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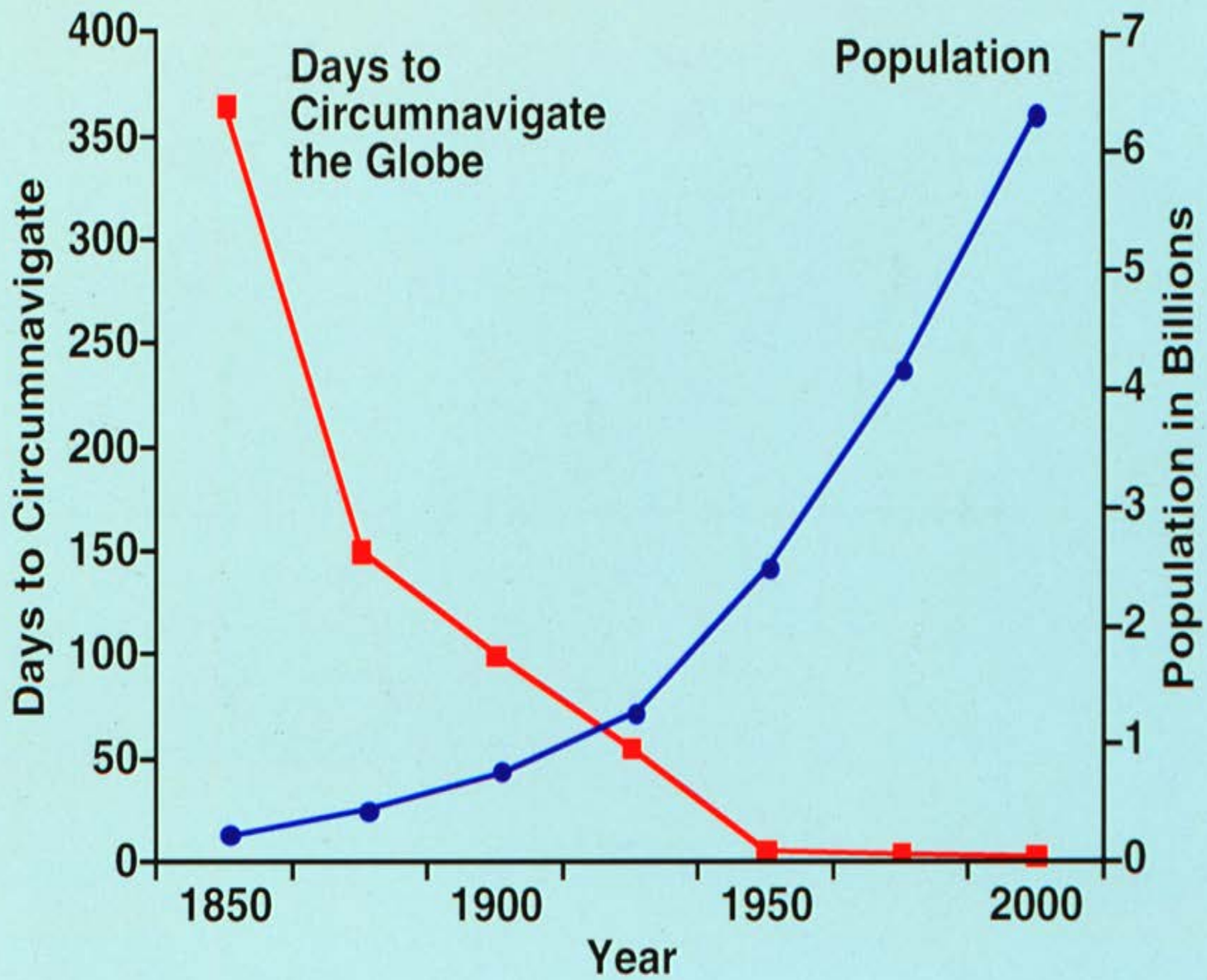
October 3rd, 2017

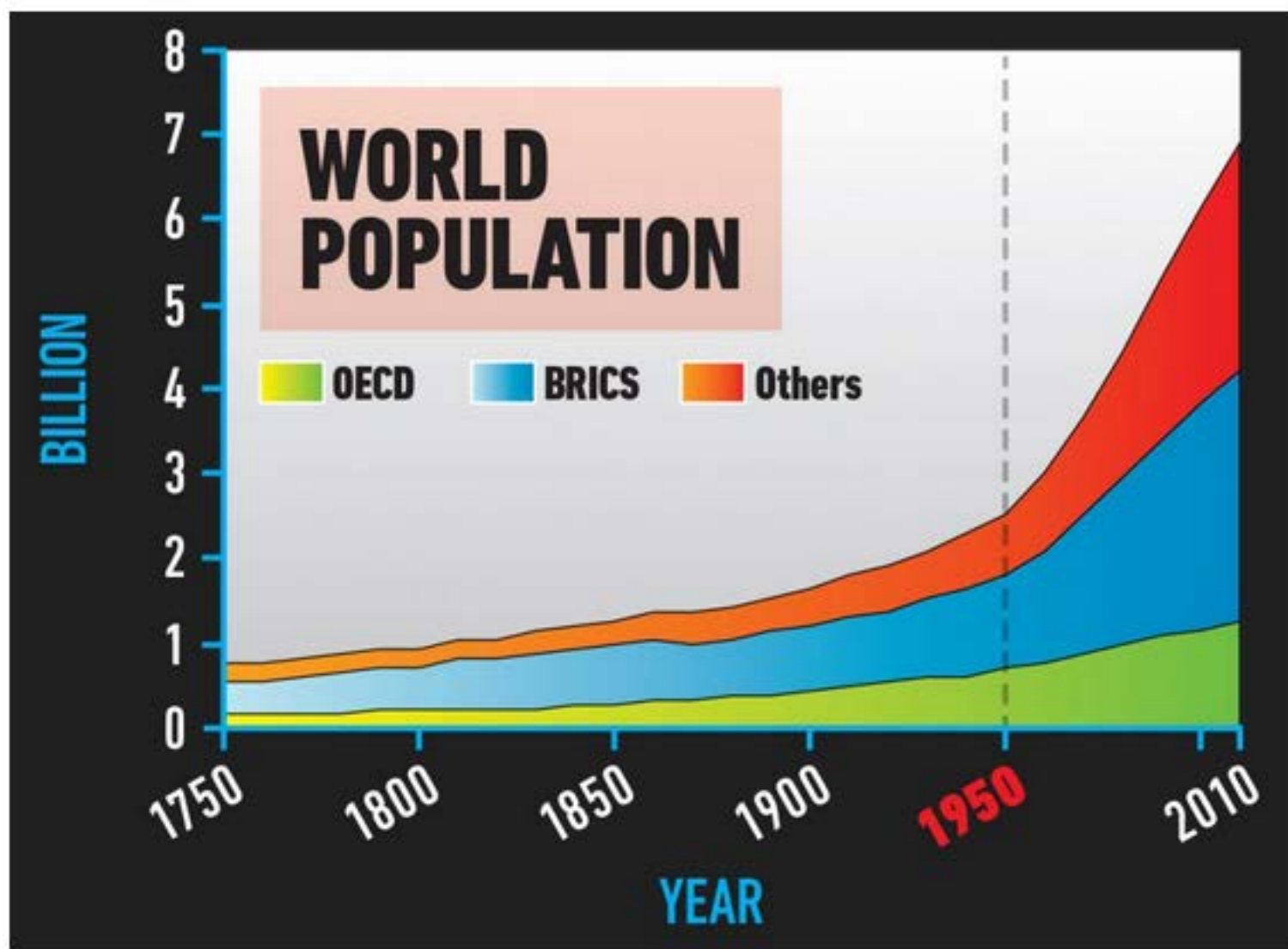
CLF Topics

- 1. Yemen / global health response**
- 2. Avian Influenza**
- 3. Post-hurricane health outcomes**
- 4. Acute flaccid myelitis**
- 5. MERS**
- 6. Bioterrorism / Gain-of-function research**
- 7. Vaccine update**
- 8. CEPI**
- 9. Movies and preparedness**
- 10. Other**

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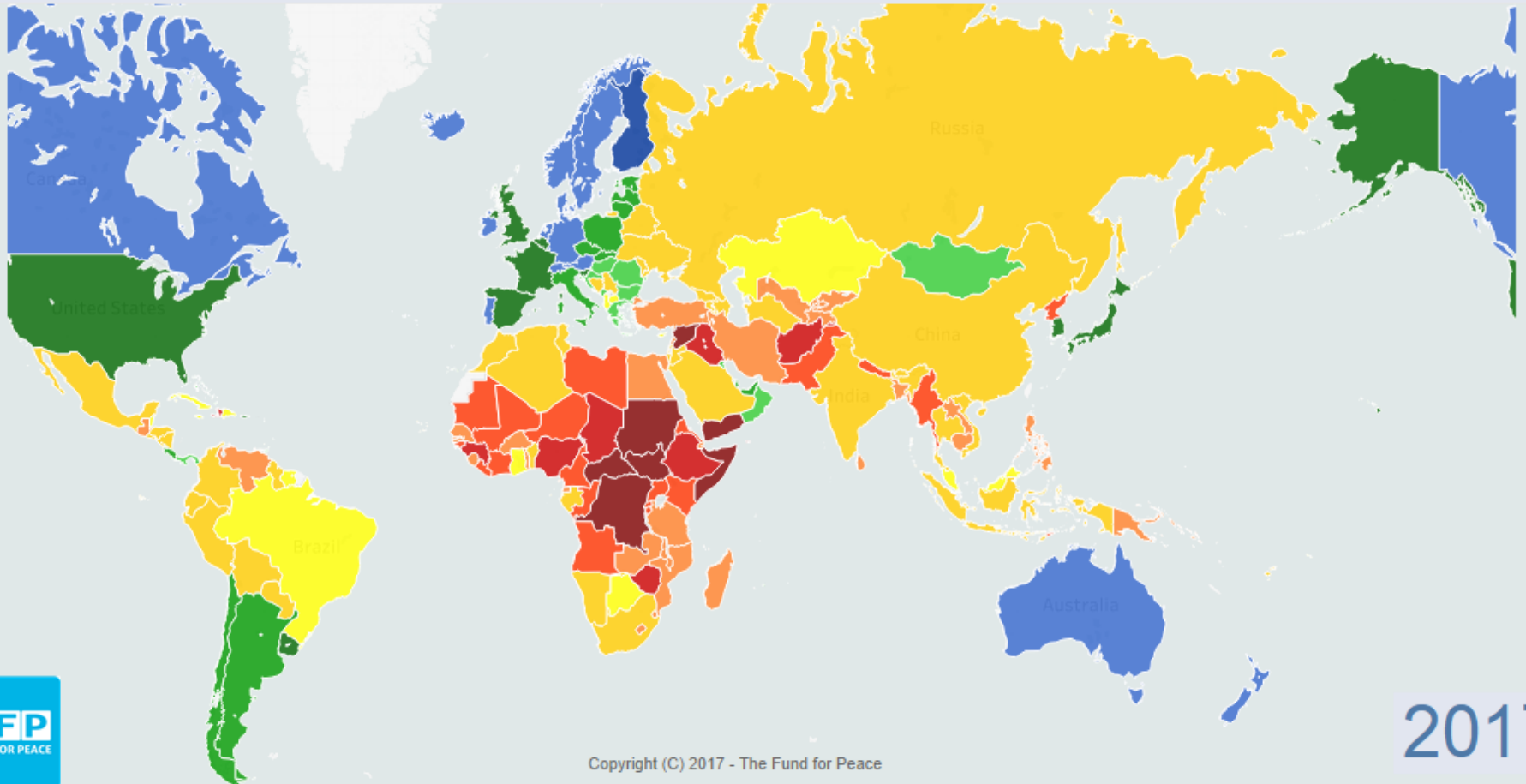
(Steffen et al 2014) Global population data according to the HYDE (History Database of the Global Environment) database. Data before 1950 are modelled. Data are plotted as decadal points.

SOURCES: HYDE database 2013; Klein Goldewijk et al. 2010.

2014 FRAGILE STATES INDEX



2017 FRAGILE STATES INDEX



2017

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Yemen's cholera epidemic called 'worst ever' by Oxfam

Filed Under: [Cholera](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Jul 21, 2017

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In just over 3 months, Yemen has reported more than 368,000 cholera cases, the most recorded in a single year, according to the nongovernmental organization Oxfam.

"It is quite frankly staggering that in just 3 months, more people in Yemen have contracted cholera than any country has suffered in a single year since modern records began," Nigel Timmins, Oxfam's humanitarian director, said in a statement.

The crisis, which began in October of 2016, picked up speed in April. Since then, there have been approximately 5,000 new cases suspected every day. The World Health Organization (WHO) said there were 368,207 suspected cases reported from Apr 27 to Jul 19, and 1,828 deaths, resulting in a case-fatality rate of 0.5%.



Simon Berry / Flickr cc

Oral rehydration solution used in cholera response.



Yemen cholera outbreak tops 400,000, draws high-level UN visit

Filed Under: [Cholera](#)

Lisa Schnirring | News Editor | [CIDRAP News](#) | Jul 26, 2017

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Suspected cholera illnesses in Yemen's outbreak have now topped 400,000 cases, the World Health Organization (WHO) said today, as leaders from three United Nations (UN) agencies wrapped up a visit to the country, which is torn by conflict and famine.

Since late April, the total has reached 402,484 suspected cases, 1,880 of them fatal, for a case-fatality rate of 0.5%. Illnesses have been reported in all but 2 of the country's 23 governorates. However, 5 governorates account for more than half of the cases: Amanat Al Asimah, Al Hudayday, Hajjah, Amran, and Ibb.

For comparison, the most cholera cases ever reported in a single year was 340,311, during Haiti's outbreak in 2011.

Worst outbreak, worst humanitarian crisis

In a statement, WHO Director-General Tedros



WFP / Abeer Etefa

From left, David Beasley, executive director of the World Food Program; Anthony Lake, executive director, UNICEF; and Tedros Adhanom Ghebreyesus, PhD (wearing cap), director-general, WHO, discuss the situation with local physicians.

Yemen's cholera outbreak passes 500,000 cases

Filed Under: [Cholera](#)

[Stephanie Soucheray](#) | [News Reporter](#) | [CIDRAP News](#) | [Aug 14, 2017](#)



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The World Health Organization (WHO) announced today that the cholera outbreak in Yemen has now pushed past 500,000 suspected cases, with nearly 2,000 dying from the disease since late April.

Though numbers have slowed down in recent weeks, some parts of the country still report up to 5,000 suspected cases each day. And the WHO estimates that 30,000 of Yemen's healthcare workers have not gotten paid in the last year.

In its daily epidemiologic update on the outbreak today, the WHO said the total stands at 504,484, with 1,975 deaths reported so far. It said the case-fatality rate is 0.4% and that all but one of the country's 23 governorates has been affected.

"Yemen's health workers are operating in impossible conditions. Thousands of people are sick, but there are not enough hospitals, not enough medicines, not enough clean water. These doctors and nurses are the backbone of the health response – without them we can do nothing in Yemen. They must be paid their wages so that they can continue to save lives," said Tedros Adhanom Ghebreyesus, PhD, WHO director-general, in a statement.



Trocaire/ Flickr cc

EXPLORE: How Yemen's cholera outbreak spread to a half-million people

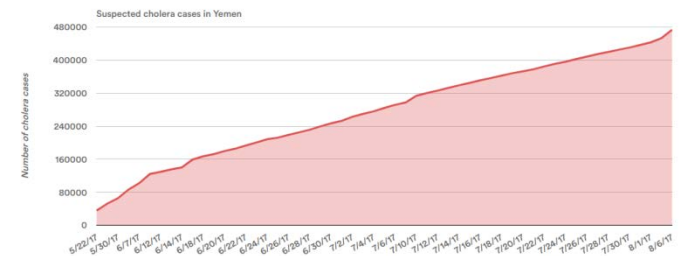
By HELEN BRANSWELL @HelenBranswell and NATALIA BRONSHTEIN @ininteraction / AUGUST 15, 2017

The numbers are mind-boggling: Over the past four months, half a million people are suspected of having contracted cholera in Yemen and 2,000 have died from the diarrheal disease.

The outbreak took off in earnest in late April, sweeping through this country of 27 million people on the Arabian Peninsula. Yemen has been engulfed in political strife for years, a factor that has greatly exacerbated the scale of this epidemic.

Cholera is caused by the bacterium *Vibrio cholerae*, which attacks the intestine. Most infections are mild, or even symptomless. But as many as 10 percent of infected people develop severe illness — vomiting and profuse, watery diarrhea that lead to a rapid loss of body fluids, which, in turn, can induce dehydration, shock and death.

This cholera outbreak is the largest currently underway in the world. Annually, [between 3 million and 5 million people](#) are infected with cholera and the infection claims an estimated 100,000 lives every year, according to the Centers for Disease Control and Prevention.



NATALIA BRONSHTEIN/STAT
SOURCE: WHO YEMEN SITUATION REPORTS 2017

Yemen's cholera epidemic hits 600,000, confounding expectations

GENEVA (Reuters) - Yemen's cholera outbreak has infected 612,703 people and killed 2,048 since it began in April, and some districts are still reporting sharp rises in new cases, data from the World Health Organization and Yemen's health ministry showed on Tuesday.

The overall spread of the epidemic has slowed in the past two months, with the daily number of new suspected cases cut to around 3,000 in recent days.

However the epidemic, the most explosive on record in terms of its rapid spread, has continually confounded expectations. Soon after it began, WHO saw a worst-case scenario of 300,000 cases within six months.

But by the end of June, WHO was hoping 218,000 cases might be the halfway mark. In late July it said the spread had peaked after infecting 400,000.

Epidemics normally decline as quickly as they arise, so the peak of the disease - which is spread by contaminated food and water - should be roughly half the eventual total caseload.



WHO plans global war on cholera as Yemen caseload nears 700,000

GENEVA (Reuters) - The World Health Organization will next month launch a strategy to stop cholera transmission by 2030, it said on Monday, as an unprecedented outbreak in Yemen raced towards 700,000 suspected cases with little sign of slowing down.

The WHO is also trying to keep the lid on a flare-up in Nigeria while tackling many entrenched outbreaks in Africa and an epidemic in Haiti, where almost 10,000 people have died since 2010.

“Once it’s out of the box, once it has spread, it’s very, very difficult to contain and we have a huge number of cases and deaths,” said Dominique Legros, the cholera focal point at WHO’s department for pandemic and epidemic diseases.

“It spreads like a forest fire.”

Epidemics often arise in war zones. The WHO is sending an expert to Bangladesh to assess the risk for Rohingya Muslims fleeing from violence in Myanmar.

Yemen cholera cases could hit 1 million by year-end: Red Cross



GENEVA (Reuters) - The humanitarian situation in Yemen is a “catastrophe”, and cholera cases could reach a million by the end of the year, the International Committee of the Red Cross said on Friday.

Warring parties in Yemen - including the western-backed Saudi-led coalition - are all using disproportionate force, leading to “very excessive” civilian casualties, said Alexandre Faite, the head of the Red Cross delegation in Yemen.

In addition, suspected cases of cholera have reached 750,000, with 2,119 deaths, Faite said, and the Red Cross expects at least 900,000 cases by the end of the year.

“The situation has really evolved in a very dramatic way and I think that it’s nothing short of a catastrophe,” Faite told a news briefing in Geneva.

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PANDEMIC

Warning signals from the volatile world of influenza viruses

February 2015

The current global influenza situation is characterized by a number of trends that must be closely monitored. These include: an increase in the variety of animal influenza viruses co-circulating and exchanging genetic material, giving rise to novel strains; continuing cases of human H7N9 infections in China; and a recent spurt of human H5N1 cases in Egypt. Changes in the H3N2 seasonal influenza viruses, which have affected the protection conferred by the current vaccine, are also of particular concern.

Viruses in wild and domestic birds

The diversity and geographical distribution of influenza viruses currently circulating in wild and domestic birds are unprecedented since the advent of modern tools for virus detection and characterization. The world needs to be concerned.

Viruses of the H5 and H7 subtypes are of greatest concern, as they can rapidly mutate from a form that causes mild symptoms in birds to one that causes severe illness and death in poultry populations, resulting in devastating outbreaks and enormous losses to the poultry industry and to the livelihoods of farmers.



Warning signals from the volatile world of influenza viruses

February 2015

The diversity and geographical distribution of influenza viruses currently circulating in wild and domestic birds are unprecedented since the advent of modern tools for virus detection and characterization. The world needs to be concerned.



Warning signals from the volatile world of influenza viruses

February 2015

Since the start of 2014, the Organisation for Animal Health, or OIE, has been notified of 41 H5 and H7 outbreaks in birds involving 7 different viruses in 20 countries in Africa, the Americas, Asia, Australia, Europe, and the Middle East. Several are novel viruses that have emerged and spread in wild birds or poultry only in the past few years.



H7N9 situation update

20 September 2017, 12:00 hours; Rome

Overview

Situation: Influenza A(H7N9) virus with pandemic potential.

Country: China; three human cases originated in China and were reported in Malaysia (1) and Canada (2).

Number of human cases: 1589 confirmed; 616 deaths (since February 2013).

Number of new findings in birds or the environment since last update (23 August 2017): 4

Number of new human cases since last update (23 August 2017): 5

Provinces/municipalities: Beijing, Chongqing, Shanghai and Tianjin Municipalities; Anhui, Fujian, Gansu, Guangdong, Guizhou, Hebei, Heilongjiang, Henan, Hubei, Hunan, Jiangsu, Jiangxi, Jilin, Liaoning, Qinghai, Shaanxi, Shanxi, Shandong, Sichuan, Taiwan, Yunnan and Zhejiang Provinces; Hong Kong SAR, Macao SAR; Guangxi, Inner Mongolia, Ningxia Hui, Tibet and Xinjiang Uyghur Autonomous Regions; Sabah (Malaysia); British Columbia (Canada).

Animal/environmental findings: around 3000 virological samples from the environment, chickens, pigeons, ducks and a tree sparrow tested positive; positives mainly from live bird markets, vendors and some commercial or breeding farms.

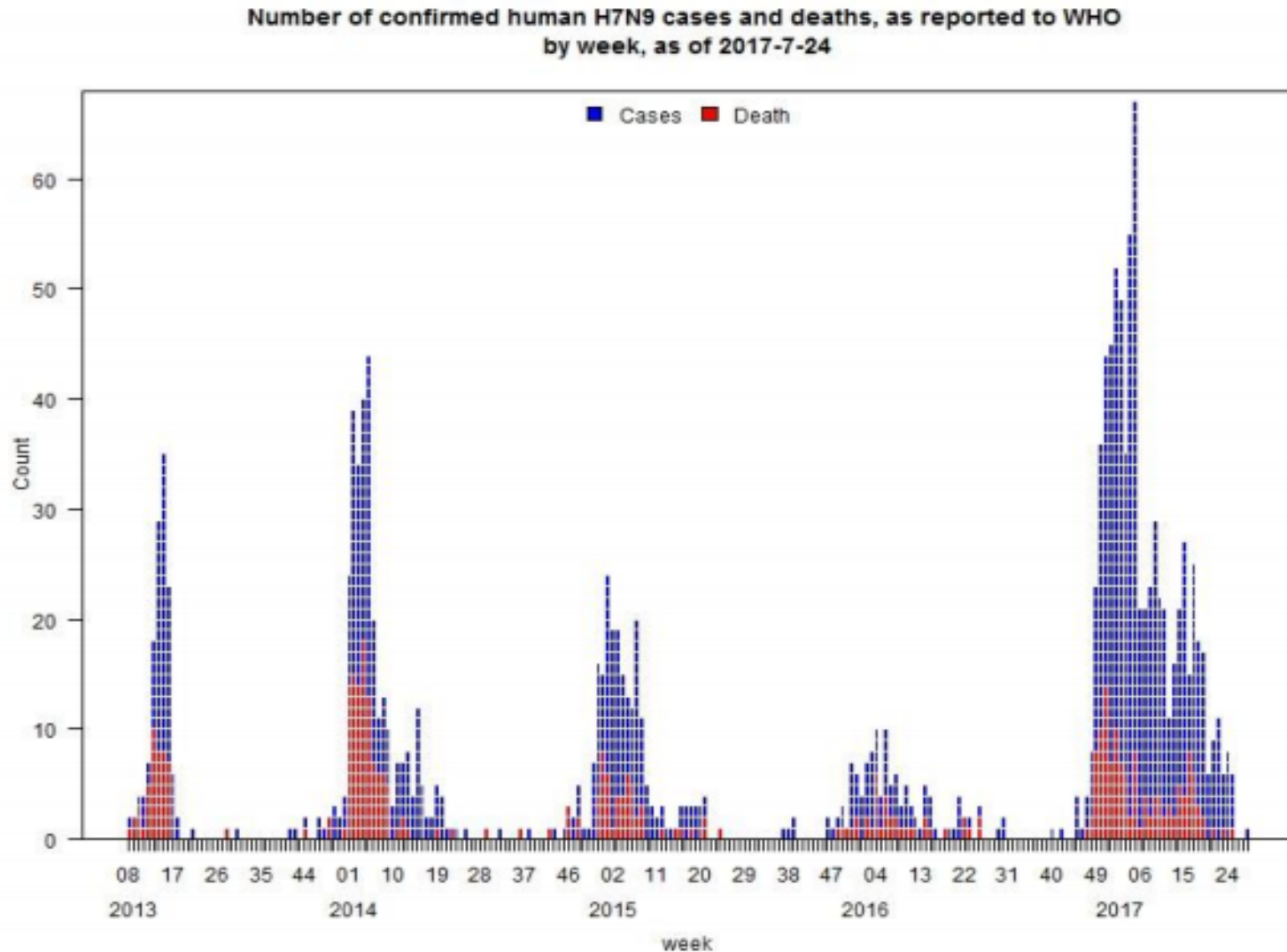
Highly pathogenic virus findings: The H7N9 highly pathogenic avian influenza virus was detected in a total of 49 poultry or environmental samples (38 chickens, 1 duck and 10 environmental samples) from 23 live bird markets (LBMs) in: **Fujian** (Longyan City), **Guangdong** (Dongguan, Guangzhou, Huizhou, Lufeng, Meijiang, Meizhou, Zhongshan Cities and Haifeng County), **Hunan** (Chenzhou City) and **Guangxi** (Guilin City) Provinces; and from 8 farms in: **Guangxi** (Guilin City), **Hebei** (a chicken layer farm in Xingtai City [reference]), **Henan** (a chicken layer farm in Pingdingshan City [reference]), **Hunan** (backyard in Chenzhou City and a large chicken layer farm in Yongzhou City [reference]), **Shaanxi** (a chicken layer farm [reference]), **Tianjin** (a chicken layer farm [reference]), **Inner Mongolia** (two chicken layer farms in Hohhot and Baotou Cities [reference 1, reference 2]), **Heilongjiang** (a chicken layer farm in Shuangyashan City [reference]) and **Anhui** (a farm in Chuzhou City, Juzhou County [reference]) Provinces.

Out of the 1589 confirmed human cases, H7N9 virus isolates from 28 human cases (including one from Taiwan Province) were found to be highly pathogenic for chickens.

FAO actions: liaise with China and partners, monitor situation, monitor virus evolution, conduct market chain analysis, risk assessment, surveillance guidance and communication.



Figure 1: Epidemiological curve of avian influenza A(H7N9) cases in humans by week of onset, 2013-2017





H7N9 situation update

20 September 2017, 12:00 hours; Rome

Map 1. Human cases and positive findings in birds or the environment



Click to enlarge - Note: Human cases are depicted in the geographic location where they were reported; for some cases, exposure may have occurred in a different geographic location. Precise location of 30 human cases in Anhui (2), Beijing (2), Guangdong (1), Guangxi (1), Hebei (3), Hunan (1), Hubei (2), Jiangsu (2), Jiangxi (6), Sichuan (2), Zhejiang (3) and unknown (5) Provinces are currently not known, these cases are therefore not shown on the map.



Avian Flu Scan for Sep 07, 2017

Wrap-up of China's fifth H7N9 waves highlights dominance of new lineage

The number of towns, provinces, and regions that reported human cases in China's unprecedented fifth wave of H7N9 avian influenza activity, which began in October 2016, is higher than the previous four waves combined, researchers from the US Centers for Disease Control and Prevention and their collaborators in China reported today in the latest edition of *Morbidity and Mortality Weekly Report (MMWR)*.

In their wrap-up of the latest epidemiologic and genetic sequencing information, the group said 759 illnesses were reported in the fifth wave, 281 of them fatal, and that among several new developments over the past months, the newly emerged Yangtze River Delta low pathogenic lineage accounted for most of the activity and scores as having the highest potential pandemic risk (moderate to high) on the CDC's Influenza Risk Assessment Tool. In February, World Health Organization (WHO) flu vaccine advisors recommended new candidate vaccine viruses for the Yangtze River Delta lineage, for which current H7N9 candidate vaccine viruses show limited protection.

Other notable features of the fifth wave were the emergence of the highly pathogenic strain in poultry, which was found in 27 of 759 cases and was most often seen in those from rural areas, people with early hospital admission, and in those who had been exposed to sick or dead poultry, according to the report.

Despite the wider geographic spread, the patterns of spread from poultry to humans and from human to humans haven't changed much, the group said. Fourteen clusters of two or three people were reported to the WHO in the fifth wave, compared to an average of nine in each of the earlier waves.

Transmission from poultry is rare and the virus doesn't pass easily among people, but when infections do occur, they are linked to severe and fatal infections, requiring close vigilance, they added.

Sep 8 MMWR report

Reported Infections with Variant Influenza Viruses in the United States since 2005

When people are infected with influenza A viruses that are known to be genetically similar to viruses circulating in swine, these viruses are called “[variant viruses](#)” and denoted with a letter “v”. The table below reflects the most current case counts for variant virus infections reported in the United States since 2005.

Most infections with variant viruses have occurred in children (persons 18 or younger) and most cases have reported direct or indirect exposure to swine prior to onset of illness. Limited transmission from close contact with an infected person has been observed in some investigations of human infections with variant viruses, but sustained human-to-human transmission has not been documented.

Table. Case Count: Detected U.S. Infections with Variant Influenza Viruses by State since December 2005

| Reporting State | H3N2v | H1N1v | H1N2v | Total Detected Influenza Variant Virus Infections |
|-----------------|-----------------------|-----------|-----------|---|
| Arkansas | | 2 | | |
| Hawaii | 1 | | | |
| Illinois | 5 | 1 | | |
| Indiana | 154 | | | |
| Iowa | 6 | 4 | 1 | |
| Kansas | 1 | | | |
| Maine | 2 | | | |
| Maryland | 12 | | | |
| Michigan | 21 | | 1 | |
| Minnesota | 9 | 4 | 6 | |
| Missouri | | 2 | | |
| New Jersey | 1 | | | |
| North Dakota | 1 | | | |
| Ohio | 131 | 3 | 2 | |
| Pennsylvania | 17 | | | |
| South Dakota | | 1 | | |
| Texas | 1 | 1 | | |
| Utah | 1 | | | |
| West Virginia | 5 | | | |
| Wisconsin | 22 | 2 | 1 | |
| Total | 390 | 20 | 11 | 421 |



Quick Links

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Testing points to a flu virus in 7 fair-goers who had close contact with swin

None of those who attended Charles County event is seriously ill with H3N2

Baltimore, MD (September 20, 2017) – The Maryland Department of Health has presumptively identified the influenza strain H3N2v (variant flu) in seven Maryland residents who had close contact with pigs at the Charles County Fair. No infected individuals has developed serious illness or been hospitalized.

Influenza is an infection caused by the influenza virus which can affect people and other animals, including pigs and birds. Symptoms for the H3N2v strain are the same as seasonal flu and include fever and respiratory symptoms, such as sore throat and cough. Historically, there is limited human to human transmission from this strain of variant flu. The treatment recommendations for this strain of influenza are the same as for seasonal flu.

Health officials recommend that people with influenza-like illness contact their healthcare provider and inform them if they had pig contact within the past seven days. Providers are advised to contact their local health departments if they suspect variant flu in their patients to coordinate appropriate testing with their local health department. The Charles County Health Department can be reached at 301-609-6900 ext. 6025 and the St. Mary's County Health Department can be reached at 475-4330.



MARYLAND Department of Health

Larry Hogan, Governor · Boyd Rutherford, Lt. Governor · Dennis Schrader, Secretary

September 21, 2017

Dear Colleague,

We are writing to alert you that the MDH has identified 7 presumptively positive cases of influenza A (H3N2) variant virus (H3N2v, colloquially known as “swine flu”) among Maryland residents who had close contact with pigs exhibited at the recent Charles County Fair (which ran September 14-17, 2017). Among pigs exhibited at the same fair, five symptomatic pigs tested positive through the National Veterinary Services Laboratory for influenza A H3N2. In response, we ask that you have heightened suspicion to identify potential human cases of variant influenza virus.

Background on variant influenza viruses

Swine flu viruses do not normally infect humans. However, sporadic human infections with influenza viruses that normally circulate in swine have occurred. When this occurs, these viruses are called “variant viruses” and are denoted by adding the letter “v” to the end of the virus subtype designation.

Since 2005, there have been 421 human cases of swine flu detected in the United States, and these have been the H1N1v, H1N2v, and H3N2v viruses. In 2017, there have been 20 reported cases; eighteen of these were H3N2v viruses (Texas [1], North Dakota [1], Pennsylvania [1], and Ohio [15]) and two were H1N2v viruses (Ohio [2]). In 2012, in Maryland, there were 13 cases among people who had direct



Maryland reports 12 more H3N2v flu cases

Filed Under: [H3N2v Influenza](#)

Lisa Schnirring | News Editor | CIDRAP News | Sep 29, 2017

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In an ongoing spike in variant H3N2 (H3N2v) influenza cases linked to Maryland county fairs, state health officials today reported 12 more presumed or confirmed cases today, as the US Centers for Disease Control and Prevention (CDC) provided more details on 32 of the most recent cases, which includes one from Delaware.

Confirmation tests are still under way for some of Maryland cases, but the state has now reported 32 presumed or confirmed H3N2v cases, making this year's H3N2v total the highest since the record year in 2012, when 309 cases were reported.

Cancelled swine exhibits

The Maryland cases so far are in people who had close contact with pigs at fairs in three counties: Charles, Anne Arundel, and Frederick.



Erika Mitchell / iStock



Flu Scan for Sep 25, 2017

Swine influenza found in more Maryland fair pigs; more human cases noted

State and county health officials in Maryland are investigating influenza in 11 pigs that were recently shown at a fair in Frederick County, the second time flu has been detected at the state's county fairs in as many weeks.

In the latest developments, preliminary tests show the pigs are infected with influenza A, but officials don't know if it's a strain that can spread to people. The Maryland Department of Agriculture (MDA) has issued a quarantine order for all pigs at the Frederick County fairgrounds until 7 days after the last pig shows signs of illness signs, the agency said in a news release.

The fair took place from Sep 15 to Sep 23. So far no human illnesses have been linked to contact with the pigs, but the local media said authorities were investigating a possible illness in a child who has a flulike illness.

On Sep 20, the state health department announced that tests had presumptively identified variant H3N2 (H3N2v) in seven Maryland resident who had close contact with pigs at the Charles County Fair. In a Sep 22 update, officials said the total of presumptive positives has risen to 10.

Sep 24 MDA press release

Sep 23 Frederick News-Post story

Sep 21 CIDRAP News scan "Seven fairgoers contract H3N2v in Maryland"



News Scan for Oct 02, 2017

Maryland reports 5 more H3N2v flu infections

In its latest update on variant H₃N₂ (H₃N₂v) flu cases linked to contact with pigs at county fairs, the Maryland Department of Health (MDH) reported 5 more presumed positive, raising the state's overall total to 37.

One more patient was hospitalized, raising that number to two. Since Sep 20, Maryland has reported infections in people who had close contact with pigs at fairs in three counties: Charles, Anne Arundel, and Frederick. Most are in children, and two were reported to be in adults older than 30.

On Sep 29 the US Centers for Disease Control and Prevention (CDC), in reporting 31 cases in Maryland, said 50 cases have been reported in six states, most of them from Maryland and Pennsylvania. CDC testing is still under way on 18 viruses identified as presumed H₃v-positive by Maryland's public health laboratory.

Led by Maryland's surge of H₃N₂v cases, the number of illnesses in the United States is the highest since the record year in 2012, when 309 cases were reported.

Sep 29 MDH case count



Flu Scan for Sep 05, 2017

Flu still rising in Australia; levels high in parts of Asia

Though flu in some Southern Hemisphere countries has plateaued or is declining, activity in Australia and New Caledonia is still rising, with parts of South and Southeast Asia also reporting increased activity, according to an update yesterday from the WHO.

Globally, H3N2 is the dominant strain, but Southern Hemisphere countries such as Australia are seeing influenza B activity, as well.

Meanwhile, India and Nepal are reporting high flu activity, mainly from the 2009 H1N1 virus. In Southeast Asian countries such as Thailand and Myanmar, flu levels have been on the rise in recent weeks, with both 2009 H1N1 and H3N2 detected. The Philippines and Vietnam are reporting illnesses from all of the seasonal flu strains.

In Southern China and Hong Kong, which saw big flu spikes this summer mainly caused by H3N2 are now reporting decreases in illness levels. In Western Africa, flu activity continues in many countries, but little activity was reported from Eastern Africa.

Low or no activity was reported in other parts of the world, and in North America, activity from flu and other respiratory viruses stayed low, with cocirculation of H3N2 and influenza B strains.

Sep 4 WHO global flu update



WHO swaps out H3N2, B strains in Southern Hemisphere flu vaccine

Filed Under: [Influenza Vaccines](#); [Influenza, General](#)

Lisa Schnirring | News Editor | CIDRAP News | Sep 28, 2017



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At their meeting this week in Melbourne, Australia, World Health Organization (WHO) vaccine advisors today recommended changing two of three components for trivalent vaccines that pharmaceutical companies will produce for the Southern Hemisphere's 2018 flu season.

The group recommended a new influenza A H3N2 strain, and swapped out the Victoria-lineage B strain with a Yamagata-lineage virus that had been recommended last year as the second B strain in quadrivalent vaccine formulations.



CIPhotos / iStock

The WHO recommends the following for the Southern Hemisphere's trivalent vaccines:

- For H1N1, an A/Michigan/45/2015-like virus
- For H3N2, an A/Singapore/INFIMH-16-0019/2016-like virus
- For B, a Phuket/3073/2013-like virus (belonging to the Yamagata lineage)

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NEWS 08/28/2017 09:34 pm ET | Updated Aug 31, 2017

Hurricane Harvey's Public Health Impact Extends Beyond Flooding

"Disasters magnify fragilities that are already present in society."

Since Hurricane Harvey hit Texas on Friday, [at least 35 people have died](#) and many others have been injured and trapped in their flooded houses. But beyond the immediate dangers posed by the flooding, experts are worried about the broader threats to public health.

Health secretary [Tom Price on Saturday declared a public health emergency](#) in Texas.

"We recognize the gravity of the situation in Texas, and the declaration of a public health emergency will provide additional flexibility and authority to help those who have been impacted by the storm," he said in a statement.

Price's concerns were widely shared by public health officials, who pointed to both immediate threats from the storm and more long-term dangers.

"In the immediate emergency there's concern around drowning, and especially for folks who are in motor vehicles where there is severe flooding, blunt trauma, fire-related injuries," said Marisa Raphael, deputy commissioner of the Office of Emergency Preparedness and Response at the New York City Health Department.

Experts: Avoid unneeded tetanus shots in wake of Harvey

Filed Under: [Tetanus](#); [Disaster Recovery](#); [Adult \(non-flu\) Vaccines](#); [Childhood Vaccines](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Aug 30, 2017

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As emergency responders and health officials continue to battle displacement and injuries after Hurricane Harvey and the resulting catastrophic flooding continue to batter Texas, some authorities are urging residents to get a tetanus shot as a necessary precaution.

US Rep. Pete Sessions (R-Tex.) said on CNN on Aug 28 that residents should get a tetanus shot before they wade into waters. And a report from National Public Radio (NPR) said Texas officials had already begun filling requests for tetanus vaccinations and sending supplies of the vaccine to affected areas.



Texas Military Department / Flickr cc

But this advice could be misconstrued at best, and wasteful of public health resources at worse. Experts are warning against offering tetanus shots to those who don't need them.

'Flesh-Eating Bacteria' From Harvey's Floodwaters Kill a Woman

By MAGGIE ASTOR SEPT. 28, 2017

From the moment the waters began rising in Texas last month, disease was on health officials' minds. Floodwaters, after all, are filthy.

When Hurricane Harvey finally moved north and the feet of flooding drained, hospitals saw a spike in skin and gastrointestinal infections, but Texans were spared some of the most serious illnesses that [contaminated water can spread](#): cholera, for instance, and typhoid.

On Tuesday, however, the Harris County medical examiner's office announced that the death of a 77-year-old woman 11 days earlier had been caused by necrotizing fasciitis: a gruesome and often deadly infection commonly known as flesh-eating bacteria.

The woman, Nancy Reed, contracted the disease when she fell inside a flooded home in Houston's Kingwood community and broke her arm, allowing bacteria from the floodwaters in through cuts. Hers was the [36th storm death recorded in Harris County](#).

Porfirio Villarreal, a spokesman for the Houston Health Department, said the city had received no other reports of necrotizing fasciitis since the storm. But a nonfatal infection was confirmed in nearby Missouri City, Tex., where J. R. Atkins, a former firefighter and paramedic, contracted the disease while helping neighbors escape the floodwaters. In Mr. Atkins's case, [The Houston Chronicle reported](#), the bacteria entered through an insect bite on his arm.

No Calm After the Storm: A Systematic Review of Human Health Following Flood and Storm Disasters

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Keywords: cyclonic storms; disaster; floods; health effects; systematic review

Abbreviations:

ARR: attributable rate ratio
CO: carbon monoxide
ECF: emergency care facility
NCD: noncommunicable disease
RR: relative risk

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Abstract

Introduction: How the burden of disease varies during different phases after floods and after storms is essential in order to guide a medical response, but it has not been well-described. The objective of this review was to elucidate the health problems following flood and storm disasters.

Methods: A literature search of the databases Medline (US National Library of Medicine, National Institutes of Health; Bethesda, Maryland USA); Cinahl (EBSCO Information Services; Ipswich, Massachusetts USA); Global Health (EBSCO Information Services; Ipswich, Massachusetts USA); Web of Science Core Collection (Thomson Reuters; New York, New York USA); Embase (Elsevier; Amsterdam, Netherlands); and PubMed (National Center for Biotechnology Information, National Institutes of Health; Bethesda, Maryland USA) was conducted in June 2015 for English-language research articles on morbidity or mortality and flood or storm disasters. Articles on mental health, interventions, and rescue or health care workers were excluded. Data were extracted from articles that met the eligibility criteria and analyzed by narrative synthesis.

Results: The review included 113 studies. Poisonings, wounds, gastrointestinal infections, and skin or soft tissue infections all increased after storms. Gastrointestinal infections were more frequent after floods. Leptospirosis and diabetes-related complications increased after both. The majority of changes occurred within four weeks of floods or storms.

Conclusion: Health changes differently after floods and after storms. There is a lack of data on the health effects of floods alone, long-term changes in health, and the strength of the association between disasters and health problems. This review highlights areas of consideration for medical response and the need for high-quality, systematic research in this area.

Saulnier DD, Brolin Ribacke K, von Schreeb J. No calm after the storm: a systematic review of human health following flood and storm disasters. *Prehosp Disaster Med.* 2017;32(5):568-579.

Introduction

The number of weather-related disasters has increased over the last 20 years. Nearly one-half of the disasters were floods, which killed 157,000 people and affected 2.3 billion. Storms were one-quarter of the disasters but were responsible for a larger proportion of fatalities, causing 220,000 deaths and affecting 660,000 people.¹ As climate change transforms the frequency and severity of weather events in the coming years, the impact of floods and storms is likely to worsen.

The health care response to a disaster should be guided by the known and expected needs of the affected population. It should be prepared for needs caused by the direct effect of the disaster and for the indirect outcomes of the initial impact. This can be achieved by knowing if and how the health of a population changes after a disaster. Response plans should use the best available evidence to understand the immediate, short-term, and long-term health outcomes after a disaster, and how ordinary health care needs are affected.

Despite the commonality of flood and storm disasters, few reviews cover the quantifiable changes in health that occur afterwards or compare the differences. Previous systematic reviews have combined floods and storms in the analysis,^{2,3} but storms have the additional hazard of strong winds. Other reviews have summarized the impact of flood or storm disasters on mortality and the causes, risk factors, or burden of specific diseases.⁴⁻⁷

Puerto Rico could become a public health catastrophe



BY TOMÁS R. GUILARTE

Florida International University



OCTOBER 02, 2017 12:00 PM



In the days since Hurricane Maria ravaged Puerto Rico, conditions on the island continue to deteriorate and become a humanitarian and public health catastrophe that could rival the damage caused by Hurricane Katrina in New Orleans.

The fact that the power grid failed creates many obvious problems and some that are not so evident. When the sewer system stops working, wastewater—aka human feces and urine—and seaborne bacteria contaminate the water supply.

This leads to bacterial infections — such as cholera, dysentery, E. coli and typhoid — that can be disastrous. The typical treatments, like tetanus shots or powerful antibiotics, are not readily available on the island, where medical supplies are quickly running out.



AFTER HURRICANE MARIA, COULD PUERTO RICO BE AT RISK OF CHOLERA?

AFTER THE DELUGE comes the deluge. First [Hurricane Irma](#) raked Puerto Rico and the US Virgin Islands in early September, and then two weeks later Hurricane Maria did the same, leaving 3.5 million people in Puerto Rico without clean water, communications, or electricity, amid damaged buildings and floodwaters.

Aid is finally reaching the islands—fuel for generators, water, medical supplies, food—but disasters always breed disasters. And that might be what's about to happen in Puerto Rico, too. “The first impact is people who were directly injured,” says [Nahid Bhadelia](#), medical director of the special pathogens unit of the National Emerging Infectious Disease Laboratories at Boston University. “Then you have an entire group of people who are critically ill, facing health care systems that are overwhelmed.”

CLF Topics

1. Yemen / global health response
2. Avian Influenza
3. Post-hurricane health outcomes
4. Acute flaccid myelitis
5. MERS
6. Bioterrorism / Gain-of-function research
7. Vaccine update
8. CEPI
9. Movies and preparedness
10. Other

A novel outbreak enterovirus D68 strain associated with acute flaccid myelitis cases in the USA (2012–14): a retrospective cohort study

Alexander L Greninger*, Samia N Naccache*, Kevin Messacar, Anna Clayton, Guixia Yu, Sneha Somasekar, Scot Federman, Doug Stryke, Christopher Anderson, Shigeo Yagi, Sharon Messenger, Debra Wadford, Dongxiang Xia, James P Watt, Keith Van Haren, Samuel R Dominguez, Carol Glaser, Grace Aldrovandi, Charles Y Chiu

Summary

Background Enterovirus D68 was implicated in a widespread outbreak of severe respiratory illness across the USA in 2014 and has also been reported sporadically in patients with acute flaccid myelitis. We aimed to investigate the association between enterovirus D68 infection and acute flaccid myelitis during the 2014 enterovirus D68 respiratory outbreak in the USA.

Methods Patients with acute flaccid myelitis who presented to two hospitals in Colorado and California, USA, between Nov 24, 2013, and Oct 11, 2014, were included in the study. Additional cases identified from Jan 1, 2012, to Oct 4, 2014, via statewide surveillance were provided by the California Department of Public Health. We investigated the cause of these cases by metagenomic next-generation sequencing, viral genome recovery, and enterovirus D68 phylogenetic analysis. We compared patients with acute flaccid myelitis who were positive for enterovirus D68 with those with acute flaccid myelitis but negative for enterovirus D68 using the two-tailed Fisher's exact test, two-sample unpaired *t* test, and Mann-Whitney *U* test.

Findings 48 patients were included: 25 with acute flaccid myelitis, two with enterovirus-associated encephalitis, five with enterovirus-D68-associated upper respiratory illness, and 16 with aseptic meningitis or encephalitis who tested positive for enterovirus. Enterovirus D68 was detected in respiratory secretions from seven (64%) of 11 patients comprising two temporally and geographically linked acute flaccid myelitis clusters at the height of the 2014 outbreak, and from 12 (48%) of 25 patients with acute flaccid myelitis overall. Phylogenetic analysis revealed that all enterovirus D68 sequences associated with acute flaccid myelitis grouped into a clade B1 strain that emerged in 2010. Of six coding polymorphisms in the clade B1 enterovirus D68 polyprotein, five were present in neuropathogenic poliovirus or enterovirus D70, or both. One child with acute flaccid myelitis and a sibling with only upper respiratory illness were both infected by identical enterovirus D68 strains. Enterovirus D68 viraemia was identified in a child experiencing acute neurological progression of his paralytic illness. Deep metagenomic sequencing of cerebrospinal fluid from 14 patients with acute flaccid myelitis did not reveal evidence of an alternative infectious cause to enterovirus D68.

Interpretation These findings strengthen the putative association between enterovirus D68 and acute flaccid myelitis and the contention that acute flaccid myelitis is a rare yet severe clinical manifestation of enterovirus D68 infection in susceptible hosts.

Funding National Institutes of Health, University of California, Abbott Laboratories, and the Centers for Disease Control and Prevention.

Introduction

Enteroviruses cause a broad spectrum of clinical illnesses, including acute respiratory infection, febrile rash, hand-foot-and-mouth disease, meningitis, encephalitis, and, rarely, acute flaccid paralysis. Enterovirus D68, which was first identified in 1962, causes respiratory illness,¹ but has also been sporadically detected in patients with acute flaccid paralysis.^{2,3} In 2014, in the USA, a nationwide outbreak of enterovirus D68 occurred in association with severe respiratory illness,⁴ with more than 1150 confirmed cases. This enterovirus D68 outbreak coincided with an apparent increase in incidence of reported cases of acute flaccid paralysis, including a temporally associated cluster

in Colorado.^{5,6} To more specifically describe this syndrome, the Centers for Disease Control and Prevention and the California Department of Public Health (CDPH) have proposed the term acute flaccid myelitis to include the subset of acute flaccid paralysis cases with myelitis primarily involving the grey matter.⁷ However, whether enterovirus D68 is an incidental finding in these patients or a newly emerging cause of acute flaccid myelitis remains uncertain.

Metagenomic next-generation sequencing (NGS) is a promising approach for the detection and discovery of pathogens in diseases that remain challenging to diagnose, such as encephalitis,^{8–11} and for investigation



Lancet Infect Dis 2015; 15: 671–82

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See Comment page 620

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Acute Flaccid Myelitis Among Children – Washington, September–November 2016

Weekly / August 11, 2017 / 66(31):826–829



Jesse Bonwitt, BVSc^{1,2}; Amy Poel, MPH²; Chas DeBolt, MPH²; Elysia Gonzales, MPH³; Adriana Lopez, MHS⁴; Janell Routh, MD⁴; Krista Rietberg, MPH³; Natalie Linton, MPH²; James Reggin, MD⁵; James Sejvar, MD⁶; Scott Lindquist, MD²; Catherine Otten, MD⁷ ([View author affiliations](#))

[View suggested citation](#)

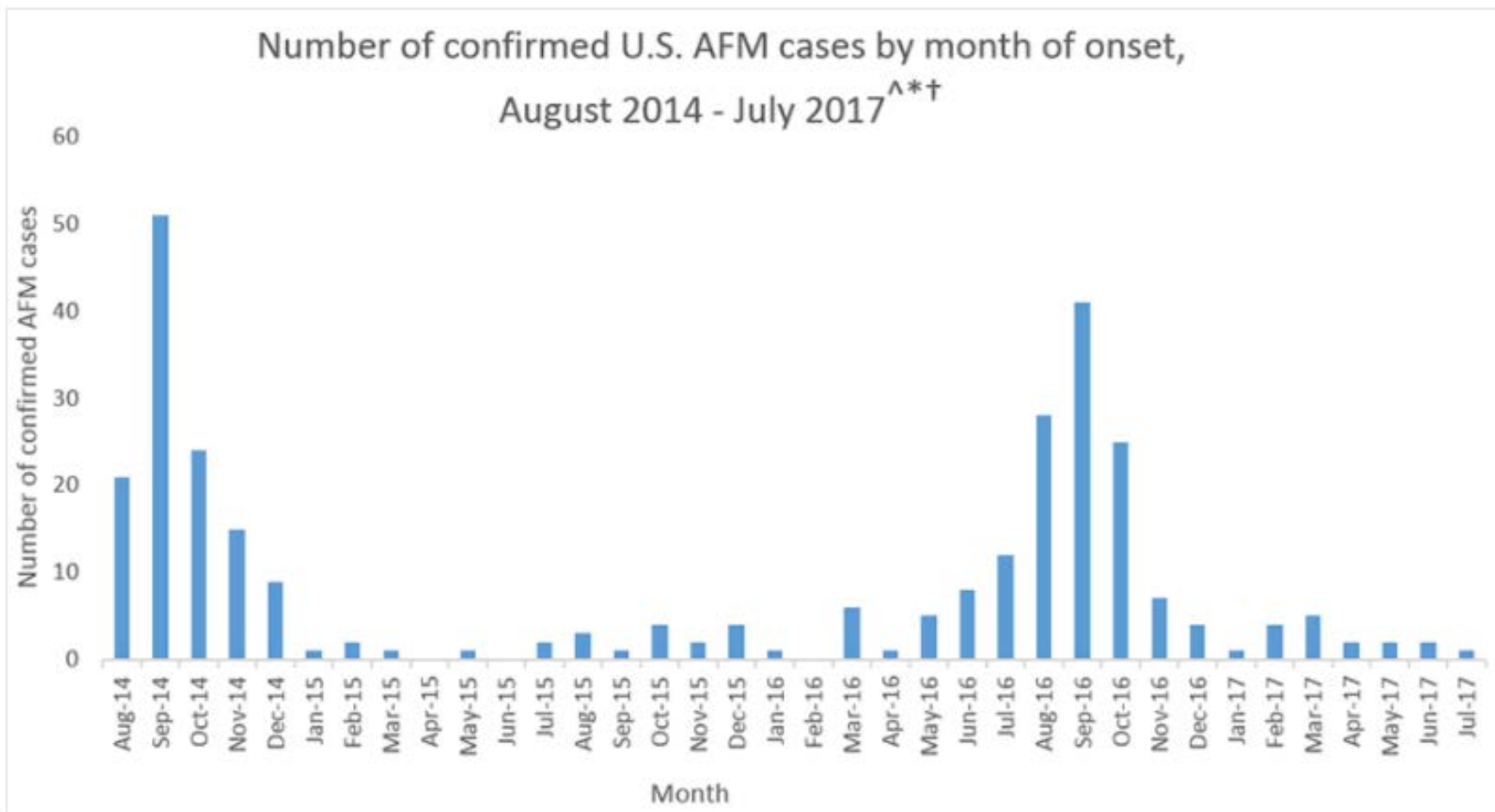
In October 2016, Seattle Children's Hospital notified the Washington State Department of Health (DOH) and CDC of a cluster of acute onset of limb weakness in children aged ≤ 14 years. All patients had distinctive spinal lesions largely restricted to gray matter detected by magnetic resonance imaging (MRI), consistent with acute flaccid myelitis (AFM). On November 3, DOH issued a health advisory to local health jurisdictions requesting that health care providers report similar cases. By January 24, 2017, DOH and CDC had confirmed 10 cases of AFM and excluded two suspected cases among residents of Washington during September–November 2016. Upper respiratory tract, stool, rectal, serum, buccal, and cerebrospinal fluid (CSF) specimens were tested for multiple pathogens. Hypothesis-generating interviews were conducted with patients or their parents to determine commonalities between cases. No common etiology or source of exposure was identified. Polymerase chain reaction (PCR) testing detected enterovirus D68 (EV-D68) in nasopharyngeal swabs of two patients, one of whom also tested positive for adenovirus by PCR, and detected enterovirus A71 (EV-A71) in the stool of a third patient. *Mycoplasma* spp. immunoglobulin M (IgM) titer was elevated in two patients, but both had upper respiratory swabs that tested negative for *Mycoplasma* spp. by PCR. Clinicians should maintain vigilance for AFM and report cases as soon as possible to state or local health departments.

On October 3, 2016, DOH and CDC were notified of a boy aged 7 years who was evaluated for acute onset of limb weakness at Seattle Children's Hospital. Eight additional patients with limb weakness were reported by the same hospital during that month, including one retrospectively identified patient with onset of weakness on September 14. MRI studies indicated distinctive lesions of the spinal cord largely restricted to gray matter in all nine patients. The clinical presentation and MRI findings among patients were similar to those reported among clusters of cases in other states during 2014 (1,2). This led to ongoing routine surveillance by DOH in Washington since 2014 and the implementation of a standard case definition for AFM* in 2015. On November 3, DOH issued a health advisory reiterating that local health jurisdictions should report suspected AFM cases.

Number of confirmed AFM cases by year of illness onset, 2014-2016

| Year | Number confirmed cases | Number of states with confirmed cases |
|--------------------------|------------------------|---------------------------------------|
| 2014 <i>(Aug-Dec)</i> | 120 | 34 |
| 2015 | 21 | 16 |
| 2016* | 144 | 37 (includes DC) |

*The case counts are subject to change.





CDC updates flaccid myelitis testing, expands search for clues

Filed Under: [Acute Flaccid Myelitis](#); [Enterovirus, Non-Polio](#)

Lisa Schnirring | News Editor | CIDRAP News | Mar 28, 2017

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The US Centers for Disease Control and Prevention (CDC) said today that it continues to receive reports of acute flaccid myelitis (AFM) cases, and because extensive testing since 2014 still hasn't identified a cause, it is modifying its testing protocols.

After an initial surge in cases in 2014, the CDC has been probing another big rise in cases in 2016, in which 136 cases were reported in 37 states. For 2017 so far, the CDC has received information for just 1 confirmed case, according to a clinical action notice sent to health providers yesterday.

The 2014 outbreak of AFM, marked by a sudden onset of limb weakness associated with spinal cord inflammation, coincided with a national outbreak of severe respiratory illness caused by enterovirus D68 (EV-D68), but testing has never consistently identified a specific pathogen in spinal fluid samples. The CDC has said several other viruses can cause AFM symptoms, including poliovirus and adenovirus.



luchschen / iStock

AFM in the United States



At a Glance

- CDC is concerned about AFM, a serious illness that we do not know all the cause of or how to prevent.
- CDC is actively investigating AFM cases. In 2016, 144 people in 37 states and DC were confirmed to have AFM.
- So far in 2017, CDC has received information for 17 confirmed cases of AFM.
- Even with an increase in cases in 2016, AFM remains a very rare disease (less than one in a million).
- CDC is [intensifying efforts](#) to understand the causes and risk factors of AFM.
- It's always important to practice general disease prevention steps, like washing your hands, staying up-to-date on vaccines, and protecting yourself from mosquito bites.

On This Page

- [What This Graph Shows](#)
- [What We Know](#)
- [What We Don't Know](#)
- [What CDC is Doing](#)

Acute flaccid myelitis (AFM) is a rare illness that anyone can get. It affects a person's nervous system, specifically the spinal cord. AFM can result from a variety of causes, including viral infections.

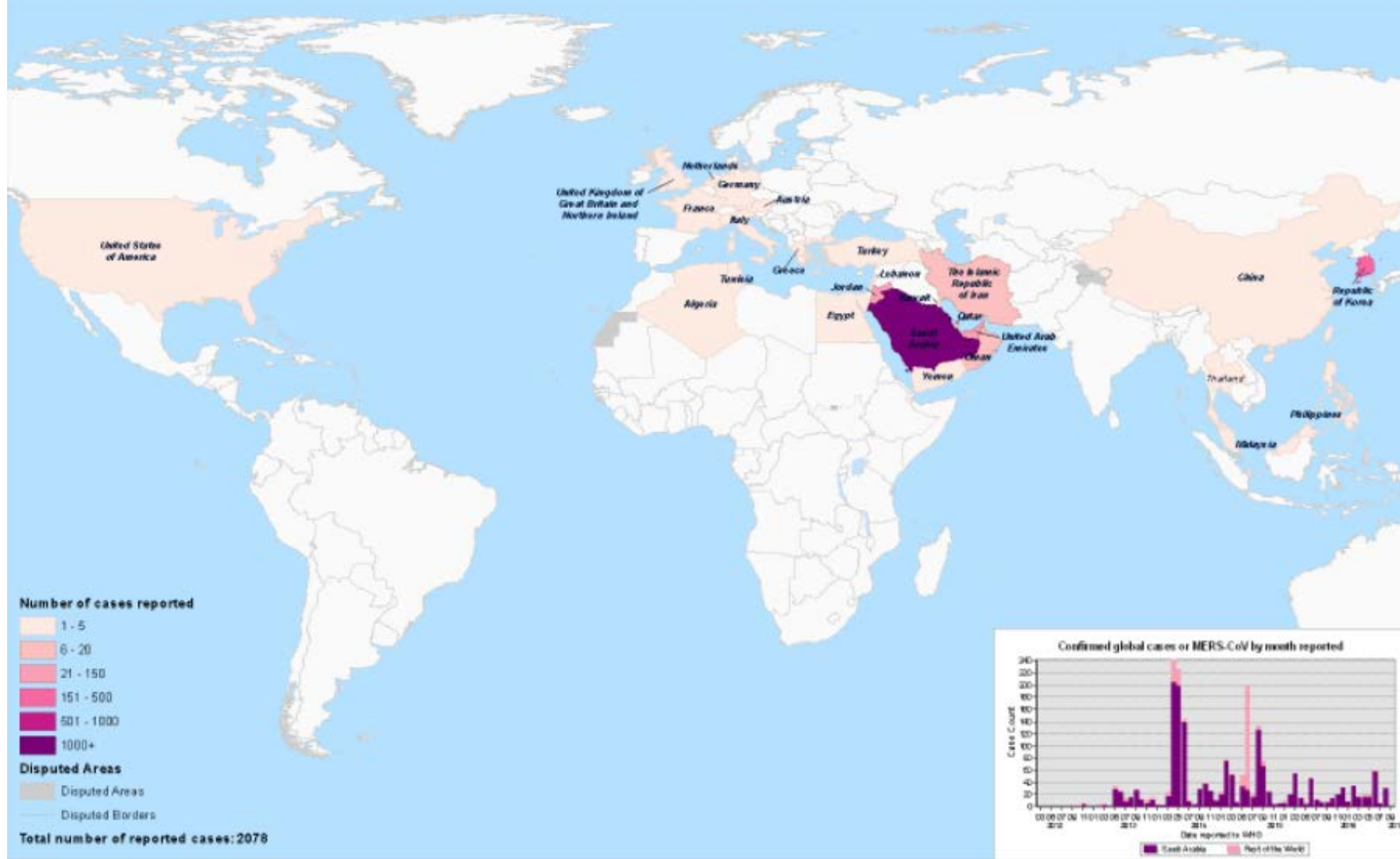
Since August 2014, CDC has been made aware of an increased number of people across the United States with AFM for which no cause could be found. Since then, CDC has been actively investigating this illness. We continue to receive information about cases of AFM. In 2016, a total of 144 people in 37 states across the country and DC were confirmed to have AFM.

CLF Topics

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2. Avian Influenza
3. Post-hurricane health outcomes
4. Acute flaccid myelitis
5. **MERS**
6. Bioterrorism / Gain-of-function research
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10. Other



CONFIRMED GLOBAL CASES OF MERS-COV 2012 - 2017



Map Scale (A2): 1:1,109,175,700
1 cm = 11,092 km

Coordinates: 216x, 902, 4802, 1644
Date: 09/2017
020, 100x

The boundaries and names shown and the designations used on this map do not imply the expression of any opinion whatsoever on the part of the World Health Organization concerning the legal status of any country, territory, city or Area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

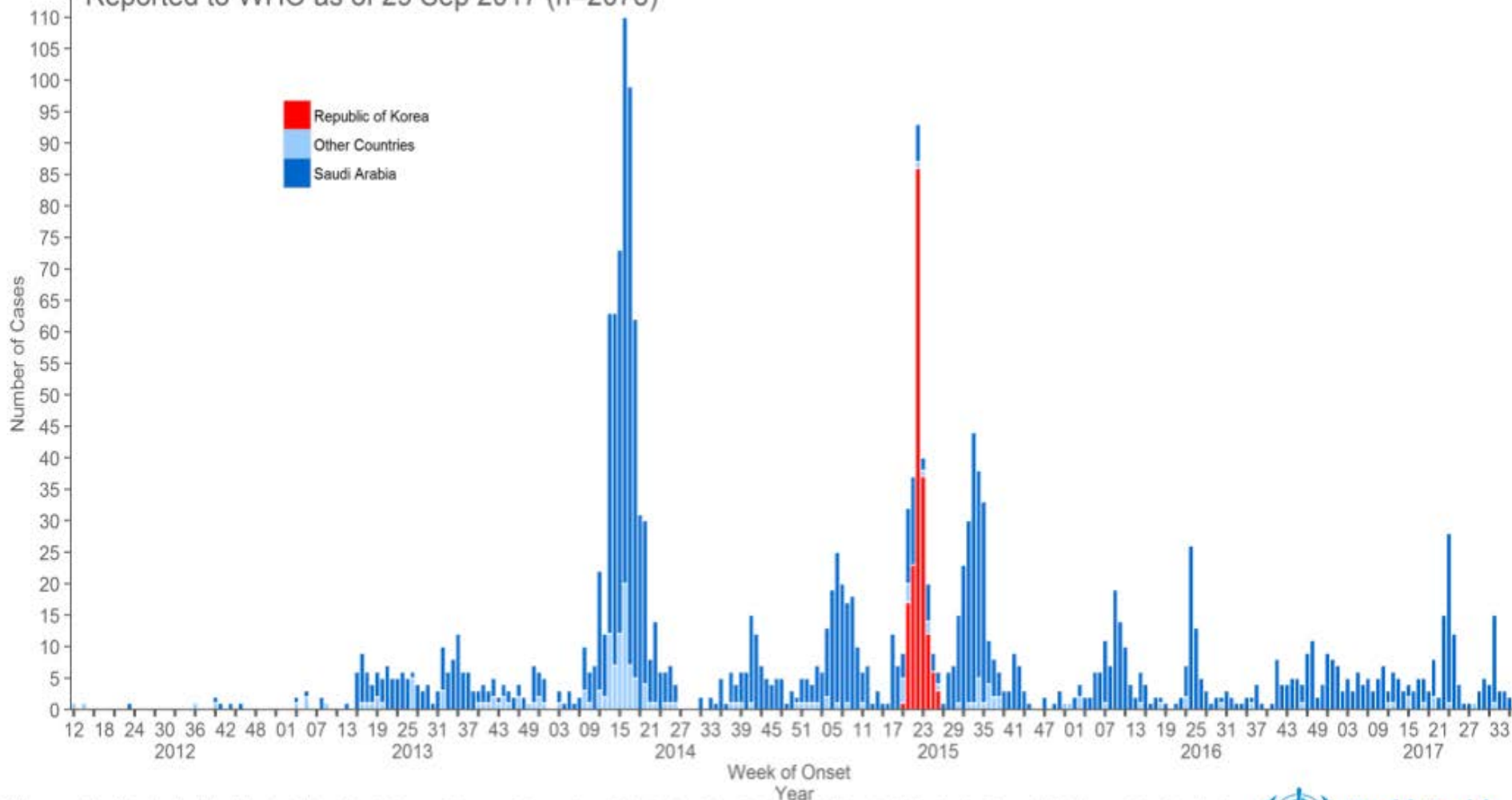
Data Source: World Health Organization
© WHO 2017. All rights reserved.
Map date: 28/09/2017



World Health Organization

Confirmed global cases of MERS-CoV

Reported to WHO as of 29 Sep 2017 (n=2078)



Other countries: Algeria, Austria, Bahrain, China, Egypt, France, Germany, Greece, Iran, Italy, Jordan, Kuwait, Lebanon, Malaysia, Netherlands, Oman, Philippines, Qatar, Thailand, Tunisia, Turkey, United Arab Emirates, United Kingdom, United States of America, Yemen

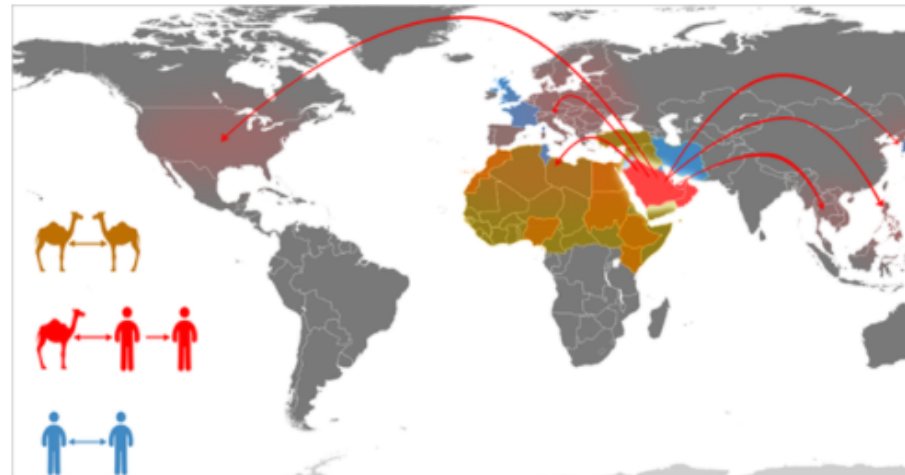
Please note that the underlying data is subject to change as the investigations around cases are ongoing. Onset date estimated if not available.

Emergencies

Countries agree next steps to combat global health threat by MERS-CoV

27 September 2017

Critical next steps to accelerate the response to the global public health threat posed by Middle-East respiratory syndrome coronavirus (MERS-CoV) have been agreed by representatives from the Ministries of Health and Ministries of Agriculture of affected and at risk countries, and experts. The virus, which circulates in dromedary camels without causing visible disease, can be fatal for humans.



WHO

At a meeting hosted by the World Health Organization (WHO), the Food and Agriculture Organization (FAO), and the World Organisation for Animal Health (OIE) in Geneva this week, more than 130 experts from 33 countries, organizations and research institutions met to share what is known about the virus, identify priority research needs, improve cross-collaboration between animal and human health sectors and agree on a plan to address crucial gaps.

Health experts zero in on camels to fight deadly MERS virus



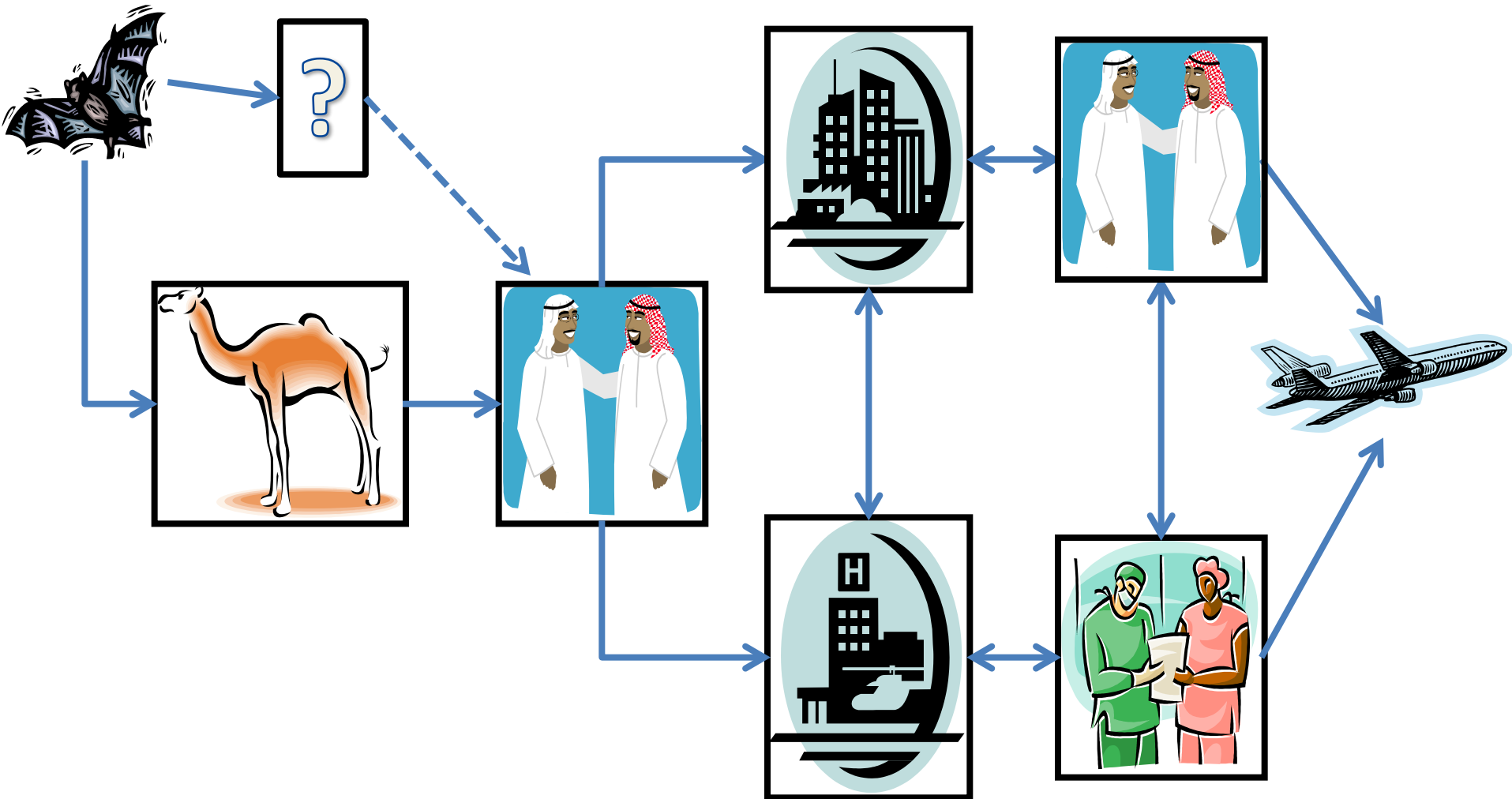
GENEVA (Reuters) - The fight against the deadly Middle East Respiratory Syndrome (MERS), which has killed at least 722 people over the past five years, is honing in on its target: camels.

MERS coronavirus (MERS-CoV), a member of a virus family ranging from the common cold to Severe Acute Respiratory Syndrome, appears to have emerged in humans in Saudi Arabia in 2012, but has now been traced back in camels to at least 1983.

Almost all the outbreaks so far originated in the Arabian Gulf, but MERS-CoV could infect humans wherever there are one-humped dromedary camels - two-humped bactrians are not affected.

That means people across a swathe of Africa, the Middle East, Pakistan and South Asia are potentially at risk. So the hunt is on for vaccinations - both for humans, and camels.

The MERS Transmission Model





WHO: Hospital outbreaks underscore MERS challenges

Filed Under: [MERS-CoV](#)

[Lisa Schnirring](#) | News Editor | [CIDRAP News](#) | Jul 25, 2017

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Though surveillance for MERS-CoV and response to suspected clusters have improved, especially in hard-hit Saudi Arabia, early identification in the community and in healthcare facilities and compliance with infection prevention and control protocols still pose major challenges, the World Health Organization (WHO) said in its latest risk assessment.

The WHO's report, issued Jul 21, is its first major risk assessment update since December and covers 199 cases in four countries reported since its last report, 190 of them in Saudi Arabia, which reported several healthcare clusters over the time span.

Illnesses linked to a spate of hospital outbreaks in Riyadh in June appear to have tapered off, and the country hasn't reported a new case in 14 days.

Overall, however, WHO experts said the epidemiology, transmission patterns, clinical presentation, and viral characteristics haven't changed since the agency's last risk assessment on Dec 5, 2016.



Wavebreakmedia / iStock



Korea highlights MERS super-spreaders, reports death

Filed Under: **MERS-CoV**

Jim Wappes | Editorial Director | CIDRAP News | Oct 26, 2015

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South Korean health officials said yesterday that five super-spreaders caused 83% of cases in its MERS-CoV outbreak this year, and they confirmed a new death from the disease in a patient who had earlier tested negative.

Major role of super-spreaders

The five super-spreaders, all of whom had pneumonia, transmitted the virus to 153 people all told out of the 186 MERS-CoV (Middle East respiratory syndrome coronavirus) cases confirmed this year in South Korea after a traveler brought the virus from the Middle East, *The Korea Herald* reported yesterday.

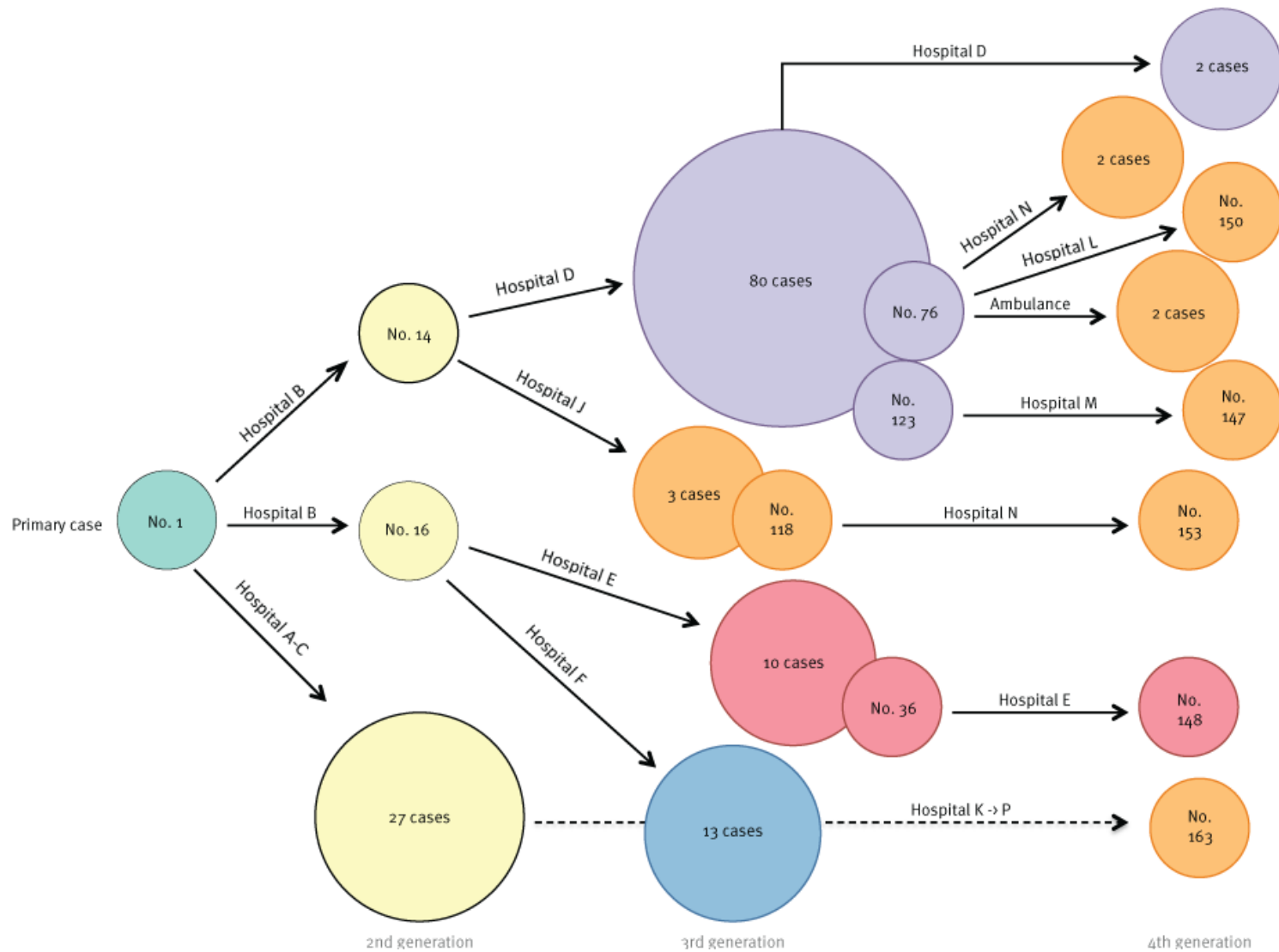


Marcel Braendi / iStock

The findings were highlighted by the country's Centers for Disease Control and Prevention yesterday but were first published Sep 5 in the agency's journal *Osong Public Health and Research Perspectives*.

FIGURE 2

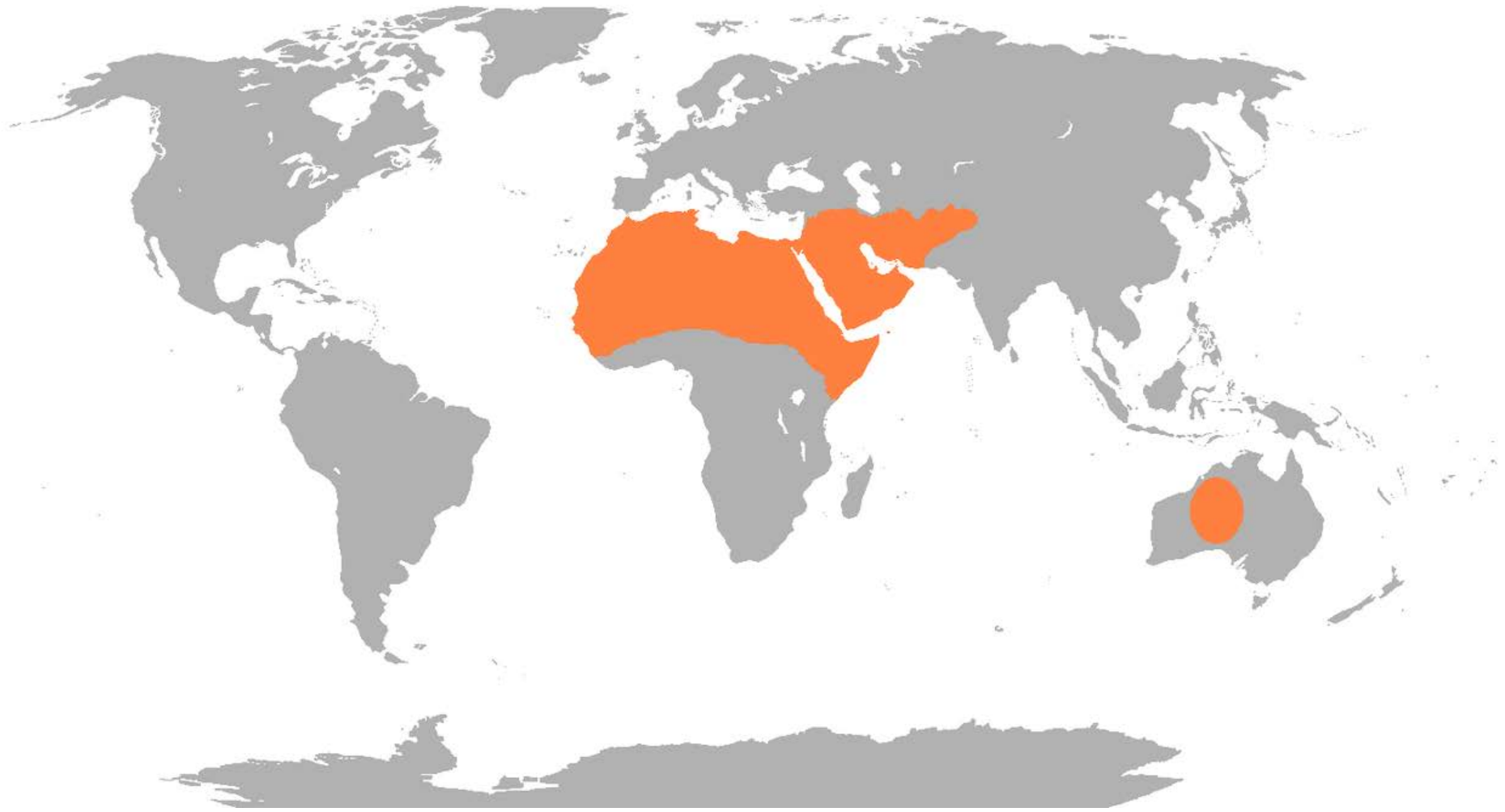
Simplified transmission diagram illustrating the superspreading events associated with Cases 1, 14, 16 and fourth-generation infections of MERS-CoV, South Korea, 11 May–19 June 2015 (n = 166)



MERS-CoV: Middle East respiratory syndrome coronavirus.

Source: Cowling BJ, Park M, Fang VJ, et al. Preliminary epidemiological assessment of MERS-CoV outbreak in South Korea, May to June 2015. *Euro Surveill* 2015 Jun 25;20(25):pii=21163





No Serological Evidence of Middle East Respiratory Syndrome Coronavirus Infection among Camel Farmers Exposed to Highly Seropositive Camel Herds: A Household Linked Study, Kenya, 2013

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Abstract. High seroprevalence of Middle East respiratory syndrome coronavirus (MERS-CoV) among camels has been reported in Kenya and other countries in Africa. To date, the only report of MERS-CoV seropositivity among humans in Kenya is of two livestock keepers with no known contact with camels. We assessed whether persons exposed to seropositive camels at household level had serological evidence of infection. In 2013, 760 human and 879 camel sera were collected from 275 and 85 households respectively in Marsabit County. Data on human and animal demographics and type of contact with camels were collected. Human and camel sera were tested for anti-MERS-CoV IgG using a commercial enzyme-linked immunosorbent assay (ELISA) test. Human samples were confirmed by plaque reduction neutralization test (PRNT). Logistic regression was used to identify factors associated with seropositivity. The median age of persons sampled was 30 years (range: 5–90) and 50% were males. A quarter (197/760) of the participants reported having had contact with camels defined as milking, feeding, watering, slaughtering, or herding. Of the human sera, 18 (2.4%) were positive on ELISA but negative by PRNT. Of the camel sera, 791 (90%) were positive on ELISA. On univariate analysis, higher prevalence was observed in female and older camels over 4 years of age ($P < 0.05$). On multivariate analysis, only age remained significantly associated with increased odds of seropositivity. Despite high seroprevalence among camels, there was no serological confirmation of MERS-CoV infection among camel pastoralists in Marsabit County. The high seropositivity suggests that MERS-CoV or other closely related virus continues to circulate in camels and highlights ongoing potential for animal-to-human transmission.

INTRODUCTION

In September 2012, Middle East respiratory syndrome coronavirus (MERS-CoV) was first detected in humans, and as of June 2016, 1,733 laboratory-confirmed human cases and 628 deaths had been reported to the World Health Organization (WHO) from 27 countries.¹ The majority of the cases have been reported from Arabian Peninsula, but cases imported to other countries have caused large hospital-linked outbreaks, such as in South Korea, in 2015.¹ Severe respiratory disease and death rate is higher in infections among older patients and those with preexisting conditions.^{2–4} Dromedary camels have been identified as a potential reservoir for the virus after detection of virus in camels in Saudi Arabia, Oman, and Qatar,^{5–7} and of a high level of seroprevalence of MERS-CoV antibodies in camel populations from a wider range of countries including countries in the Middle East and Africa.^{8–14} Notably, however, Australia has documented absence of MERS-CoV antibodies among camels.^{15,16} Most MERS-CoV infections in humans are not linked to camel exposure and are thought to be due to human-to-human transmission particularly in health-care settings. The low frequency of camel-to-human infections is supported by the finding that MERS-CoV seroprevalence among the general human population in Saudi Arabia is less

than 0.5%, though significantly higher in camel shepherds (2.3%) and slaughterhouse workers (3.6%).¹⁷

According to the Food and Agriculture Organization, the world population of camels in 2001 was 19 million camels, of which, 17 million were dromedary camels and approximately 65% of these were found in the eastern African countries of Sudan, Somalia, Ethiopia, and Kenya.¹⁸ Despite the fact that the majority of dromedary camels are in Africa, no case of MERS-CoV in humans has been reported in Africa, except for a cluster of three family members in Tunisia, in 2013, associated with an imported index case and no history of exposure to camels.¹⁹ A retrospective study carried out in Kenya detected MERS-CoV antibodies in more than 90% of camels from various parts of the country.⁸ A recent study that analyzed > 1,000 human sera from among pastoralists who did not keep camels reported two likely asymptomatic humans (< 0.2%) positive for MERS-CoV neutralizing antibodies.²⁰

To understand the risk of transmission between camels and humans living in close contact, we conducted a serosurvey in camels and humans in same households to determine the prevalence of MERS-CoV antibodies among pastoral communities in northern Kenya that live in close association with camels and investigated risk factors associated with seropositivity in camels and humans.

METHODS

Study site and design. In 2013, we conducted a cross-sectional serosurvey of humans and camels in Marsabit County,²¹ using a two-stage random sampling methodology.

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†These authors contributed equally to this work.



News Scan for Oct 02, 2017

New MERS cases confirmed in Saudi Arabia

After a lag in reporting last week, the Saudi Arabian Ministry of Health (MOH) updated it information on MERS-CoV cases over the weekend, noting three new cases since the agency last reported on Sep 25.

On Sep 26, the MOH said a 52-year-old Saudi man from Taif had been diagnosed as having MERS-CoV (Middle East respiratory syndrome coronavirus). He was reported to be in critical condition. The man had direct contact with camels, a known risk factor for MERS transmission.

The following day a 76-year-old Saudi man from Nifi was diagnosed as having the disease. He was also symptomatic and is in stable condition. The man's source of infection is listed as "primary," meaning it's unlikely he contracted the disease from another person.

Finally, on Sep 30, the MOH said a 31-year-old Saudi man from Bishah was in critical condition with a MERS-CoV infection. That man also had direct contact with camels.

None of the newly reported patients are healthcare workers. The new cases raise Saudi Arabia's MERS count to 1,726 since 2012, including 699 deaths. Four people are currently being treated for the disease.

Sep 26 MOH report

Sep 27 MOH report

Sep 30 MOH report



Researchers find novel bat coronaviruses, akin to MERS, SARS

Filed Under: [MERS-CoV](#); [SARS](#)

Lisa Schnirring | News Editor | CIDRAP News | Apr 05, 2017

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Two new studies shed more light on coronaviruses in bats, one identifying a novel coronavirus similar to MERS-CoV in a bat from Uganda and the other finding wide diversity in China that includes strains similar to the SARS virus.

The new findings add to an expanding list of coronaviruses identified in bats and strengthen the case that the viruses known to cause severe disease in humans originate in bats.

MERS-like virus said to pose no human threat

The study detailing the finding in the Ugandan bat was conducted by a team from the United States and Uganda, part of the US Agency for International Development Emerging Pandemic threats PREDICT project. The researchers published the results yesterday in *mBio*.



Adam Zdebel / Flickr cc

CLF Topics

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BILL GATES: A new kind of terrorism could wipe out 30 million people in less than a year – and we are not prepared

Bill Gates, Bill & Melinda Gates Foundation

🕒 Feb. 18, 2017, 9:00 AM 🔥 240,926

The following op-ed was exclusively provided to Business Insider to coincide with a speech Bill Gates is giving for the Munich Security Conference. The following is an abridged version of his remarks.

When I decided 20 years ago to make global health the focus of my philanthropic work, I didn't imagine that I'd be speaking at a conference on international security policy. But I'm speaking here at the Munich Security



Mike Nudelman/Business Insider

AMERICA IS ONE KILLER ORGANISM AWAY FROM A LIVING NIGHTMARE
THAT THREATENS ALL WE HOLD DEAR....

LIVING TERRORS

"Osterholm sounds a frightening alarm...the threats
he describes are bone chilling."—*Publishers Weekly*



**What America Needs to Know
to Survive the Coming Bioterrorist Catastrophe**

**MICHAEL T. OSTERHOLM, Ph.D., M.P.H.,
and JOHN SCHWARTZ**

Everything we know about North Korea's bioweapons program



Kevin Loria [✉](#) [📧](#) [🐦](#)

🕒 Jul. 26, 2017, 12:05 PM 🔥 5,294

North Korea's successful launch of an intercontinental ballistic missile on July 4 heightened global fears about the deadly threat of nuclear war.

But nuclear weapons are not the only weapons of mass destruction that experts think North Korea is developing. They warn that the secretive state also possesses chemical weapon stores and may maintain an ongoing biological weapons program as well.

Biological weapons are particularly scary, since they could



South Koreans rush out into the street during an anti-chemical, biochemical and radiological terror exercise against a possible terrorist attack. Chung Sung-Jun/Getty Images

Terrorists, rogue nations could easily access dangerous biological research

■ US National Academies says there are 'multiple shortcomings' in the systems designed to stop risky research from being published.

By Immanuel Jotham

September 17, 2017 12:16 BST



Building biological weapons could be done easily by downloading instructions in the form of research off the internet (Usaf/Getty Images)

The US National Academies of Sciences, Engineering, and Medicine has said that biological research of viruses, bacteria, and other pathogens can be easily accessed by people or states that might want to build weapons out of them.

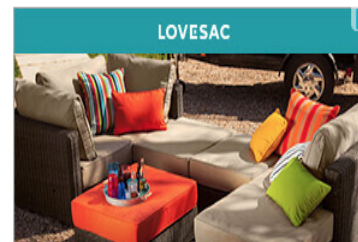
A report by the National Academy pointed out that such publications could actually contain information on how to weaponize pathogens.

More from IBTimes UK

- Terrorists can get their hands on WMDs via tech available on Dark Web - UN
- Inside the US Army's top secret chemical and biological weapons testing facility
- I treated chemical attack victims - antidotes should be made available on street corners

According to the National Academy, a majority of scientists and researchers in this field have limited awareness when it comes to biosecurity issues. New Scientist pointed out the incident where 22 people were infected and five were killed after a government scientist sent Anthrax spores via mail in 2001.

The academy also said that there were "multiple shortcomings" in the systems designed to stop potentially risky research from being published.



In the US, there is a restriction in place on research concerning 15 different pathogens and toxins called the "dual-use research of concern". These are materials that have the dual use of medical research as well as be fashioned to kill.

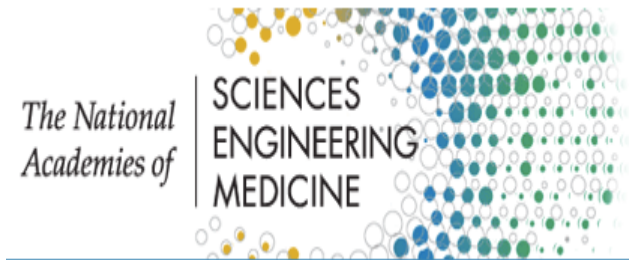
The National Academies of
SCIENCES • ENGINEERING • MEDICINE

CONSENSUS STUDY REPORT




**DUAL USE
RESEARCH
OF CONCERN
IN THE LIFE
SCIENCES**

**Current Issues
and Controversies**



Dual Use Research of Concern in the Life Sciences: Current Issues and Controversies (2017)

 Consensus Study Report

The potential misuse of advances in life sciences research are raising concerns about national security threats. The current report examines the U.S. strategy for reducing biosecurity risks in life sciences research and considers mechanisms that would allow researchers to manage the dissemination of the results of research while mitigating the potential for harm to national security.

US rules for 'dual-use' research found lacking



BY REBECCA TRAGER | 22 SEPTEMBER 2017

US policies governing the dissemination of so-called 'dual-use' research – legitimate work in the life sciences that could pose a national security or public health threat if misused – are fragmented and have multiple weaknesses, [warns a new National Academies report](#). Its authors suggest that most life scientists have little awareness of biosecurity issues, and they say better training is needed.

The panel says the US government's current policy emphasis and definition of dual-use research of concern (DURC) – which focuses on 15 select agents and toxins and seven types of experiments – fails to address all biosecurity concerns in various research fields. In particular, emerging areas like synthetic biology, computational modelling, genome editing and the isolation of new micro-organisms and toxins are falling through the cracks.

The report argues that current US rules in this arena can unnecessarily constrain certain types of scientific endeavours, including research with so-called pathogens of pandemic potential. Its authors also emphasise that journal editors and researchers who do not work at federally funded institutions currently have little guidance on how to manage manuscripts or research activities that raise potential biosecurity concerns.

Regulations may overlook studies of concern and needlessly hamper other work





Canadian group creates poxvirus, prompting dual-use discussion

Filed Under: [Dual-Use Research](#); [Smallpox](#)

[Stephanie Soucheray](#) | News Reporter | [CIDRAP News](#) | Jul 07, 2017



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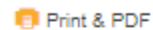
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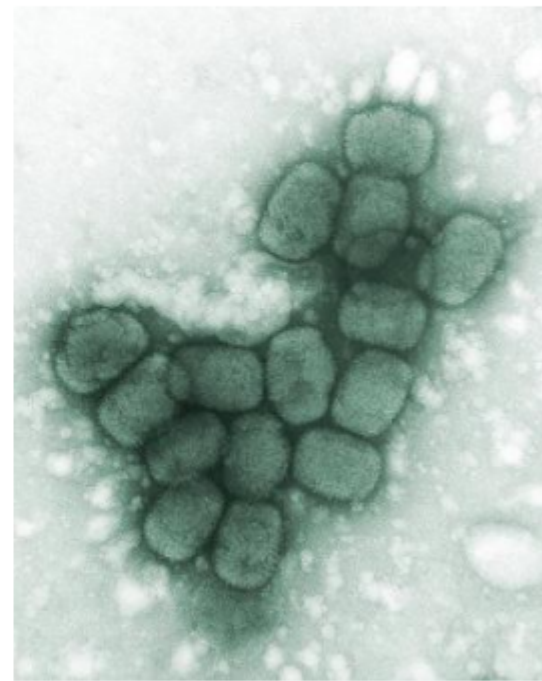
Yesterday, *Science* magazine published a story about a group of Canadian researchers at the University of Alberta who, for about \$100,000, created a horse poxvirus that had been extinct.

While many news agencies and scientists expressed their shock at this development, several researchers say this discovery has been expected for a long time.

"This shouldn't surprise anyone," said Paul Duprex, PhD, director of cell and tissue imaging at the National Emerging Infectious Diseases Laboratories at Boston University. "It's just molecular biology, and we've had the ability to do this for ages."

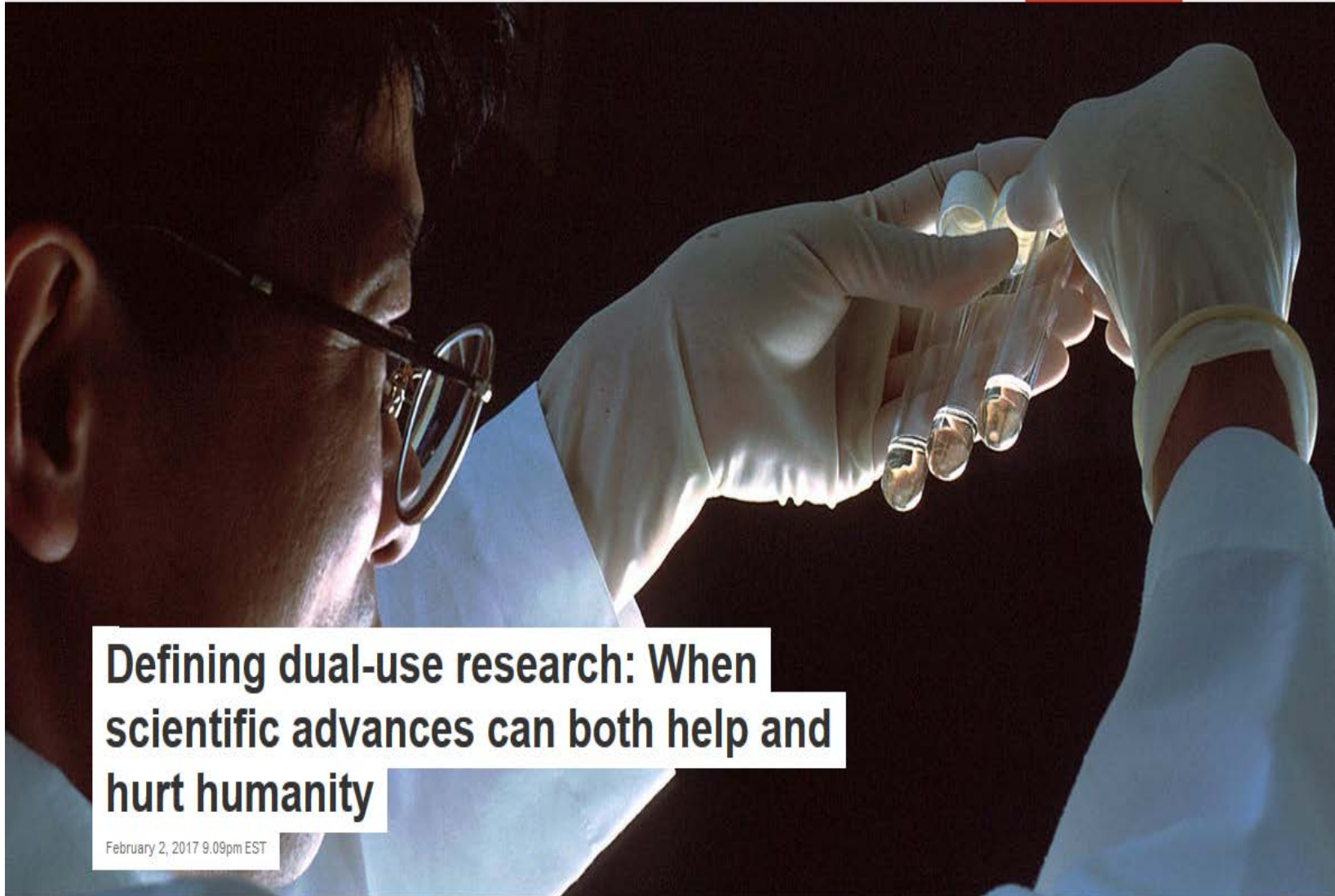
Valid research goal, but dual-use questions

Duprex said the Canadian group's paper on their recreation of a horsepox virus, closely related to the smallpox virus, has yet to be published. The group said their work was done via genetic pieces ordered in the mail, and their objective was to understand the



CDC-Dr Fred Murphy/ Flickr cc

The smallpox virus shown here is similar to the horsepox virus that the Canadian team recreated.



Defining dual-use research: When scientific advances can both help and hurt humanity

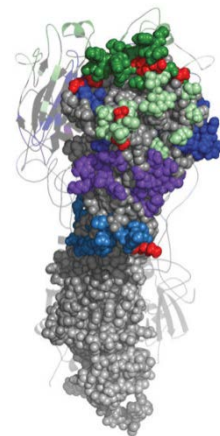
February 2, 2017 9:09pm EST

CLF Topics

1. Yemen / global health response
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3. Post-hurricane health outcomes
4. Acute flaccid myelitis
5. MERS
6. Bioterrorism / Gain-of-function research
7. Vaccine update
8. CEPI
9. Movies and preparedness
10. Other

Why flu vaccines so often fail

By [Jon Cohen](#) | Sep. 20, 2017 , 2:30 PM



The influenza virus has yet to hit the Northern Hemisphere, but flu vaccine season is already in full swing, with banners outside pharmacies urging: "Get Your Flu Shot Now." What's not advertised, however, is just how lackluster the vaccine is. The most commonly used flu shots protect no more than 60% of people who receive them; some years, effectiveness plunges to as low as 10%. Given that a bad flu season can kill 50,000 people in the United States alone, "10% to 60% protection is better than nothing," says Michael Osterholm, an epidemiologist at the University of Minnesota in Minneapolis. "But it's a terribly inadequate vaccine for a serious public health threat." Now, researchers are striving to understand why it fails so often—and how to make a markedly better one.

They're questioning what was once received wisdom: that the vaccine fails when manufacturers, working months ahead of flu season, incorrectly guess which strains will end up spreading. And they're learning instead that the vaccine may falter even when the right strains were used to make it, perhaps because of how it is produced or quirks of individual immune systems. "It's much more complicated than we thought," Osterholm says. "I know less about influenza today than I did 10 years ago."

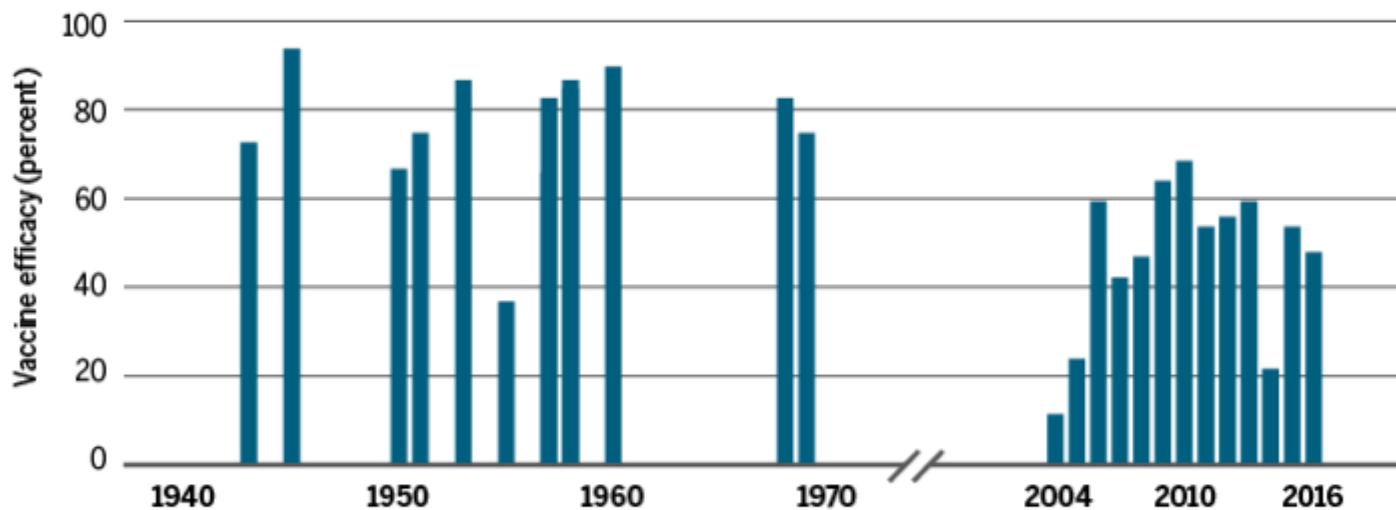
The influenza vaccine teaches the body to produce antibodies against the head of the virus's surface protein, hemagglutinin (HA). Those antibodies ideally prevent HA from attaching to cellular receptors, thwarting infection. But HA's head is highly mutable, which is why vaccinemakers must come up with a new formula every year.

Why flu vaccines so often fail

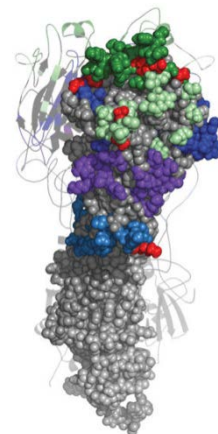
By Jon Cohen | Sep. 20, 2017, 2:30 PM

Loss of confidence

For decades, tests suggested the flu vaccine worked extremely well, but in the past 15 years a better test revealed many infections in vaccinated people who would previously have been deemed protected.



CREDITS: (GRAPHIC) G. GRULLÓN/SCIENCE; (DATA) F. M. DAVENPORT ET AL. *MED J AUST.* 1973; SUPPL 33-38; CENTERS FOR DISEASE CONTROL & PREVENTION





Study signals association between flu vaccine, miscarriage

Filed Under: [Influenza Vaccines](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Sep 13, 2017



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A study published today in *Vaccine* suggests a strong association between receiving repeated doses of the seasonal influenza vaccine and miscarriage.

The authors said the study is an unexpected signal that calls for deeper investigation and highlights the challenges of monitoring the safety of annual vaccines.

"We are not saying this is a causal relationship," said James Donahue, DVM, PhD, MPH, a senior epidemiologist at the Marshfield Clinic in Wisconsin and the lead author of the study, meaning the data don't necessarily show that the flu vaccine causes miscarriages. "There's no biological basis for this phenomenon, so the study represents something that wasn't expected."



wissanuo1 / iStock

A new finding of a possible flu shot-miscarriage link shows science prioritizes vaccine safety

By MICHAEL T. OSTERHOLM / SEPTEMBER 13, 2017



When I first heard about [the study](#) published in the journal *Vaccine* on Tuesday that linked getting a flu shot to having a spontaneous abortion (or what is more commonly called miscarriage) over the course of the next 28 days, I knew it was likely to make waves.

Few things today can evoke as much concern, if not downright panic, as declaring that doing something that is routinely recommended, like getting your annual [flu shot](#), may be harmful, like causing a pregnant woman to have a miscarriage. Yet while this story may be potentially bad news for newly pregnant women who get a flu shot, it is also a good news story about science, showing that the science community is doing its job, painstakingly watching for any signals that a recommended intervention might be harmful to health.

The researchers, from the Marshfield Clinic, Kaiser Permanente, Group Health Research Institute, and the Centers for Disease Control and Prevention, emphasized that the results may be just a chance finding, something that occurs when you do a number of studies. It's like flipping a coin five times: Three times out of 100 you can expect all five flips to result in heads. That is a rare finding, but it's due to chance alone, not to some causal effect.



FALSE ALARM

The Pregnancy Vaccine Scare That Should Have Never Been

Why that CDC study on flu shots during the first trimester should never have been published.



PAUL A. OFFIT 09.24.17 12:00 AM ET

Last week, researchers at the Centers for Disease Control and Prevention (CDC) warned that an influenza vaccine given in the first trimester of pregnancy might have caused miscarriages. News outlets all over America picked up the story.

The CDC's claim wasn't trivial. About 50 percent of all pregnant women in the U.S. receive an annual influenza vaccine. Now, some expectant mothers were wondering whether they had done the right thing **by getting their flu shots** ■.

These women had no need to worry. For several reasons, this CDC study should have never been published. Why?


- The CDC's observation was inconsistent. Researchers had studied two influenza-vaccine seasons: 2010-2011 and 2011-2012. The problem of first-

Officials highlight flu vaccination gaps, progress ahead of season

Filed Under: [Influenza Vaccines](#)


Lisa Schnirring | News Editor | [CIDRAP News](#) | Sep 28, 2017

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In an annual event to build support for flu vaccination and take stock of the nation's uptake trends, federal officials said today that vaccination rates rebounded slightly last season, led by better coverage in adults over age 50, but immunization reached only 46.8% of the population.

Health officials and other experts, speaking at a media briefing in Washington, D.C., focused on the latest coverage levels in specific populations targeted for vaccination, including kids, pregnant women, healthcare workers, and older people. The US Centers for Disease Control and Prevention (CDC) published the findings on its FluVaxView Web site and in two reports in the latest edition of *Morbidity and Mortality Weekly Report (MMWR)*.

Health and Human Services Secretary Tom Price, MD, said flu seasons are difficult to predict, but vaccination can help blunt the impact of the disease and cut hospitalizations and deaths. "Today, I am leading by example and getting vaccinated against flu. I urge everyone 6 months and older to do the same as soon as vaccine is available in their community," he said.



Penn State / Flickr cc



Sanofi halts work on Zika vaccine amid federal funding cuts

Filed Under: [Zika](#)

Lisa Schnirring | News Editor | CIDRAP News | Sep 05, 2017

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Late Friday on the eve of the long Labor Day weekend, Sanofi announced it would suspend work on a candidate Zika vaccine that it has been developing with Walter Reed Army Institute of Research (WRAIR), based on news it received of scaled-back federal support.

Rocky vaccine landscape

After a surge of activity in the Americas, Zika activity has dropped off sharply this year, after tearing through populations who weren't exposed to it before who now are thought to have some protection based on herd immunity.

As with the 2013-16 Ebola outbreak, a steep drop in new cases poses obstacles to testing new vaccines and treatments. Though globally there are about 20 Zika vaccines at different stages of development, the Sanofi vaccine is one of a few at the advanced stage.



Guschenkova / iStock

The race for a Zika vaccine slows, a setback for efforts to head off future outbreaks

By HELEN BRANSWELL @HelenBranswell / SEPTEMBER 13, 2017



The development of a type of Zika vaccine that authorities had hoped to usher to the market has proven more challenging than some scientists and pharmaceutical companies had expected, people involved in the research have told STAT, posing a setback for efforts to avoid future outbreaks of the disease.

Although vaccines typically take years to produce, test, and license, U.S. health officials had voiced confidence that Zika would not be a difficult target, and some predicted that [a vaccine](#) could be made and fully tested, ready for Food and Drug Administration assessment, within two to three years. Others predicted a licensed Zika vaccine could be available sometime in 2020.

Even the more cautious forecast now seems optimistic.

Early this month, the vaccine maker Sanofi Pasteur [quietly pulled the plug](#) on its Zika vaccine efforts, a reflection of some complications in the development of the vaccine as well as of evaporating market prospects and limited U.S. government funding.

The company said the latter factor — word that the government would not fully fund the vaccine work — was the key. Without full government funding of the program “we could not continue development of a Zika vaccine,” said Jon Heinrichs, the Sanofi executive who led the effort. “We still don’t see that this would be a profitable vaccine for Sanofi Pasteur.”

Is there a future for a Zika vaccine?

By SETH BERKLEY / SEPTEMBER 18, 2017



When a leading vaccine manufacturer announced earlier this month that it was [pulling out of the race](#) to develop a [vaccine against the Zika virus](#), it effectively shelved what was widely considered to be one of front-running candidates. Along with the dramatic drop in the number of new cases of Zika in recent months, does this signal that the threat has now passed, or does it mean we are now no closer to a vaccine should a resurgence of the disease eventually occur?

Neither, in fact. When Zika does start to spread again, which seems likely, the loss of this one vaccine is unfortunate, particularly because it is from a major manufacturer. But there are [numerous other Zika vaccine candidates](#) currently in the works.

While it's not entirely clear what lies behind Sanofi Pasteur's decision, it is worrisome, suggesting that a deeper problem is at play and highlighting one of the biggest challenges in vaccine development.

WELCOME TO THE WHO VACCINE TRIAL TRACKER



| Pathogen | Month of most recent update | Updating Partner | Further Information |
|-------------------------|-----------------------------|------------------|---|
| HIV | | | |
| Malaria | March 2017 | | |
| TB | March 2017 | Collaborator | |
| Dengue | March 2017 | WHO Secretariat | |
| RSV | March 2017 | PATH | |
| Enterics | June 2017 | PATH | |
| Zika | April 2017 | WHO Secretariat | |
| Lassa, MERS-CoV, Nipah | May 2017 | CEPI | http://cepi.net/pipeline-dataset |
| Ebola/Marburg | June 2017 | Oxford | |
| Pneumococcal infections | June 2017 | MSF Epicentre | |

GeneOne Life Science Receives Approval for Phase I/IIa MERS-CoV Vaccine Trial in Korea

GeneOne Life Science Receives Approval of IND by the Korean Ministry of Food and Drug Safety (KMFDS) of MERS-CoV Plasmid DNA vaccine, GLS-5300, for a Phase I/IIa Clinical Trial in Korea

SEOUL (PRWEB) SEPTEMBER 17, 2017

GeneOne Life Science, Inc. announces that it has received approval from the South Korean Ministry of Food and Drug Safety (KMFDS) for an Investigational New Drug application for a Phase I/IIa study of its investigational vaccine, GLS-5300, against the Middle East Respiratory Syndrome coronavirus (MERS-CoV). The study in Korea represents the second clinical trial for GLS-5300.

A US clinical trial of GLS-5300 at the Walter Reed Army Institute of Research (NCT02670187, <http://www.ClinicalTrials.Gov>) has completed all study visits. GLS-5300 was well tolerated and induced high levels of antibodies and T-cell responses when administered intramuscularly (IM) and followed by electroporation (EP) using the CELLECTRA® device. All dose levels, 0.67 mg, 2 mg, and 6 mg were equally immunogenic. GLS-5300 has been shown to be fully protective in pre-clinical studies in non-human primates. The trial in Korea will assess the responses of GLS-5300 given intradermally (ID) and followed by EP at doses of 0.3 and 0.6 mg.



“Regulatory approval for this Phase I/IIa clinical trial will enable GeneOne to bring the GLS-5300 MERS-CoV vaccine into Korea”

CLF Topics

1. Yemen / global health response
2. Avian Influenza
3. Post-hurricane health outcomes
4. Acute flaccid myelitis
5. MERS
6. Bioterrorism / Gain-of-function research
7. Vaccine update
8. CEPI
9. Movies and preparedness
10. Other

This New Group Wants to Stop Pandemics Before They Start

Alexandra Sifferlin

Jan 19, 2017

TIME
Health

For more, visit [TIME Health](#).



Global epidemics tend to follow an unfortunate pattern: An emerging disease—like [Zika](#) or [Ebola](#)—infects thousands of people, but vaccines and drugs are not developed fast enough to be of any real benefit. This week, a global group called the [Coalition for Epidemic Preparedness Innovations](#) (CEPI) launched with significant funding and the aim to develop vaccines for known infectious disease threats. The goal is to have vaccines ready before an epidemic starts.

CEPI was announced Wednesday at the [World Economic Forum](#) in Davos, Switzerland, with initial funding of \$460 million from the governments of Germany, Japan and Norway, as well as the Bill & Melinda Gates Foundation and the Wellcome Trust. The group hopes to shorten the amount of time it takes to develop new vaccines for emerging diseases by embracing innovative vaccine technology and funding labs that are able to respond quickly to outbreaks.

Coalition for Epidemic Preparedness Innovations (CEPI)

Presentation to the WHO

21 July, 2017

Professor John-Arne Røttingen, Interim CEO, CEPI



Norwegian Ministry
of Foreign Affairs

BILL & MELINDA
GATES foundation

wellcome trust



DEPARTMENT OF BIOTECHNOLOGY
Ministry of Science & Technology

Why CEPI?

1

Global consensus that new and sustainable partnership models are needed for product development (vaccines, diagnostics, therapeutics) to contain outbreaks of EIDs

2

Recent outbreaks – SARS, Ebola and Zika - reveal gaps such partnerships should fill

- need for coordinated and proactive R&D and increased funding
- stronger advanced development and manufacturing capabilities
- regulatory innovations and harmonization of regulatory requirements

3

Comprehensive policy ecosystem required with a collective end-to-end vision

- Ebola response reviews/panels suggest lack of mechanisms to unite funders, developers, regulators
 - Effective coordination will require dedicated mechanisms and resources, as well as end-to-end coordination of R&D and access



News Scan for Sep 12, 2017

CEPI calls for proposals for rapid vaccine production

The Coalition for Epidemic Preparedness Innovations (CEPI) last week announced support for the development of vaccine platforms that will speed production in hopes of making the world better prepared for the next epidemic.

CEPI, in collaboration with the Bill & Melinda Gates Foundation and the US National Institute of Allergy and Infectious Diseases (NIAID), invited research and development institutions, companies, and foundations to submit proposals for new approaches to vaccine development "to radically reduce the time required for the development of new vaccines," the organization said in a news release.

"CEPI will fund vaccine platform technologies that will enable rapid vaccine development, elicit the rapid onset of immunity, and whose production can be scaled up quickly to respond to outbreaks of new or previously unrecognised infectious diseases," the release said.

New platforms should be able to identify a vaccine virus component and be ready for clinical testing in 16 weeks, have the vaccine show clinical benefit within 6 weeks of its first administration, and be able to release 100,000 vaccine doses 8 weeks after production scale-up.

Richard Hatchett, CEO of CEPI said, "Vaccines can be the insurance policy we need to combat that epidemic when it comes. Today's announcement is a call to develop vaccine platform technologies that can rapidly generate safe and effective vaccines against emerging threats. Having such platforms at the ready will represent a major advance in global health security for the whole world."

Sep 5 CEPI news release

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DUSTIN
HOFFMAN

RENE
RUSSO

MORGAN
FREEMAN

This animal carries
a deadly virus...
and the greatest
medical crisis in the world
is about to happen.



OUTBREAK

Try to remain calm.

WARNER BROS. presents

by ARNOLD KOPELSON Producer in Association with PUNCH PRODUCTIONS, INC. a WOLFGANG PETERSEN film

DUSTIN HOFFMAN RENE RUSSO MORGAN FREEMAN "OUTBREAK" CUBA GOODING, JR. PATRICK DEMPSEY and DONALD SUTHERLAND and KEVIN SPACEY

Music by JAMES NEWTON HOWARD Lyrics by KEEL TRAVIS Lyrics and Lyrics by LANCE KLEINMAN Lyrics and Lyrics by WILLIAM MOY Lyrics by WILLIAM SHIBEL

Produced by MICHAEL BALLHAUS and JAMES DUNCAN HENDERSON and ANNE KOPELSON Story by LAURENCE DUBOIS and ROBERT ROY POOL

Directed by ARNOLD KOPELSON, WOLFGANG PETERSEN and SAL KATZ Screenplay by WOLFGANG PETERSEN





MARION COTILLARD MATT DAMON LAURENCE FISHBURNE JUDE LAW GWYNETH PALTROW KATE WINSLET

NOTHING SPREADS LIKE FEAR
C O N T A G I O N



participant  imagination

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CNN FILMS

UNSEEN ENEMY

A WORLD HEALTH DAY PRESENTATION



Documentary Unseen enemy

Unseen Enemy
Written and directed by
Janet Tobias, USA, 2017.
117 mins.
For more on **Unseen Enemy** see
<http://www.takesallofus.com/>

"There is something that destroys the soul of a community when an epidemic is out of control", explains Larry Brilliant, early in *Unseen Enemy*. "It is not just the large number of casualties and the deaths, it is what it does to the social fabric". The well-meaning but flawed documentary is a call to arms. The world must ready itself for the next major disease outbreak.

A trip to a Chinese wet market offers a vivid example of the conditions from which dangerous pathogens can emerge. Bowls of blood-reddened water stand stagnant in the sun. The vendors work with disinterested efficiency, slaughtering hundreds of ducks and chickens and rinsing them in the same water in the same vessel. Customers wait in the immediate vicinity. In 2016, two-thirds of the water samples the Pasteur Institute tested in the market were positive for H5N1 influenza virus.

Influenza features prominently in *Unseen Enemy*. The film neatly outlines the dangers of the virus and the gaps in research. A foray to Minnesota personalises the tale with an account of the death of a teenage girl from seasonal influenza. The world is due an influenza pandemic, narrator Jeffrey Wright reminds us, and if it resembles the 1918 Spanish flu, a monumental number of deaths will occur. The film is on shakier ground when it advances the argument that the influenza vaccine should be taken up by everyone. It is not certain that this is either practical or desirable, especially given the vaccine's suboptimal effectiveness. Still, it is an interesting debate, and it is reasonably fleshed out.

The spread of Zika virus and its terrible effect on unborn children is ably addressed, as is the contribution of fruit bats and climate change to the emerging diseases of the past 50 years or so. But when it comes to the more complicated story of the Ebola virus disease epidemic in west Africa, *Unseen Enemy* flounders. There is no real sense of the ineptitude of the initial response, the widespread mayhem caused by the disease, the factors that led to its spread, and how a similar scenario can be avoided in the future. *Unseen Enemy* labours

but it provides scant details on what an adequate level of preparation would entail. It is not enough to simply point out that far more is spent on homeland security than is spent on biosecurity, or that an unchecked pandemic would cost trillions of dollars. The audience has to be told where the shortfalls lie, and how best they can be resolved.

When Ebola virus struck west Africa, it came out of nowhere. There was no vaccine, public awareness of the risk factors was virtually non-existent, and health-care systems were woefully ill prepared. The story offers a rich opportunity for a filmmaker to come to grips with the cultural, logistical, and scientific obstacles that threaten epidemic response. But *Unseen Enemy* spurns its chance. It skates over virtually everything of importance when assessing the Ebola virus disease outbreak. The tale of a valiant Liberian doctor is heartening, but it is not placed within the context of wider events. A glimpse of an unmanned border post between Liberia and Sierra Leone is not accompanied by a meaningful explanation of how free movement exacerbates epidemics. The crucial detail that a vaccine was eventually rushed into production is also excluded from the account.

The documentary does mention the hysterical reaction from certain quarters of the USA, where there were calls for Africans to be denied entry to the country. But this was thousands of miles from the epicentre of the outbreak. The point that epidemics generate panic is well taken, but it hardly comes as a surprise.

A discussion of smallpox feels similarly incomplete. Brilliant was part of the eradication campaign in India in the 1970s. In an intriguing aside, he explains how he was involved in the forcible vaccination of a tribe that had refused the vaccine on religious grounds. The incident elucidates the ethical tension inherent in epidemic response: individual freedom versus collective good. But *Unseen Enemy* does not add that smallpox was a disease for which there was an effective vaccine and no animal reservoir. Eradication was feasible, so the calculus involved in decisions concerning

All of which is disappointing, particularly given the impressive roster of interviewees assembled by director Janet Tobias (Peter Piot, Director of the London School of Hygiene and Tropical Medicine, and a Professor of Global Health is a particularly engaging and thoughtful presence). The resistance to delve into detail suggests a lack of faith in the audience, and it undermines the film's efforts to differentiate between the featured diseases. "Epidemics are inevitable, pandemics are not", concludes Brilliant. That might well be true, but *Unseen Enemy* singularly fails to make the case.

Talha Burki

CLF Topics

1. Yemen / global health response
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5. MERS
6. Bioterrorism / Gain-of-function research
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9. Movies and preparedness
10. Other

CDC Is Deactivating the Emergency Operations Center for the Zika Response



Press Release

For Immediate Release: Friday, September 29, 2017

Contact: [Media Relations](#)

(404) 639-3286

CDC is deactivating its emergency response for Zika virus (Zika) to transition efforts to normal program operations on September 29, 2017. On January 22, 2016, CDC activated its Emergency Operations Center (EOC) in response to the devastating effects of Zika virus infection during pregnancy. A team of experts from across the agency, called the Zika Coordination and Operations Transition Team (ZCOTT), will lead the transition from EOC activation to routine, long-term activities and will ensure timely coordination and collaboration on scientific, communication, and policy activities.

CDC's EOC is the agency's command center for monitoring and coordinating emergency response to public health threats and has been activated previously for events such as natural disasters, the 2009 H1N1 influenza pandemic, and the 2014 Ebola outbreak, among others. Since the 2016 EOC activation for Zika, experts from across the agency have worked to protect Americans, especially pregnant women, fetuses, and infants, from the emerging virus and its devastating consequences. CDC will continue its work to protect these groups by providing support for healthcare providers as they counsel pregnant women affected by Zika and provide follow-up care to their infants. CDC recognizes the continued need for coordination among federal, state, and local levels to provide services for families affected by Zika and will provide technical assistance as resources permit.

Deactivation does not mean that the threat of Zika has lessened in importance or that people are no longer at risk of infection. Zika continues to be a public health threat in the United States and internationally. Zika is still a risk for pregnant women, and the continental United States and Hawaii will continue to see some travel-related cases as travelers visit countries and territories with risk of Zika transmission. The possibility of local transmission in the continental United States and Hawaii still exists. CDC remains committed to protecting the health of Americans and will continue working to protect the nation from the threat of Zika.

As a reminder, CDC recommends travelers to [areas with a risk of Zika](#) take steps to prevent Zika by [preventing mosquito bites](#) and [sexual transmission](#) of Zika during and after travel. CDC continues to recommend that pregnant women avoid travel to areas with risk of Zika.

For more information on Zika, visit www.cdc.gov/zika.



Single mutation tied to Zika's ability to cause microcephaly, GBS

Filed Under: [Zika](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Sep 28, 2017



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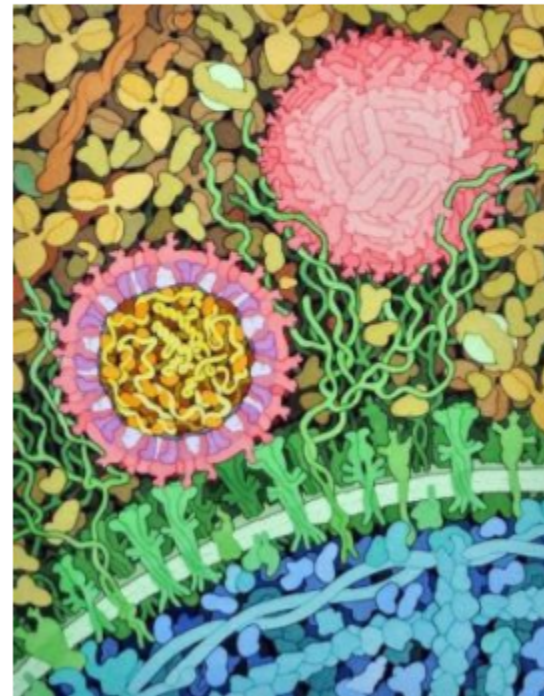
A study today in *Science* posits that a single genetic mutation that occurred in the Zika virus in 2013 allowed the mosquito-borne pathogen to become more infective and cause microcephaly and Guillain-Barre syndrome.

The work was done by researchers from the Chinese Academy of Sciences in Beijing. They compared Zika virus strains from the 2015 and 2016 South American epidemics with an ancestral Cambodian virus that was circulating in 2010.

According to the study, one change, known as S139N, which switched a serine to a glutamine at the 139th position of a structural protein within the pathogen's protective coat, made the virus deadlier to neuron precursor cells.

Evolution to congenital pathogen

To demonstrate if this change led to microcephaly and



RCSB Protein Data Bank, Wellcome Images

Media centre

WHO scales up response to plague in Madagascar

News release

1 OCTOBER 2017 | GENEVA - WHO is rapidly scaling up its response to an outbreak of plague in Madagascar that has spread to the capital and port towns, infecting more than 100 people in just a few weeks.

The Government of Madagascar has confirmed that the death of a Seychellois national was due to pneumonic plague. The basketball coach died in hospital in Antananarivo on Wednesday (September 27) while visiting the island nation for a sports event.

Health authorities are tracing people with whom he came into contact in recent days and who may have become exposed to the illness. Once identified, they will be given antibiotics to prevent infection as a precautionary measure.

The incident brings the death count to 21 since the outbreak was identified in late August; at least 114 people have been infected.

“WHO is concerned that plague could spread further because it is already present in several cities and this is the start of the epidemic season, which usually runs from September to April,” said Dr. Charlotte Ndiaye, WHO Representative in Madagascar.



News Scan for Oct 02, 2017

WHO steps up Madagascar plague outbreak response as cases top 130

The World Health Organization (WHO) announced yesterday that it is scaling up its response to a plague outbreak in Madagascar that has spread to the capital and port cities in recent weeks over the past few weeks, resulting in more than 100 infections.

In an update today, the WHO said that, as of Sep 30, Madagascar has reported 73 suspected, probable, and confirmed cases of pneumonic plague, 17 of them fatal. Besides the pneumonic cases, Madagascar has reported 58 cases of bubonic plague, 7 of them fatal. The latest totals reflect increases of 22 pneumonic and 5 bubonic plague cases since the WHO's first outbreak announcement on Sep 29.

A case of septicemic plague has also been reported, for a total of 132, which is 27 more cases than the WHO reported just 3 days ago. The event is Madagascar's second plague outbreak this year.

Ten cities have reported pneumonic plague cases, including the capital city of Antananarivo and its suburbs, Toamasina and Faratsiho.

On Sep 27, a basketball player from the Seychelles who was in Madagascar participating in championship games died in a Madagascar hospital from pneumonic plague, triggering an investigation into his close contacts, who have received prophylactic treatment.



POLICY FORUM

GLOBAL HEALTH

Reducing antimicrobial use in food animals

Consider user fees and regulatory caps on veterinary use

By Thomas P. Van Boeckel,¹ Emma E. Glennon,^{2,3} Dora Chen,^{2,4} Marius Gilbert,^{5,6} Timothy P. Robinson,^{7,8} Bryan T. Grenfell,^{4,9} Simon A. Levin,^{4,10} Sebastian Bonhoeffer,¹ Ramanan Laxminarayan^{2,10}

The large and expanding use of antimicrobials in livestock, a consequence of growing global demand for animal protein, is of considerable concern in light of the threat of antimicrobial resistance (AMR). Use of antimicrobials in animals has been linked to drug-resistant infections in animals (1) and humans (2). In September 2016, the United Nations (UN) General Assembly recognized the inappropriate use of antimicrobials in animals as a leading cause of rising AMR. In September 2018, the interagency group established by the UN Secretary General will report on progress in the global response to AMR, including antimicrobial consumption in animals. We provide a baseline to monitor efforts to reduce antimicrobial use and assess how three global policies might curb antimicrobial consumption in food animal production: (i) enforcing global regulations to cap antimicrobial use, (ii) adherence to nutritional guidelines leading to reduced meat consumption, and (iii) imposing a global user fee on veterinary antimicrobial use.

The rise of AMR in zoonotic pathogens, including to last-resort drugs such as colistin (3), is an important challenge for human

medicine because it can lead to untreatable infections. Evidence linking AMR between animals and humans is particularly strong for common foodborne pathogens resistant to quinolones, such as *Campylobacter* spp. and *Salmonella* spp. (4). AMR is also a threat to the livestock sector and thus to the livelihoods of millions who raise animals for subsistence (5).

The primary driver for the accumulation of harmful resistance genes in the animal reservoir is the large quantity of antimicrobials used in animal production (6). Antimicrobial use in livestock, which in many countries outweighs human consumption (7), is primarily associated with the routine use of antimicrobials as growth promoters or their inappropriate use as low-cost substitutes for hygiene measures that could otherwise prevent infections in livestock.

In Europe, regulations have been the principal instrument to limit antimicrobial use in animal production. In the United States, consumer preferences have driven companies to reduce antimicrobial use in animals, although the impact on livestock rearing practices is still nascent (8). Some European countries maintain highly productive livestock sectors while using less than half the current global average amount of antimicrobial per kilogram of animal (50 mg/kg). Therefore, this threshold has been proposed as a potential target for global regulations on veterinary antimicrobial use (9). However, the impact that such policies would have on the global consumption of antimicrobials has yet to be quantified.

A second solution to reduce antimicrobial consumption in animal production may be

this measure could have an indirect but substantial impact on the global consumption of veterinary antimicrobials. A third solution to cut antimicrobial use would be to charge a user fee, paid by veterinary drug users, on sales of antimicrobials for nonhuman use (11). This approach has recently received support from the World Bank (12) on the basis that the associated revenues could be injected into a global fund to stimulate discovery of new antimicrobials and support efforts to preserve existing drugs (13). Without further analysis, however, it is unclear whether a user fee policy could achieve a meaningful reduction in the global consumption of veterinary antimicrobials, let alone generate sufficient revenues to support improved livestock rearing practices or the development of new drugs, vaccines, and diagnostics.

GLOBAL TRENDS

Veterinary antimicrobial sales volumes were obtained via public records for 38 countries and self-governing dependencies and estimated for 190 more (supplementary materials). In 2013, the global consumption of all antimicrobials in food animals was estimated at 131,109 tons [95% confidence interval (CI) (100,812 to 190,492 tons)] and is projected to reach 200,235 tons [95% CI (150,848 to 297,034 tons)] by 2030. Consumption levels varied considerably between countries, ranging from 8 mg/population correction unit (PCU) (a kilogram of animal product) in Norway to 318 mg/PCU in China (see fig. S1). As the largest consumer of veterinary antimicrobials, both in relative (per PCU) and in absolute terms, China has an important leadership role with regard to its response to AMR and has already set precedents in phas-

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Questions, Comments and Discussion



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