MERS-CoV—in its current guise—is unlikely to cause a pandemic.” (Bauch et al., 2013)<sup>3</sup>

In the same vein, Ian Jones, a virologist from the University of Reading, stated that “overall risk [of MERS-CoV] remains very low” and that “the most pressing need is to identify where the virus is coming from so that these occasional infections can be prevented.” (Aljazeera, 2013)<sup>12</sup>. When asked to comment on the restrictiveness of Erasmus Medical Center’s MTAs, Keiji Fukuda,

the WHO assistant director-general, insisted that the WHO was completely focused on detecting the disease and preventing it from spreading further (Arab News, 2013)<sup>18</sup>.

Jones and Fukuda's responses to the MERS outbreaks exemplify Wald's critique of narratives reliant on authoritative stories grounded in scientific predictability, validity, and patterns. They are indeed necessary in the grand scheme of global pandemic preparedness, but they are not the only narratives that emerge from the ontologically mobile landscape of the MERS virus. In addressing the lack of uniformity, systematic disease naming based on clouded etiologies can lead to geographies of blame with political and economical ramifications. Beneath the moral justifications of responsible global public health, there can be hidden agendas behind MTAs and patents claimed by research laboratories or a nation's declaration of viral sovereignty—often founded upon research recognition, profit, and mistrust.

In light of a lack of sufficient epidemiological knowledge of MERS-CoV, these discourses create a space of vulnerability that disrupts and obscures the structural and institutional responsibilities of key stakeholders to equitable health and security. A unilateral focus on simply addressing the need for epidemiological knowledge is inadequate. At the closing of the 66<sup>th</sup> World Health Assembly, Margaret Chan remarks, "We understand too little about this virus when viewed in magnitude of its potential threat. Any new disease that is emerging faster than our understanding is never under control" (WHO, 2013)<sup>35</sup>. By making spaces of biopolitical disruptions and viral myths visible amid the dominant outbreak narrative, there is simultaneously space to address the human obstacles of public health preparedness—or as Wald compassionately suggests, to "tell the story of disease emergence and human connection in the language of social justice rather than of susceptibility" (Wald, p. 268, 2008). Just as the MERS virus is ontologically mobile beyond the human boundaries we attempt to place it within, the

global community must strive for unanimity in transparency and trust to accommodate for future emerging infectious diseases.

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