House Committee on Natural Resources
Oversight and Investigations Subcommittee

Hearing on
"Preventing Pandemics through US Wildlife-borne Disease Surveillance."

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Introduction

Good morning. Thank you, Chair Porter, Ranking Member Moore, and distinguished members of the subcommittee for the opportunity to testify in today's hearing. My name is Colin Carlson, and I am an assistant professor at Georgetown University's Center for Global Health Science and Security, as well as the director of Verena (viralemergence.org), a National Science Foundation-funded scientific research team working to predict and prevent future viral emergence. Today I want to share three conclusions about how we can better monitor for disease emergence within the borders of our nation

Zoonotic risk in the United States

First, the United States faces a substantial threat both from animal infections that can be transmitted to humans (zoonotic diseases), and from complacency about the domestic risk that they pose. Historically, the United States has handled pandemics in a paradigm that treats the risk of emergence within our borders as comparatively low. The risk of disease emergence is generally believed to be higher in tropical countries with more animal biodiversity (*1*), weaker health systems (*2*), and high-risk interfaces like wildlife markets (*3*) that allow viruses to jump from animals to humans. But risk only goes so far while planning for a once-in-a-generation event.

We live alongside wildlife, and alongside zoonosis, even here in the nation's capital. In March, the CDC reported that in 2018, our local rat problem was responsible for two cases of a haemorrhagic fever called Seoul hantavirus (*4*). Only a few weeks later, a rabid fox bit Representative Ami Bera just outside this building. Thanks to the miracle of vaccines, the Congressman is safe, healthy, and back at work. However, the stakes of these encounters can be much higher. In fact, the deadliest pandemic in recent history started within our borders. Though it's often called "Spanish flu," the 1918 pandemic of influenza was first detected on a military base in Kansas, and is believed to have originated on a nearby farm. As one 2004 historical account wrote: "If the virus did cross into man in a sparsely populated region of Kansas, and not in a densely populated region of Asia, then such an animal-to-man cross-over can happen anywhere." (*5*) This remains true today; a pandemic can start anywhere. It might start here next time.

As the country with by far and away the greatest total number of poultry chickens, it remains entirely possible another influenza pandemic could start in the United States. A recent surge of domestic cases of high pathogenicity avian influenza in poultry, particularly in the Midwest, speaks to this possibility—but also to the strength of existing outbreak surveillance and transparent reporting in the agricultural sector.

On the other hand, the domestic emergence risk of wildlife viruses is considered less often. Coronaviruses are generally thought of as a low risk for emergence in the United States, because the lineage of viruses related to SARS-CoV and SARS-CoV-2 are not currently known to circulate in bats in the Americas; however, another lineage that includes viruses like the Middle Eastern Respiratory Syndrome coronavirus (MERS-CoV) has been detected in bats in Mexico (*6*), and other species of bats throughout the Americas are suspected to possibly host similar viruses (*3*, *7*). It is likely that further zoonotic surveillance throughout North America will uncover similar viruses in coming years. Similarly, a high number of rodent species are known to be reservoirs of zoonotic diseases in the United States, including respiratory and haemorrhagic pathogens like hantaviruses (*8*, *9*); a 2015 study predicted that the global hotspot of undiscovered reservoirs might be in Kansas and Nebraska (*10*). Overall, the Americas are believed to have a large number of undiscovered mammal viruses (*11*)—a pattern driven by gaps in zoonotic surveillance that are, in turn, driven by lower perceived urgency of zoonotic risk. (For example, the USAID PREDICT project's work sampling for wildlife viruses and building a surveillance workforce in Latin America was mostly concluded several years before the main program ended in Africa and Asia.)

Further risks exist in terms of the possibility of importation immediately before or after spillover takes place at the animal-human interface. Wildlife trade, and the pet trade in particular, poses a major risk, underscored by the 2003 outbreak of monkeypox to the United States originating in imported African rodents. These risks were also recently discussed in a Senate hearing ("Stopping the Spread: Examining the Increased Risk of Zoonotic Disease from Illegal Wildlife Trafficking"; July 22, 2020). Pathogens also cross borders with humans: a recent study reported that several medical professionals had traveled to Haiti in 2017 to assist in Zika virus outbreak response, and returned with an unknown illness. Both the outbreak and its cause—canine coronavirus, a well-known virus not generally believed to infect humans until last year—were essentially unknown to the world until reported in an October 2021 study. It remains possible that the next coronavirus pandemic could be the United States' to prevent.

Climate change and zoonotic risk

Second, the risk posed by zoonotic disease is growing rapidly. One reason in particular stands out: one of the Subcommittee's mandates is to "investigate the sources and impacts of climate change, the single biggest issue that affects every aspect of the Committee's work." A growing body of evidence now suggests that climate change could also become a global crisis for pandemic prevention.

In a study published only a few hours ago today in the journal *Nature,* our team reports that, as mammal species are forced to track warming temperatures towards the Arctic and up mountainsides, zoonotic diseases will arrive in new places, and encounter new animals, some of which will likely serve as a stepping stone to reach a human host. Every simulation we conducted was unambiguous: climate change is creating innumerable hotspots of future zoonotic risk right in our backyard.

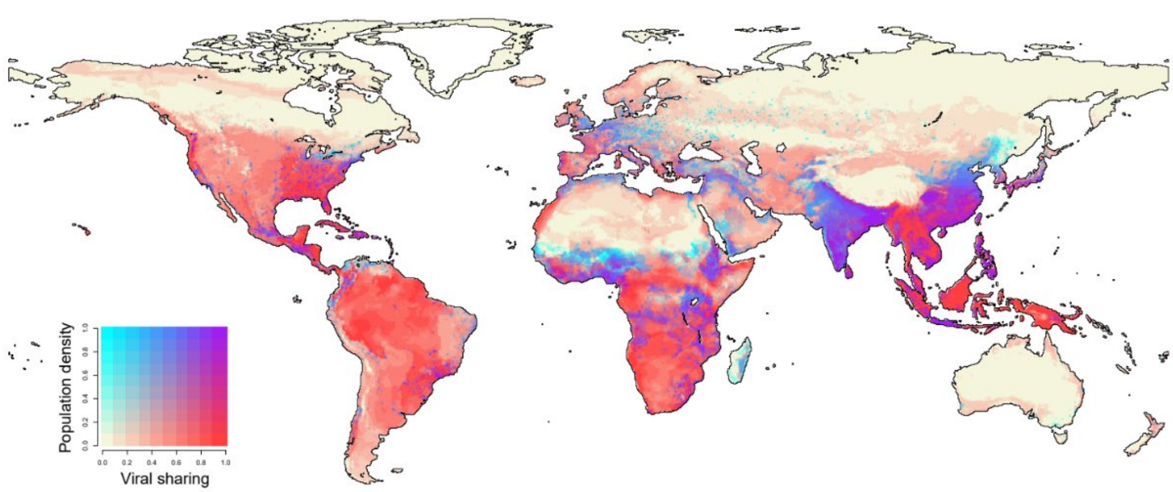

Figure 1. Climate change makes zoonotic disease emergence a global problem. As a result of climate change, by 2070, predicted hotspots of viral host jumps among mammal species (red) will sometimes coincide with human settlements (blue), including in several parts of the United States (purple). (From Carlson *et al.,* "Climate change increases cross-species viral transmission risk", *Nature,* 2022)

We also believe this process is already likely underway in some ecosystems. In 2004, a virus closely related to measles called phocine distemper virus was first reported in Alaskan sea otters. Working with several state and federal agencies, a team of researchers spent the next 15 years monitoring wildlife health throughout the northern Pacific (*12*). They found that melting Arctic sea ice appears to have removed barriers to animal movement, allowing the virus to spread between otters, seals, and sea lions. Phocine distemper virus is unlikely to ever pose a threat to human health, but as we spotlight in our study, the same process will happen to the hosts of Ebola virus, and coronaviruses, and any other zoonotic disease—even here at home, in the United States.

Benefits of strengthening and integrating domestic surveillance systems

Third, to face that growing risk, the most urgent priority is surveillance. Our country leads the world in zoonotic disease research, but modernizing our surveillance system, sharing data more openly, and increasing connections among state and federal agencies would do immeasurable good.

For example, in a recent study, my colleagues and I found that, since 1950, climate change has increased environmental suitability for bubonic plague in the western United States by up to 40% in some areas (*13*). We were only able to detect that signal thanks to decades of both human case surveillance by public health agencies and the wildlife data collected by the USDA's National Wildlife Disease Program. However, data also accounts for our study's biggest limitation: the California Department of Public Health has long curated its own independent surveillance system for plague, and the absence of that data creates a noticeable hole in our risk maps. Other studies have also used these data to assess potential consequences of climate change for plague transmission in California (*14*), leading to a fragmented picture of total impacts.

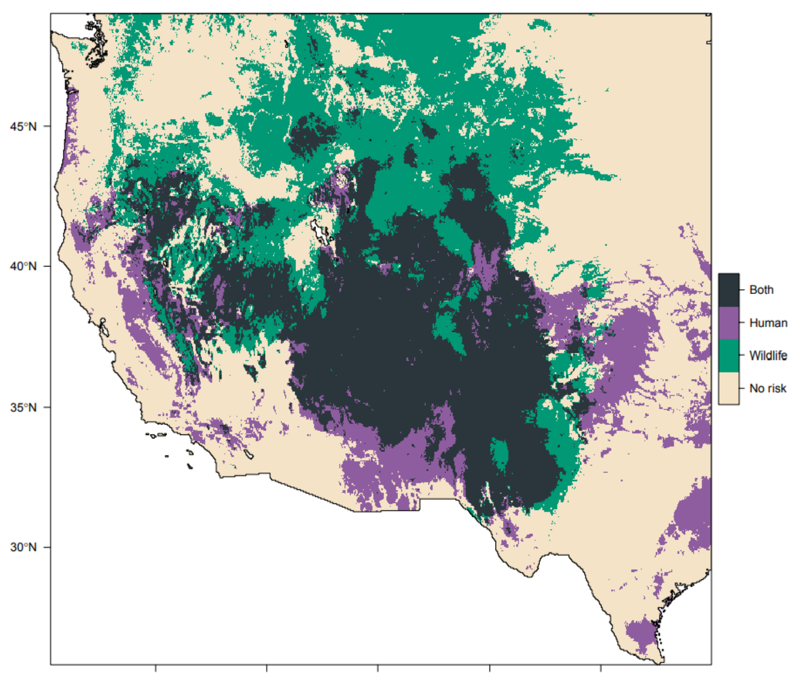

Figure 2. Gaps in zoonotic disease surveillance create gaps in preparedness. A map of plague reservoirs based on wildlife antibody data (green) misses key at-risk areas in California, which are identifiable from county-level human case surveillance (purple). California maintains its own system of wildlife plague surveillance separate from USDA. (From Carlson *et al.,* "Plague risk in the western United States over seven decades of environmental change", *Global Change Biology,* 2022)

Any steps we take towards more comprehensive, connected, and open zoonotic surveillance will massively benefit scientific efforts to predict and prevent the next pandemic. It's easy to miss in all the other pandemic science, but our field is currently headed into something of a scientific revolution. We can do things today we couldn't do a decade ago, like use artificial intelligence to identify animal viruses with zoonotic potential only a few hours after we've sequenced their genome (*15*). Teams like Verena are working towards further advances in what we can do with machine learning, particularly when we harness the genomic revolution, big data, and private sector advances in technology. We're headed in leaps and bounds towards true prediction: knowing which viruses pose a threat, and which animals we need to test; building early warning systems that predict disease spillover like the weather; and using that information to develop and deploy countermeasures like universal vaccines that can stop an outbreak in its tracks. That vision offers renewed hope the Covid-19 pandemic could, in fact, be the last one.

All of that exists by the grace of scientific data, and the patchwork of programs the federal government funds to collect, consolidate, and immortalize that data. Many of the most important programs the United States funds are the cornerstone of open scientific research not just here but around the world: particularly notable is the National Center for Biotechnology Information, where a small core staff works tirelessly to maintain GenBank, the scientific database of record for all genetic and genomic data around the world. Programs like these foster transparency in scientific research, and the data they store have an incalculably high return on investment, not just to prevent outbreaks but during outbreak response as well.

The same can be said of the immense value of disease surveillance conducted by several federal agencies, including CDC, USDA, USGS, and USFWS; other federal agencies and agencies in every state and territory; and by NIH- and NSF-funded scientists in the academic sector. However, the mandate of domestic surveillance for zoonotic disease is fragmented across these institutions, and as a result, researchers might nevertheless be forced to spend months or years hunting for the data they need to answer one scientific question. Building a more centralized infrastructure for zoonotic disease surveillance could easily be the lowest-cost, highest-return way to make our country more prepared for both the pandemic era and the health hazards of a warming world.

I look forward to discussing this with you further, and will gladly answer any questions that the Committee may have.

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