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University of Minnesota

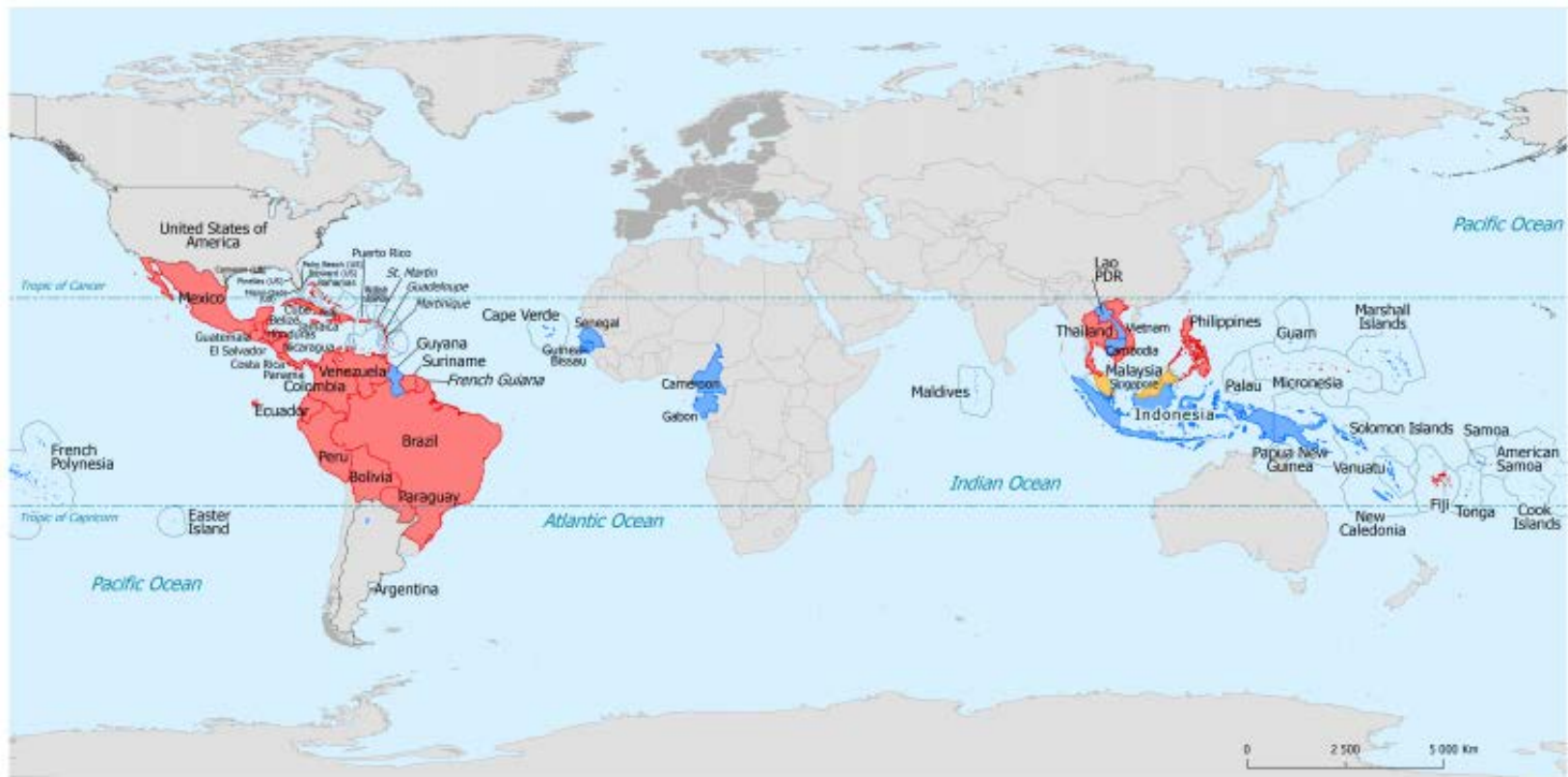
**CIDRAP Leadership Forum
Infectious Disease BRIEFING**

December 14th, 2016

- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
 - Flu vaccine
- 3. Antimicrobial resistance**
- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

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- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

Countries or territories with reported confirmed autochthonous cases of Zika virus infection in the past three months, as of 9 December 2016



- Widespread transmission in the past three months
- Sporadic transmission in the past three months
- Past transmission (2007 – three months ago)
- EU/EEA Member States, including outermost regions
- Other countries and territories
- Maritime Exclusive Economic Zones for non-visible areas

Molecular evolution of Zika virus as it crossed the Pacific to the Americas

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Accepted 20 September 2016

Abstract

Zika virus was previously considered to cause only a benign infection in humans. Studies of recent outbreaks of Zika virus in the Pacific, South America, Mexico and the Caribbean have associated the virus with severe neuropathology. Viral evolution may be one factor contributing to an apparent change in Zika disease as it spread from Southeast Asia across the Pacific to the Americas. To address this possibility, we have employed computational tools to compare the phylogeny, geography, immunology and RNA structure of Zika virus isolates from Africa, Asia, the Pacific and the Americas. In doing so, we compare and contrast methods and results for tree search and rooting of Zika virus phylogenies. In some phylogenetic analyses we find support for the hypothesis that there is a deep common ancestor between African and Asian clades (the “Asia/Africa” hypothesis). In other phylogenetic analyses, we find that Asian lineages are descendent from African lineages (the “out of Africa” hypothesis). In addition, we identify and evaluate key mutations in viral envelope protein coding and untranslated terminal RNA regions. We find stepwise mutations that have altered both immunological motif sets and regulatory sequence elements. Both of these sets of changes distinguish viruses found in Africa from those in the emergent Asia–Pacific–Americas lineage. These findings support the working hypothesis that mutations acquired by Zika virus in the Pacific and Americas contribute to changes in pathology. These results can inform experiments required to elucidate the role of viral genetic evolution in changes in neuropathology, including microcephaly and other neurological and skeletomuscular issues in infants, and Guillain-Barre syndrome in adults.

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Introduction

Zika virus is a flavivirus that has recently emerged as an agent of severe disease in humans and human fetuses in the Americas after island-hopping across the Pacific. Flaviviridae are a family of positive sense single-stranded RNA viruses that include Dengue virus, Yellow fever virus, West Nile Virus and Japanese Encephalitis virus among others. The Zika virus reference genome sequence (National Center for

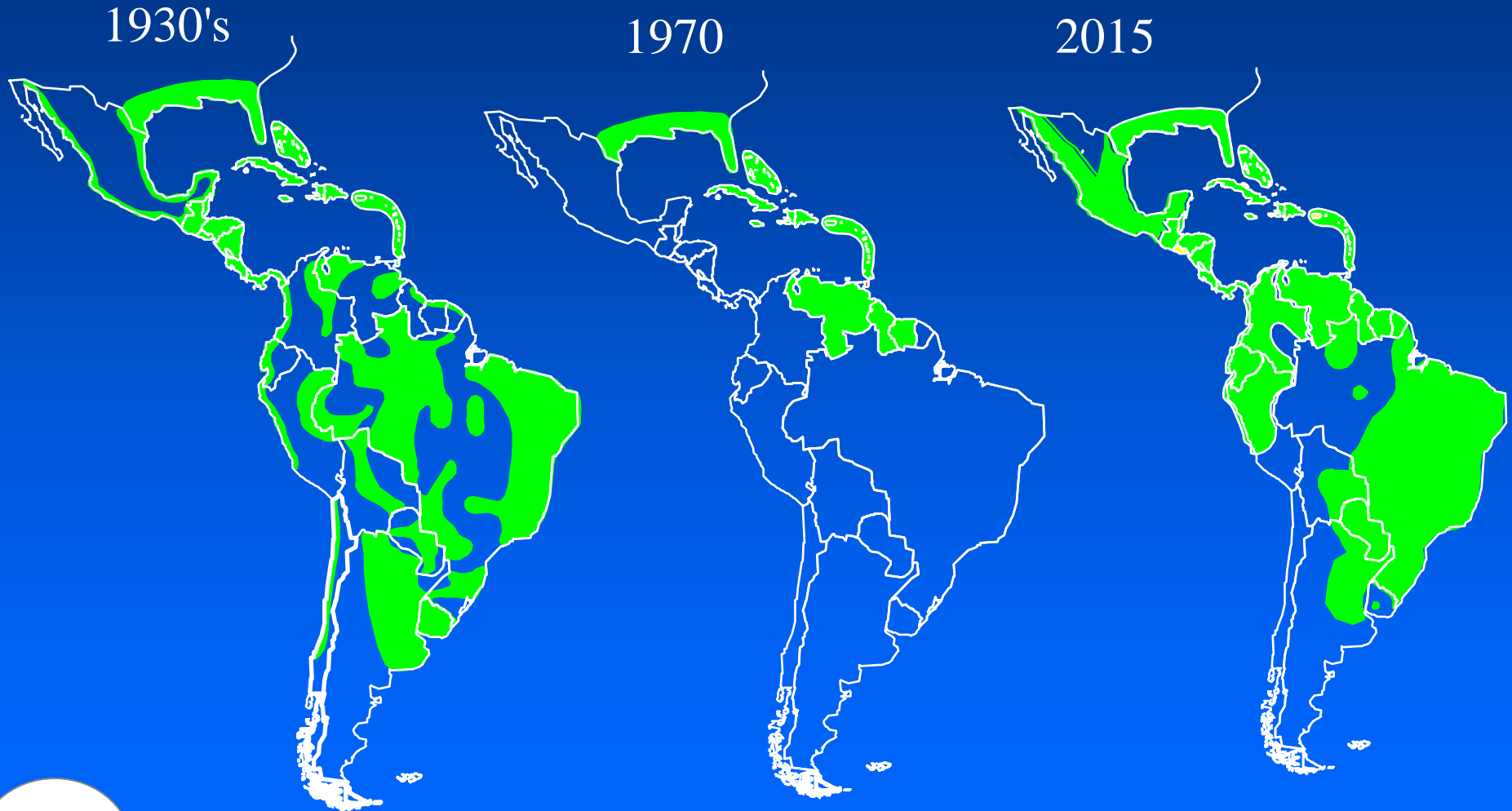
Biotechnology Information (NCBI; ncbi.nlm.nih.gov) accession NC_012532.1; strain MR766 from Uganda) comprises 10 794 bases of linear RNA. The 5' and 3' untranslated regions of the Zika virus genome form complex RNA structures that interact and regulate the replication, gene expression and tissue tropism of the virus when it infects a host cell. The remainder of the Zika virus genome codes for a 3419 amino acid polyprotein with at least 12 proteins (Haddow et al., 2012).

Zika virus was initially discovered by isolation from

Aedes aegypti



Aedes aegypti Distribution in the Americas



Adapted from Gubler, 1998



Study confirms 4-fold rise in Zika microcephaly in Colombia

Filed Under: [Zika](#)

[Lisa Schnirring](#) | News Editor | [CIDRAP News](#) | Dec 09, 2016

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Over the past year, experts have wondered if Colombia —hit with Zika virus after Brazil—would see a rise in Zika-related microcephaly similar to that witnessed in Brazil. Colombia has officially reported some microcephaly cases (476, including 44 pregnancy losses), but nowhere near the level seen in Brazil, raising questions about the impact of the virus.

Today researchers from Colombia and the US Centers for Disease Control and Prevention (CDC) reported a fourfold increase in microcephaly following the country's Zika outbreaks, suggesting that the rise isn't unique to Brazil and signaling that other outbreak countries are likely to see similar rises.

The report adds more evidence to the body of literature linking the virus to a rise in microcephaly cases.



PAHO / Flickr cc

Zika Pregnancies And Big Questions In Puerto Rico

November 29, 2016 · 10:04 AM ET



The number of new Zika cases in Puerto Rico has dropped dramatically in recent weeks, yet health officials worry the full effect of the outbreak on the island may not be known for months or years to come.

Puerto Rico has [confirmed more than 34,000](#) Zika infections since the virus was first detected on the island in November 2015.

Tyler M. Sharp, acting head of epidemiology at the Center for Disease Control and Prevention's Dengue Branch in San Juan, says the outbreak peaked during the summer.

"In mid-August we were at more than 2,000 [confirmed] lab cases per week coming in," [Sharp](#) says. "Now we are at a little over 200 per week, so the numbers are down from where they were at the worst part of the outbreak. But there is continued transmission, so there's continued risk both to pregnant women and everybody else who's present on the island."

The Telegraph

First case of sexually transmitted Zika virus in the UK



By **Telegraph Reporters**

1 DECEMBER 2016 • 1:30AM

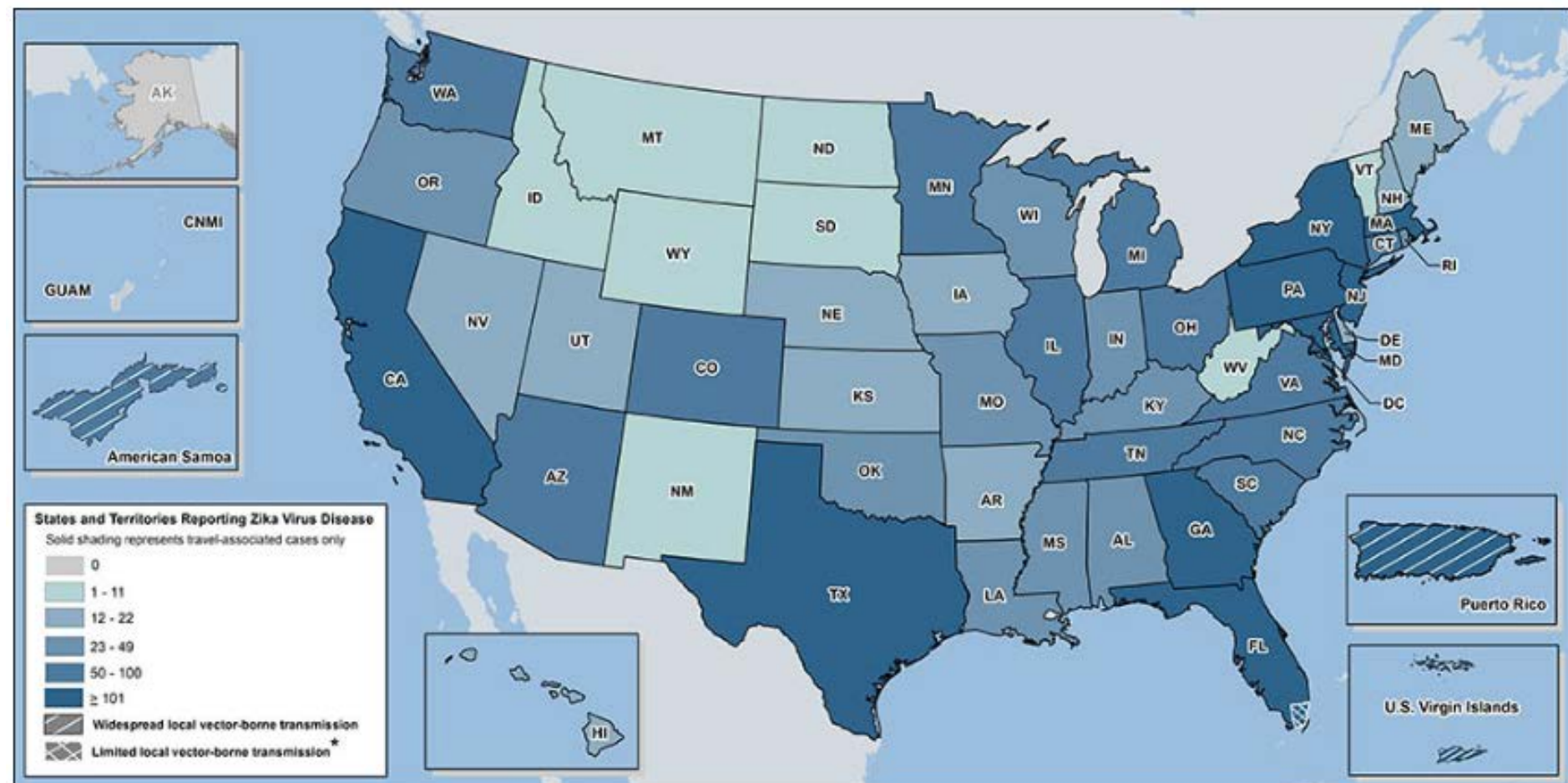
A woman in the UK is thought to have been infected with the Zika virus through sexual transmission, health officials have said.

Public Health England (PHE) said that one case of "likely sexual transmission" of Zika virus infection has been reported in the UK.

Meanwhile, of the 265 travel-associated cases reported in Britain, seven have been diagnosed in pregnant women, PHE said.

Zika Cases Reported in the United States

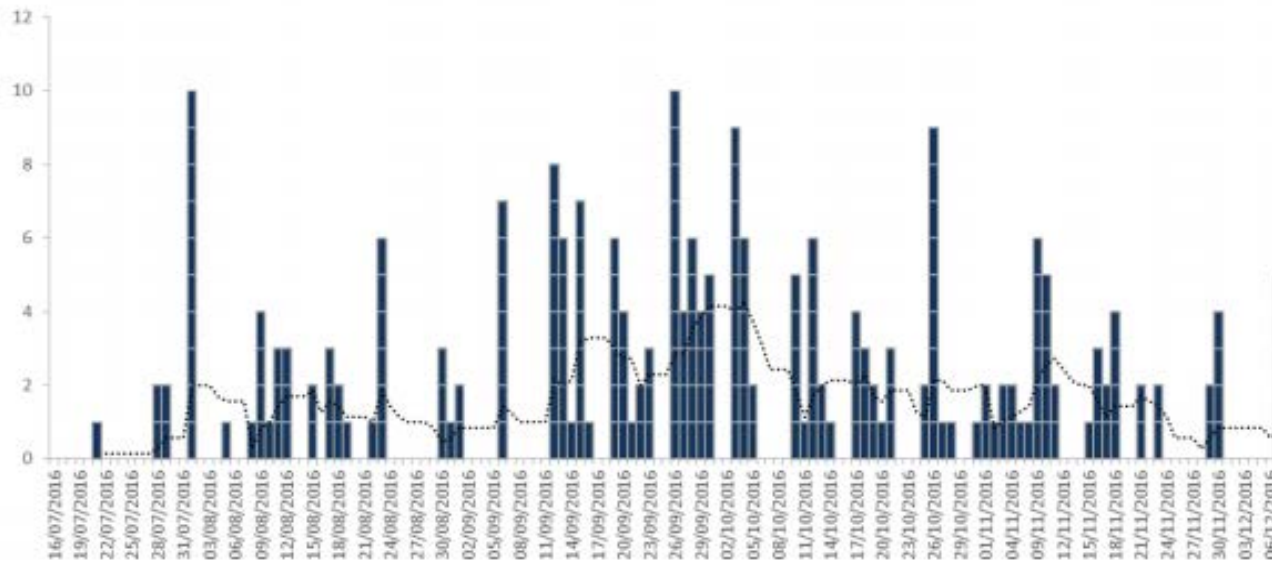
Laboratory-confirmed Zika virus disease cases reported to ArboNET by state or territory (as of December 7, 2016)



Distribution of locally acquired Zika cases in Florida State (US), by reporting date, from 16 July 2016 to 7 December 2016

ECDC: (Adapted from Florida health department and media)

Distribution of locally acquired Zika cases* in Florida State in Florida residence, by reporting date, from 16 July 2016 to 7 December 2016



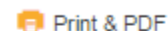
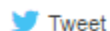
..... Moving average over seven days period

* Due to reclassification 19 cases are not visible in this graph

Zika counts rise in Florida as more nations note microcephaly

Filed Under: [Zika](#)

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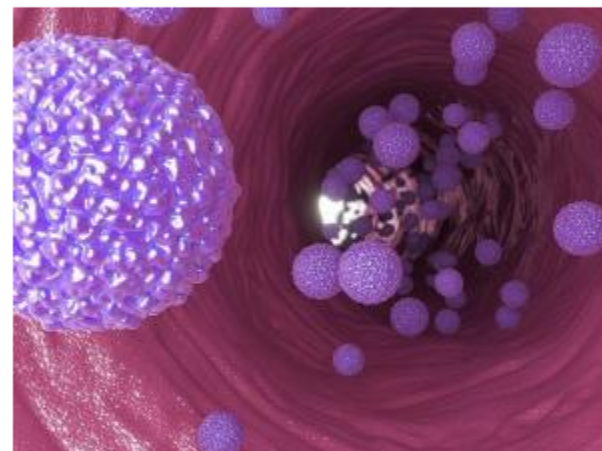
Florida officials have confirmed more locally transmitted Zika, and Argentina and Guadeloupe have reported their first congenital microcephaly cases.

Ongoing spread in Miami Beach, Little River

The Florida Department of Health (Florida Health) reported six new cases of locally acquired Zika yesterday and today.

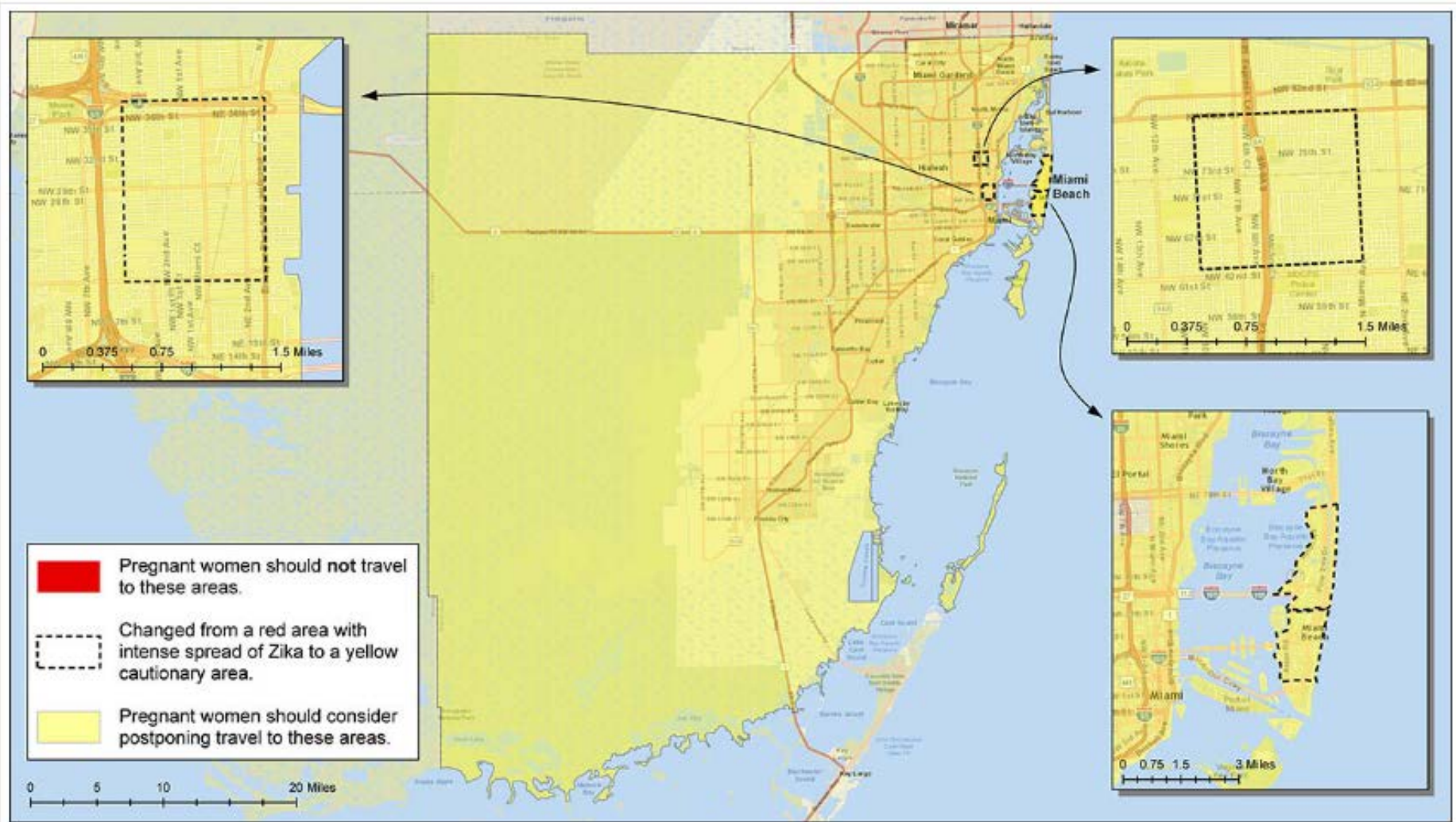
Yesterday the Florida Health reported three new locally acquired cases of Zika, and one new case in a non-Florida resident who had recently traveled to Miami. Two of the local cases occurred in Miami-Dade County residents, and the other involves a Broward County resident.

Though investigations are still under way to determine where the four cases were acquired, Florida Health says that Miami Beach and Little River, two neighborhoods in Miami-Dade County, are still the only places in the state where active transmission is taking place.



Maurizio De Angelis, Wellcome Images / Flickr cc

Active Zika Virus Transmission in Florida



Miami-Dade County, FL. Red shows areas where pregnant women should not travel. Yellow shows areas where pregnant women should consider postponing travel.



Rio Grande Valley, Texas, reports first case of local Zika

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Today the Texas Department of State Health Services (TDSHS) reported a case of locally acquired Zika in Cameron County, a first for a state that has been on high alert for local transmission since the beginning of October and the first local US case outside of Florida.

"We knew it was only a matter of time before we saw a Zika case spread by a mosquito in Texas," John Hellerstedt, MD, TDSHS commissioner, said in a press release. "We still don't believe the virus will become widespread in Texas, but there could be more cases, so people need to protect themselves from mosquito bites, especially in parts of the state that stay relatively warm in the fall and winter."

So far, one patient, a non-pregnant woman with no recent travel or sexual transmission risks, has been diagnosed as having locally acquired Zika. The disease was confirmed through urine analysis late last week. According to the US Centers for Disease Control and Prevention (CDC) the patient lives in Brownsville, Texas.



Jimmy Emerson, DVM / Flickr cc

Cameron County Courthouse in Brownsville, where local transmission has been confirmed.

Zika zones end in Florida as Texas reports 4 new cases

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Lisa Schnirring | News Editor | CIDRAP News | Dec 09, 2016

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In a flurry of Zika developments today, Florida said local transmission has ended in the final affected area of Miami, and Texas reported four more locally acquired cases.

Florida lifts final zone

At a media briefing in Miami Beach today, Florida Gov. Rick Scott announced that the final Zika transmission zone has been lifted, a 1.5-square-mile area of South Miami Beach, the *Miami Herald* reported.

Officials said today that the South Miami Beach area has now met the Centers for Disease Control and Prevention (CDC) criteria for when transmission ends: 45 days without a new case inside the designated zone. Florida announced its first local case on Jul 29, and at one time had four active transmission areas. So far the state has reported 249 local cases, with 15 more people who may have been exposed locally or abroad.



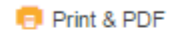
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Groups report first Zika glaucoma, new 'minibrain' findings

Filed Under: [Zika](#)

Lisa Schnirring | News Editor | CIDRAP News | Dec 01, 2016



Adding another serious condition to the list of Zika complications, a team from Brazil and the United States published the first report of glaucoma in a baby born with severe virus-related birth defects.

Clinicians have already documented eye problems in the posterior part of the eye in babies born with Zika virus, but the new report, published in the journal *Ophthalmology*, is the first to describe a problem involving the anterior chamber. Glaucoma can permanently damage the optic nerve, leading to blindness.

In other developments, researchers reported new findings on the vulnerability of developing fetal brain cells to Zika virus, while health officials released new case updates, including England's first sexually transmitted infection, more local cases in Florida, and Bolivia's first Zika-related Guillain-Barre syndrome (GBS) case.



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More data show Zika viremia in mothers, fetal infection link

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Spanish researchers today reported more evidence of Zika replication in the fetus or placenta, describing persistent viremia lasting more than 100 days after symptom onset in a mother of a baby born with microcephaly.

In other developments, Florida reported five more local Zika cases, all involving people who were sick earlier this fall, and researchers from England who reviewed studies on the effectiveness of mosquito control methods found weak evidence for some of the common strategies.

Prolonged viremia and fetal infections

The patient in the Spanish report is a woman who contracted a Zika infection in December 2015 while visiting Colombia, her home country. The group reported the findings in a letter to the *New England Journal of Medicine*.

Her Zika symptoms began when she was 9 weeks pregnant, and blood tests for Zika virus were positive for 89 days—until she was 29 weeks along. The reverse-transcriptase polymerase chain reaction (RT-



Ken Hurst / iPhoto



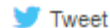
Zika linked to hearing and vision complications in adults

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[Stephanie Soucheray](#) | [News Reporter](#) | [CIDRAP News](#) | [Dec 08, 2016](#)



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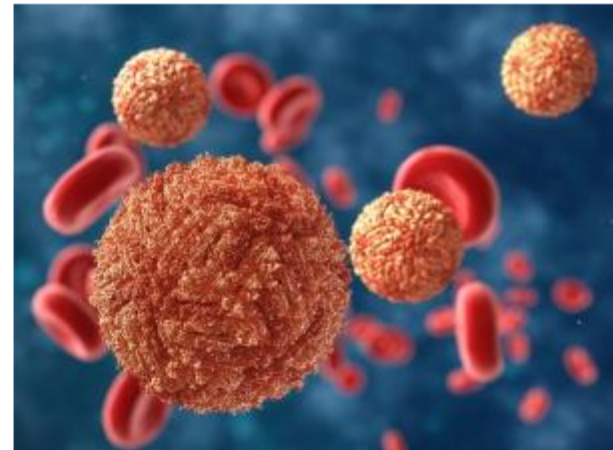


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Two studies released today detail Zika-related ear and eye problems while the US Centers for Disease Control and Prevention (CDC) and World Health Organization (WHO) updated their weekly Zika numbers.

Acute hearing loss, eye inflammation

In a new study published in *Clinical Infectious Diseases*, Brazilian researchers detailed three cases of acute, transient hearing loss in adults who were infected with Zika virus. All patients were admitted to an ear, nose, and throat emergency department in the summer of 2015. One patient had laboratory-confirmed Zika, and the other two were probably infected with the flavivirus.



urfinguss / iStock

These are the first cases of acute hearing losses described during the current epidemic that began in Brazil.

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Zika Virus Infection in Pregnant Women in Rio de Janeiro

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ABSTRACT

BACKGROUND

Zika virus (ZIKV) has been linked to central nervous system malformations in fetuses. To characterize the spectrum of ZIKV disease in pregnant women and infants, we followed patients in Rio de Janeiro to describe clinical manifestations in mothers and repercussions of acute ZIKV infection in infants.

METHODS

We enrolled pregnant women in whom a rash had developed within the previous 5 days and tested blood and urine specimens for ZIKV by reverse-transcriptase–polymerase-chain-reaction assays. We followed women prospectively to obtain data on pregnancy and infant outcomes.

RESULTS

A total of 345 women were enrolled from September 2015 through May 2016; of these, 182 women (53%) tested positive for ZIKV in blood, urine, or both. The timing of acute ZIKV infection ranged from 6 to 39 weeks of gestation. Predominant maternal clinical features included a pruritic descending macular or maculopapular rash, arthralgias, conjunctival injection, and headache; 27% had fever (short-term and low-grade). By July 2016, a total of 134 ZIKV-affected pregnancies and 73 ZIKV-unaffected pregnancies had reached completion, with outcomes known for 125 ZIKV-affected and 61 ZIKV-unaffected pregnancies. Infection with chikungunya virus was identified in 42% of women without ZIKV infection versus 3% of women with ZIKV infection ($P<0.001$). Rates of fetal death were 7% in both groups; overall adverse outcomes were 46% among offspring of ZIKV-positive women versus 11.5% among offspring of ZIKV-negative women ($P<0.001$). Among 117 live infants born to 116 ZIKV-positive women, 42% were found to have grossly abnormal clinical or

The authors' full names, academic degrees, and affiliations are listed in the Appendix. Address reprint requests to Dr. Brasil at Laboratório de Doenças Febris Agudas, INI, Fiocruz, 4365 Av Brasil, Rio de Janeiro-RJ 21040-900, or at patricia.brasil33@gmail.com, or to Dr. Nielsen-Saines at the Division of Pediatric Infectious Diseases, David Geffen School of Medicine at UCLA, MDCC 22-442, 10833 LeConte Ave., Los Angeles, CA 90095, or at knielsen@mednet.ucla.edu.

A preliminary version of this article was published on March 4, 2016, at NEJM.org.

N Engl J Med 2016;375:2321-34.

DOI: 10.1056/NEJMoa1602412

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4 in 10 babies born after Zika infection may have brain defects, researchers say

By HELEN BRANSWELL [@HelenBranswell](#)

DECEMBER 13, 2016

The toll that Zika virus takes on pregnancies appears to be even higher than was previously estimated, with a [newly updated study](#) from Brazil suggesting that 42 percent of infants infected in the womb may have significant [birth defects](#).

When the authors factored in stillbirths and miscarriages suffered by women who had been infected with Zika, 46 percent of pregnancies were affected. Microcephaly — a condition in which babies are born with smaller than normal heads — was seen in only about 3 percent of babies in the study.

“Microcephaly is just the tip of the iceberg. It’s definitely not where the focus should be,” said Dr. Karin Nielsen-Saines, the paper’s senior author. “For every case of microcephaly you’re probably going to have 10 cases of other problems that haven’t been recognized.”

JAMA | Original Investigation

Birth Defects Among Fetuses and Infants of US Women With Evidence of Possible Zika Virus Infection During Pregnancy

Margaret A. Honein, PhD; April L. Dawson, MPH; Emily E. Petersen, MD; Abbey M. Jones, MPH; Ellen H. Lee, MD; Mahsa M. Yazdy, PhD; Nina Ahmad, MD; Jennifer Macdonald, MPH; Nicole Evert, MS; Andrea Bingham, PhD; Sascha R. Ellington, MSPH; Carrie K. Shapiro-Mendoza, PhD; Titilope Oduyebo, MD; Anne D. Fine, MD; Catherine M. Brown, DVM; Jamie N. Sommer, MS; Jyoti Gupta, MPH; Phillip Cavicchia, PhD; Sally Slavinski, DVM; Jennifer L. White, MPH; S. Michele Owen, PhD; Lyle R. Petersen, MD; Coleen Boyle, PhD; Dana Meaney-Delman, MD; Denise J. Jamieson, MD; for the US Zika Pregnancy Registry Collaboration

IMPORTANCE Understanding the risk of birth defects associated with Zika virus infection during pregnancy may help guide communication, prevention, and planning efforts. In the absence of Zika virus, microcephaly occurs in approximately 7 per 10 000 live births.

OBJECTIVE To estimate the preliminary proportion of fetuses or infants with birth defects after maternal Zika virus infection by trimester of infection and maternal symptoms.

DESIGN, SETTING, AND PARTICIPANTS Completed pregnancies with maternal, fetal, or infant laboratory evidence of possible recent Zika virus infection and outcomes reported in the continental United States and Hawaii from January 15 to September 22, 2016, in the US Zika Pregnancy Registry, a collaboration between the CDC and state and local health departments.

EXPOSURES Laboratory evidence of possible recent Zika virus infection in a maternal, placental, fetal, or infant sample.

MAIN OUTCOMES AND MEASURES Birth defects potentially Zika associated: brain abnormalities with or without microcephaly, neural tube defects and other early brain malformations, eye abnormalities, and other central nervous system consequences.

RESULTS Among 442 completed pregnancies in women (median age, 28 years; range, 15-50 years) with laboratory evidence of possible recent Zika virus infection, birth defects potentially related to Zika virus were identified in 26 (6%; 95% CI, 4%-8%) fetuses or infants. There were 21 infants with birth defects among 395 live births and 5 fetuses with birth defects among 47 pregnancy losses. Birth defects were reported for 16 of 271 (6%; 95% CI, 4%-9%) pregnant asymptomatic women and 10 of 167 (6%; 95% CI, 3%-11%) symptomatic pregnant women. Of the 26 affected fetuses or infants, 4 had microcephaly and no reported neuroimaging, 14 had microcephaly and brain abnormalities, and 4 had brain abnormalities without microcephaly; reported brain abnormalities included intracranial calcifications, corpus callosum abnormalities, abnormal cortical formation, cerebral atrophy, ventriculomegaly, hydrocephaly, and cerebellar abnormalities. Infants with microcephaly (18/442) represent 4% of completed pregnancies. Birth defects were reported in 9 of 85 (11%; 95% CI, 6%-19%) completed pregnancies with maternal symptoms or exposure exclusively in the first trimester (or first trimester and periconceptional period), with no reports of birth defects among fetuses or infants with prenatal exposure to Zika virus infection only in the second or third trimesters.

CONCLUSIONS AND RELEVANCE Among pregnant women in the United States with completed pregnancies and laboratory evidence of possible recent Zika infection, 6% of fetuses or infants had evidence of Zika-associated birth defects, primarily brain abnormalities and microcephaly, whereas among women with first-trimester Zika infection, 11% of fetuses or infants had evidence of Zika-associated birth defects. These findings support the importance of screening pregnant women for Zika virus exposure.

← Editorial

+ Supplemental content

Author Affiliations: Author affiliations are listed at the end of this article.

Group Information: The US Zika Pregnancy Registry Collaboration members are listed at the end of this article.

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Study: Zika virus can linger on hard surfaces

Filed Under: [Zika](#)

[Lisa Schnirring](#) | News Editor | [CIDRAP News](#) | Nov 15, 2016

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Zika virus can be transmitted from an environmental source—underscored by a worker infected from a needle stick injury in a Pennsylvania lab earlier this year—and a study today found that it can survive several hours on nonporous surfaces but is easily killed by commonly used disinfectants.

In other developments, the California Department of Public Health (CDPH) in a holiday travel warning yesterday said local spread is occurring in many of Mexico's most popular tourist destinations and in one state that borders Arizona.



Vicheslav / iStock

Disinfection differed on surfaces with blood

The study of Zika survival on surfaces was presented in Denver at the annual meeting of the American Association of Pharmaceutical Scientists (AAPS).

Zika can live on hard, nonporous surfaces for as long as 8 hours, and possibly longer if the environment contains blood, common in real-world healthcare settings, S. Steve Zhou, PhD, study lead and director of virology at Pittsburgh-based Microbac Laboratories, said in an AAPS press release.



Zika



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Last updated Dec 2, 2016

Latest Cases & General Information

[Zika virus \(CDC landing page\)](#)

[Latest Zika situation reports \(WHO\)](#)

[Zika virus infections and complications called Public Health Emergency of International Concern \(WHO, Feb 1, 2016\)](#)

[Zika virus disease, frequently asked questions about Zika virus \(WHO Emergencies Preparedness, Response\)](#)

[Zika virus infection \(PAHO/WHO landing page\)](#)



Maps

[Current Zika transmission \(ECDC\)](#)

[2016 Zika outbreak timeline map \(HealthMap\)](#)

[Pacific Disaster Center maps \(updated periodically\)](#)

[Zika in the United States, explained in 9 maps \(Vox, Aug 4, 2016\)](#)

[Zika cases in the United States \(New York Times, Jul 29, 2016\)](#)

[Maps predict possible Zika hot spots \(USA Today, Apr 28, 2016\)](#)

[Mapping global environmental suitability for Zika virus \(eLife study, Apr 19, 2016\)](#)

Yellow Fever Epidemic in Africa Shows Gaps in Vaccine Pipeline

Global Health

By DONALD G. McNEIL Jr. DEC. 5, 2016

The yellow fever outbreak in Africa this year came closer to being a disaster than is widely recognized, public health experts recently disclosed. The epidemic also revealed glaring weaknesses in the emergency vaccine supply pipeline.

The first deaths in Angola were misdiagnosed as food poisoning; the global emergency vaccine stockpile was depleted before even one city was fully protected; and diagnostic laboratories were so far away that it was months before the scope of the outbreak was clear and [a worldwide alarm was raised](#).

Ultimately, the yellow fever outbreak was halted only by a huge vaccination campaign that stretched supplies by diluting doses, and even that succeeded only because some unusual donors stepped in.

Brazil contributed 18 million doses of yellow fever vaccine — three times the amount in the emergency stockpile — to contain the African outbreak. Even South Sudan, one of the world's poorest nations, gave up 400,000 doses intended for its children.





News Scan for Nov 21, 2016

PAHO reports 231 new chikungunya cases in the Americas

After reporting well over 100,000 new chikungunya cases a week ago, the Pan American Health Organization (PAHO) late last week reported only 231 new cases, mostly in Guatemala.

Countries and territories in the Americas this year have now reported 441,306 suspected, confirmed, and imported cases, according to the Nov 18 PAHO update. The 2 previous weeks saw increases of 440 and 137,528 new cases, respectively.

Guatemala saw the largest increase, with 209 new cases and 5,036 for the year. Costa Rica had 87 new cases, to bring its 2016 total to 3,215. Colombia, in contrast, dropped its official count by 121 cases, from 19,399 to 19,278.

Many countries, however, have not reported for several weeks. Brazil, which was largely responsible for the previous week's large spike as it did catch-up reporting, has yet to report on its most recent 9 weeks of data. Brazil has by far the most cases this year, at 352,810.

PAHO reported no new chikungunya-related deaths last week, leaving that figure at 135.

Starting in late 2013 on the Caribbean island of St. Martin, the Americas' chikungunya outbreak has now sickened 2,319,746 people.

Nov 18 PAHO update



News Scan for Dec 12, 2016

PAHO reports only 256 new chikungunya cases

For the third update in a row, the Pan American Health Organization (PAHO) late last week reported low chikungunya numbers, with only 256 new cases.

The previous two updates noted only 231 and 305 new cases, respectively. Countries and territories in the Americas this year have now reported 441,867 suspected, confirmed, and imported cases, according to PAHO's Dec 9 report.

Guatemala reported the most new cases, with 133. It now has 5,169 cases for the year. Bolivia was next with 31 new cases and 20,804 for the year.

Many nations, however, are behind in their reporting to PAHO on the disease. Brazil, for example, which has logged about 80% of the cases so far in 2016 and noted more than 100,000 new cases in a catch-up report in early November, has not reported on the latest 3 months' of data.

The outbreak started in late 2013 on the Caribbean island of St. Martin, and has now sickened 2,320,307 people.

Dec 9 PAHO update

- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
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- 3. Antimicrobial resistance**
- 4. Ebola**
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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.



ALL Findings

Update on Avian Influenza Findings Poultry Findings Confirmed by USDA's National Veterinary Services Laboratories

Animal Health
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Program Overview
Animal Disease Information
Emergency Management
Export from the U.S.
Import into the U.S.
Laboratory Information Services

223
Detections Reported

48,091,293
Birds Affected

12/19/14
First Detection Reported

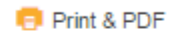
6/17/15
Last Detection Reported



H5N8 expands reach along Baltic, other parts of Europe

Filed Under: [Avian Influenza \(Bird Flu\)](#)

[Stephanie Soucheray](#) | [News Reporter](#) | [CIDRAP News](#) | [Nov 10, 2016](#)



Croatia confirmed H5N8 in wild swans, while the Netherlands and Denmark are investigating suspected cases of the highly pathogenic avian flu. Germany also found the strain in a new region of that country.

The events signal ongoing rapid developments in the spread of H5N8, first to India and then to several countries in Europe.



dicaug58 / Flickr cc

Croatia confirms H5N8 as disease spreads along Baltic

Yesterday and today more countries across Europe reported H5N8, a highly pathogenic avian influenza that experts predicted would be spreading southward and westward after the H5 clade was found in migratory birds in Russia in June. The strain targets wild birds, waterfowl, and poultry, and will likely circulate through next spring.


The World Organization for Animal Health (OIE) reported Croatia's first case of H5N8 in 10 wild swans found dead in the River Bidj, near the border with Bosnia and Herzegovina. The outbreak occurred on Oct 30 and is ongoing. Only two of the swans were available for laboratory testing, and H5N8 was confirmed. Last week, Hungary also reported H5N8 in wild swans.

H5N8 noted in more European nations, spreading elsewhere

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Lisa Schnirring | News Editor | CIDRAP News | Nov 28, 2016

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Three more countries in Europe—Finland, France, and Romania—reported their first highly pathogenic H5N8 avian influenza outbreaks over the past few days, part of a recent wave of activity linked to migratory birds from Russia, bringing the number of affected European countries to 13.

Meanwhile, veterinary officials in India and Iran reported more H5N8 outbreaks, while earlier affected European countries reported new developments, including major poultry culls.

Outbreaks in Finland, France, Romania

The three newest detections in Europe all involved waterfowl—wild ducks in Finland and France and wild swans in Romania.

Finland's agriculture ministry said about 60 tufted ducks were found dead in locations around the Aland islands, southwest of the mainland in the Baltic Sea, on Nov 12, according to a Nov 25 report to the World Organization for Animal Health (OIE). So far, of four birds sent for testing, two are positive for H5N8.



Incessant Flux / Flickr cc

Bird flu: Netherlands culls 190,000 ducks

🕒 27 November 2016 | [Europe](#)



About 190,000 ducks have been culled in the Netherlands as the authorities try to prevent the spread of bird flu across northern European countries.

The slaughter involved six farms, following the discovery of a virus in the village of Biddinghuizen, some 70km (43 miles) east of Amsterdam.

Outbreaks of the highly contagious H5N8 strain have been reported in Denmark, Sweden, Germany and Finland.

The Dutch authorities have not said which strain is involved.

Officials said they were checking for bird flu at farms within three kilometres of the original site and imposed a ban on transporting poultry products within a 10km (six mile) radius.

What is bird flu?

Avian influenza - bird flu - is an infectious disease of poultry and wild birds.

The H5N8 strain first appeared in South Korea in early 2014.

The virus later spread to Japan, North America and Europe, causing outbreaks at poultry farms between autumn 2014 and spring 2015.

Europe Culls 400,000 Birds to Prevent Spread of Avian Flu

NOVEMBER 30, 2016 12:52 PM

Outbreaks of the highly pathogenic H5N8 avian influenza are spreading across Europe, prompting the culling of thousands of birds.

The **World Organization for Animal Health** has confirmed avian influenza in 10 European countries, including France, Croatia, Germany, Sweden and Russia.

An estimated 27,000 birds in Europe have died in just a few weeks from the flu.

Reports say officials in Sweden alone are culling **200,000 laying hens** to stop the virus from spreading further.

In 2015, the U.S. experienced its own infestation of the avian flu, affecting more than 50 million birds.

390,000 ducks and hens in northern Europe culled over bird flu fears

The birds were culled in the space of three days in Sweden and the Netherlands following a resurgence in the virus across Europe.

Nov 28th 2016, 2:45 PM

DUTCH OFFICIALS HAVE culled 190,000 ducks on a central Netherlands farm where inspectors have confirmed the presence of a highly infectious strain of bird flu, according to officials and local media.

Last Thursday, officials announced the discovery of the virus in a farm in southwest Sweden, and that 200,000 birds would be culled to prevent the spread of bird flu, which has seen a resurgence across Europe.

The outbreak in the Netherlands was detected at a farm in Biddinghuizen, about 70 kilometres (43 miles) west of Amsterdam, where about 180,000 ducks were put down over the weekend together with another 10,000 within a one kilometre radius, the Dutch food and safety watchdog NVWA said.

“There are three other poultry farms within a three kilometre radius and they are being monitored,” the NVWA added in a statement.



Image: Shutterstock/Red On



OIE: First high-path avian flu in Tunisia

Filed Under: [Avian Influenza \(Bird Flu\)](#)

[Stephanie Soucheray](#) | News Reporter | [CIDRAP News](#) | Dec 01, 2016



Today the World Organization for Animal Health (OIE) released three new reports that show highly pathogenic avian flu spreading in both northern Africa and northern Europe.

Tunisia confirms H5 in wild birds

Thirty wild wigeons and coots were found dead in Ichkeul National Park, on the northern tip of Tunisia, according to an OIE report. The birds tested positive for highly pathogenic H5 on Nov 30, but the subtype is still unknown.

This is the first time Tunisia has reported a highly pathogenic avian strain. The country, however, is located in the center of a migration corridor that takes birds from Europe to northern Africa during the winter months, and Ichkeul Lake and the surrounding wetlands is a major stopover point for migratory birds.

As more countries in Europe and the Middle East report instances of high-path avian flu, the risk of more wild birds in North Africa could rise.




Len Blumin / Flickr cc

H5N8 expands in France as H5N6 strikes more Korean farms

Filed Under: [Avian Influenza \(Bird Flu\)](#)

[Lisa Schnirring](#) | News Editor | CIDRAP News | Dec 02, 2016

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French veterinary officials today said the highly pathogenic H5N8 avian flu strain spreading quickly though Europe has been detected for the first time in the country's poultry in the south.

Also South Korea is reporting several new outbreaks of H5N6 avian flu, which, according to a new report from China, has replaced H5N1 as the dominant strain in that country's poultry.

French outbreak strikes foie gras ducks

In a report today to the World Organization for Animal Health (OIE), France's agriculture ministry said H5N8 struck an open-air farm in Tarn department that raises ducks for foie gras production. An increase in duck deaths was noted on Nov 25, and samples taken on Nov 28 yielded positive results for H5N8 yesterday.



Barry Lewis / Flickr cc

Ducks in Tarn department, France, where H5N8 recently struck.



More avian flu reported in Germany, France

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Dec 05, 2016



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H5N8 outbreaks in central Europe

Today the World Organization for Animal Health (OIE) said Germany reported 24 more outbreaks of H5N8, a highly pathogenic avian influenza. The outbreaks occurred in wild birds and waterfowl found in various locations throughout the country, including in towns along the Baltic Sea and along the Austrian border.

Several towns reported finding H5N8 in just one dead gull, goose, swan, or duck, while other places reported up to five dead birds found in a cluster. Germany first began reporting cases of H5N8 3 weeks ago, as the virus followed seasonal migration patterns that brought birds from Russia to Europe.

Avian Flu Diary (AFD), an infectious disease tracking blog, said the French Ministry of Agriculture is confirming today that H5N8 has been found on seven poultry farms and in two wild birds in that country.



Eric Page / Flickr cc



H5N8 outbreaks expand to Serbia

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Lisa Schnirring | News Editor | CIDRAP News | Dec 06, 2016



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Serbia today became the latest country in Europe to report highly pathogenic H5N8 avian influenza, as France and the United Kingdom took new steps to protect poultry flocks from the virus.

Serbia's detection involves swans

Serbia's agriculture ministry said today that the virus was found in six mute swans found dead in a nature park near Novi Sad in the north central part of the country, according to a report to the World Organization for Animal Health (OIE). The outbreak began on Nov 30, and testing at Serbia's national lab were positive for the virus on Dec 2.



jAYkROW / Flickr cc

Three of Serbia's neighbors—Croatia, Hungary, and Romania—have already been hit by the virus. H5N8 has now been confirmed in 14 European countries, and it is suspected in an H5 outbreak reported by Ukrainian officials in late November. Outside of the region, the virus has also turned up in Egypt, India, Iran, Israel, and Tunisia.



Hungary reports widespread avian flu in poultry

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Dec 07, 2016



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The World Organization of Animal Health (OIE) today released a slew of European avian influenza reports that included details of multiple outbreaks in Hungarian poultry, while Japan says highly pathogenic avian flu has been found in 41 wild birds.

Poultry, wild bird outbreaks in Europe

The OIE said Hungary had 24 outbreaks of highly pathogenic H5N8 in poultry in the southern part of that country, leading to the death and culling of thousands of ducks and geese.

All of the outbreaks occurred in either backyard or commercial farms between Nov 18 and 24. The largest involved 26,000 ducks on a farm near the town of Csolyospalos. A total of 38,230 birds have been destroyed as of yesterday among 241,967 susceptible poultry. More than 10,000 died from H5N8 infection.




Lisa / Flickr cc

Europe weighs H5N8 threat as Russia reports new outbreak

Filed Under: [Avian Influenza \(Bird Flu\)](#)


Lisa Schnirring | News Editor | CIDRAP News | Dec 08, 2016

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Experts from several European countries today weighed in on the quickly expanding highly pathogenic H5N8 avian flu outbreaks that have hit more than a dozen countries, noting that some of the lessons they learned during outbreaks in 2014 and 2015 are useful for response preparations.

In new outbreak developments, Russia reported H5 infections affecting a large poultry farm, and Taiwan officials said tests have now confirmed H5N8 in two outbreaks in backyard birds that it first reported in early November.



Rob Faulkner / Flickr cc

European experts urge preparedness

The H5N8 virus turned up in Europe in October and has rapidly spread across central Europe, as well as India and parts of the Middle East. The virus has mainly affected waterfowl, but also birds of prey that feed on the carcasses, introducing the virus into local bird populations, the experts wrote.



H5N8 reported on poultry farms in Hungary, France

Filed Under: [Avian Influenza \(Bird Flu\)](#)

[Stephanie Soucheray](#) | News Reporter | [CIDRAP News](#) | Dec 13, 2016



The World Organization for Animal Health (OIE) reported 33 more outbreaks of highly pathogenic H5N8 avian flu in Hungary today, including several on farms that house ducks, chickens, and other poultry. France, meanwhile, noted four new H5N8 outbreaks in poultry.

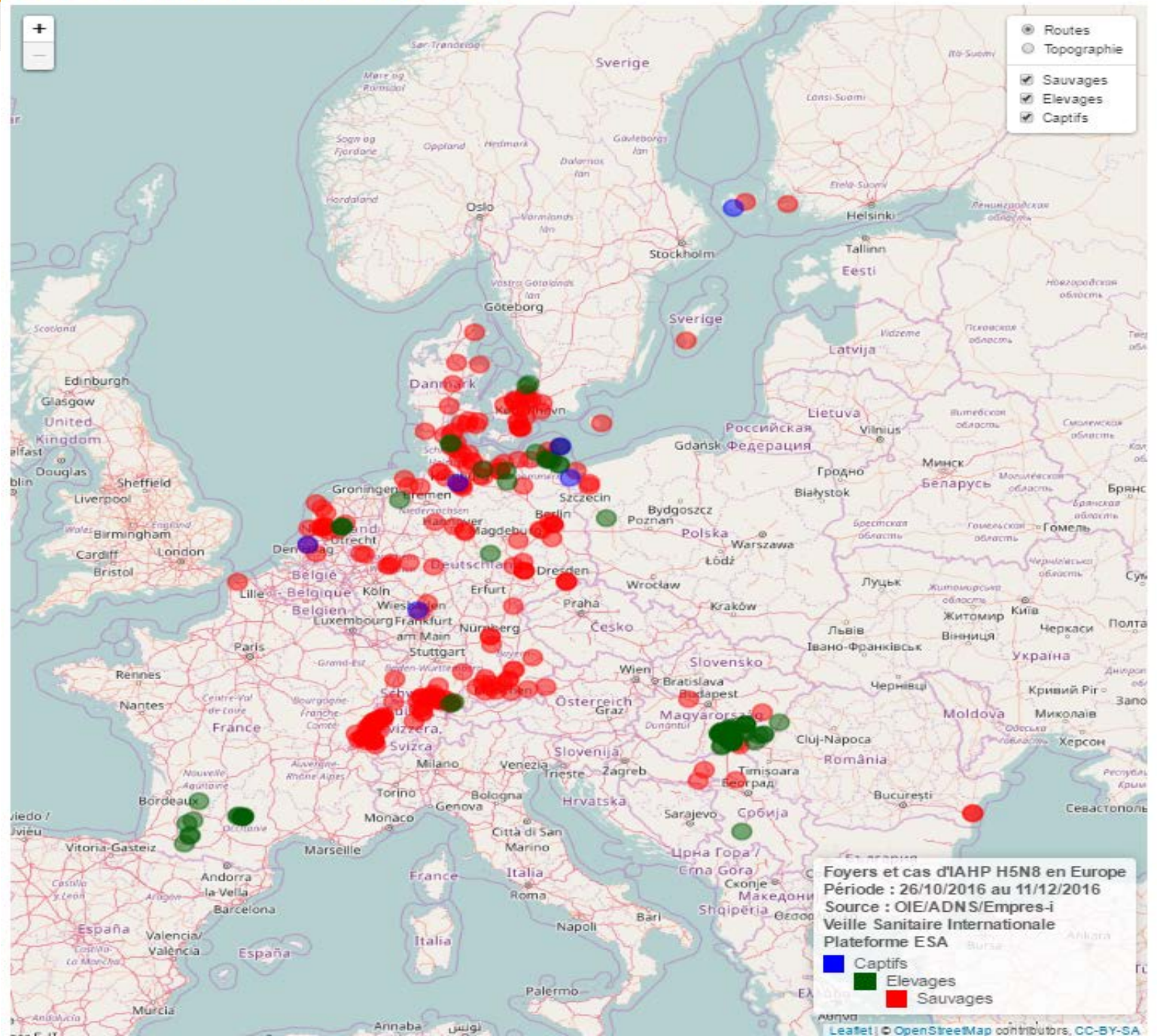
The affected Hungarian farms are clustered in the south-central and southeastern parts of the country.

A total of 303,141 turkeys, geese, ducks, and chickens are housed on the farms experiencing the outbreaks, which first began on Nov 25. The largest flocks are on a farm in Kompoc housing 70,000 broiler chickens and on a farm near Szank with 21,500 ducks and geese.

Hungary first reported H5N8 on Nov 4, when 2,374 turkeys died after they possibly contracted the disease from wild birds and 7,827 were destroyed to curb disease spread. Wild birds, including waterfowl, likely carried H5N8 from Siberia as they have migrated west and south for the winter months.



USAID / Flickr cc




H5N8 expands in France as H5N6 strikes more Korean farms

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Lisa Schnirring | News Editor | CIDRAP News | Dec 02, 2016

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French veterinary officials today said the highly pathogenic H5N8 avian flu strain spreading quickly though Europe has been detected for the first time in the country's poultry in the south.

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French outbreak strikes foie gras ducks

In a report today to the World Organization for Animal Health (OIE), France's agriculture ministry said H5N8 struck an open-air farm in Tarn department that raises ducks for foie gras production. An increase in duck deaths was noted on Nov 25, and samples taken on Nov 28 yielded positive results for H5N8 yesterday.



Barry Lewis / Flickr cc

Ducks in Tarn department, France, where H5N8 recently struck.



Sweden confirms H5N8 as H5N6 spreads in South Korea

Filed Under: [Avian Influenza \(Bird Flu\)](#)

[Stephanie Soucheray](#) | [News Reporter](#) | [CIDRAP News](#) | [Nov 23, 2016](#)



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Sweden today joined the growing list of European countries facing highly pathogenic avian influenza (HPAI), while South Korea detailed four outbreaks of H5N6, and Russia reports H5 avian flu activity.

According to the Swedish Ministry of Agriculture, officials detected H5N8 avian flu in two locations in the southern tip of the country. [Avian Flu Diary](#), an infectious disease blog, posted the developments today.

The disease was detected in Vellinge and Helsingborg, two villages near the Danish border. Vellinge confirmed that a wild bird was found dead and tested positive for H5N8, while a flock of laying hens outside of Helsingborg were infected with an H5 avian influenza, but officials have yet to determine the exact type.



Olga / Flickr cc



H5N6 hits more Korean farms as study hints at reassortment

Filed Under: [H5N6](#); [Avian Influenza \(Bird Flu\)](#)

Lisa Schnirring | News Editor | CIDRAP News | Nov 28, 2016



South Korea has reported 12 more highly pathogenic H5N6 avian influenza outbreaks, and an initial analysis from the country's agriculture ministry suggests that the outbreak strain is a new reassortant, making it different from the strain detected in China and Hong Kong.

Korean outbreaks span 3 provinces

Most of the new detections in South Korea were reported at duck farms, though one was reported from among egg-laying hens. One of the outbreaks struck a farm in the newly affected Gyeonggi province, with the others occurring in the previously affected North Chungcheong and South Jeolla provinces, according to a Nov 24 report to the World Organization for Animal Health (OIE).

Among the 12 new outbreaks, the virus killed 4,020 of 137,600 susceptible birds, and authorities destroyed the remaining ones to control the spread of the virus.



kylieellway / iStock

More avian flu expected in Europe, US

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Stephanie Soucheray | News Reporter | CIDRAP News | Nov 16, 2016



The World Organization for Animal Health (OIE) said yesterday that Europeans should expect more avian flu this season, adding that highly pathogenic avian influenza (HPAI) strains are also apt to appear in America.

In an interview with Reuters, Matthew Stone, BVSc MVS, deputy director general of the OIE, said the level of exposure in wild birds is indicative of high avian flu activity.

In the last few weeks eight European countries, in addition to India and Israel, have reported outbreaks of H5N8, a strain that can infect waterfowl, other migratory birds, and poultry. Though the risk to human health is considered low, mutation or reassortment with other strains of influenza could make H5N8 dangerous and potentially lethal.

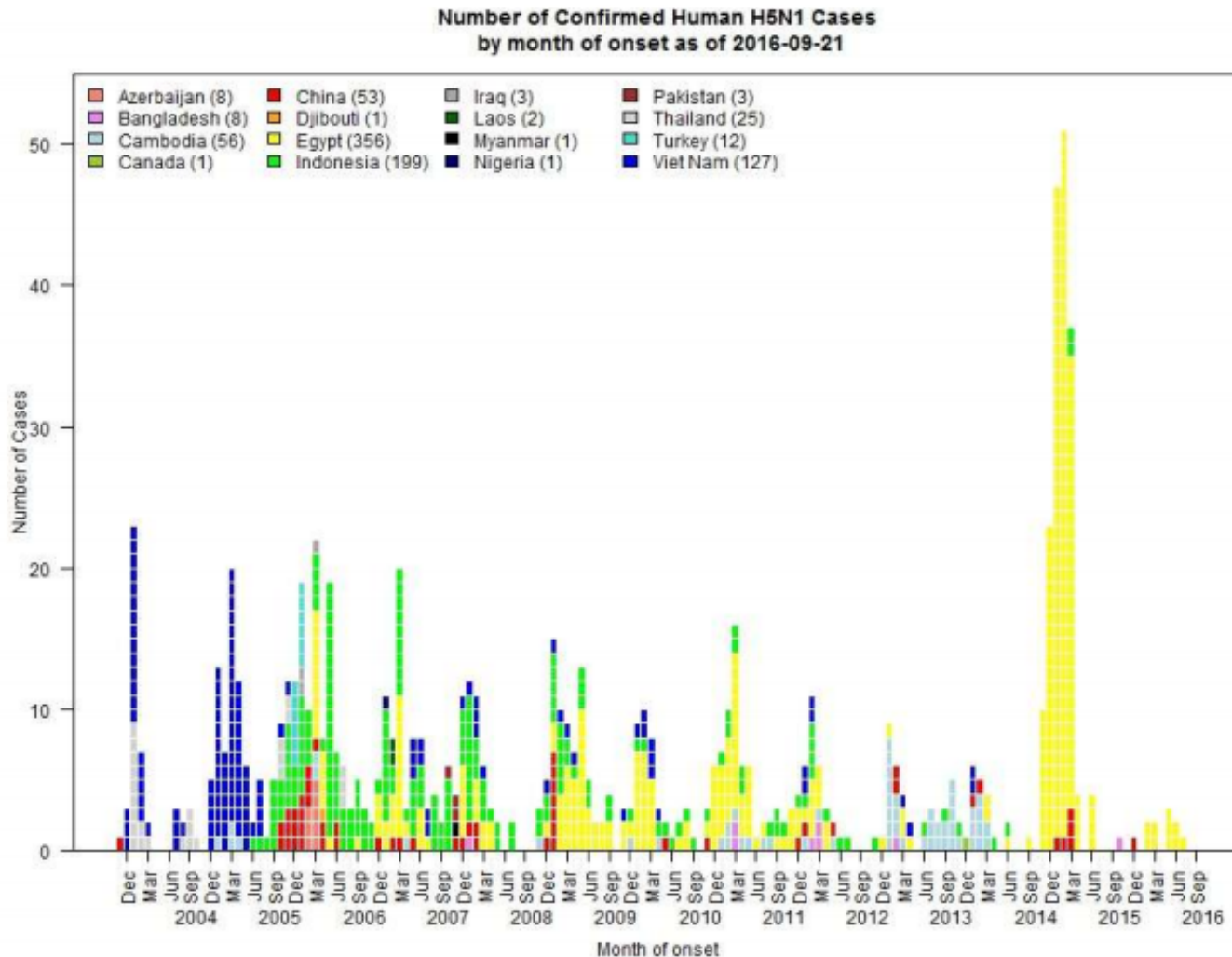
Stone also said the OIE's main concern is domestic poultry that could be exposed to HPAI by wild birds. In 2014, thousands of poultry in Europe were destroyed by avian influenza, and earlier this year an outbreak in France decimated the foie gras industry.



Bernard Spragg, NZ / Flickr cc



Figure 1: Epidemiological curve of avian influenza A(H5N1) cases in humans by week of onset, 2003-2016





China reports H5N6 in poultry; study finds high H5N1 seroprevalence

Filed Under: [Avian Influenza \(Bird Flu\)](#)

Jim Wappes | Editorial Director | CIDRAP News | Oct 10, 2016

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Chinese officials yesterday reported two outbreaks of highly pathogenic H5N6 avian flu, while a study out of Indonesia reports that 84% of Indonesian poultry workers have evidence of previous infection with H5N1 avian flu in their bloodstream.

Elsewhere, the World Health Organization (WHO) confirmed two recent H5N1 human cases in Egypt.

H5N6 in China

The two H5N6 outbreaks are in separate provinces and have affected more than 100,000 poultry, Chinese officials reported in a World Organization for Animal Health (OIE) report.

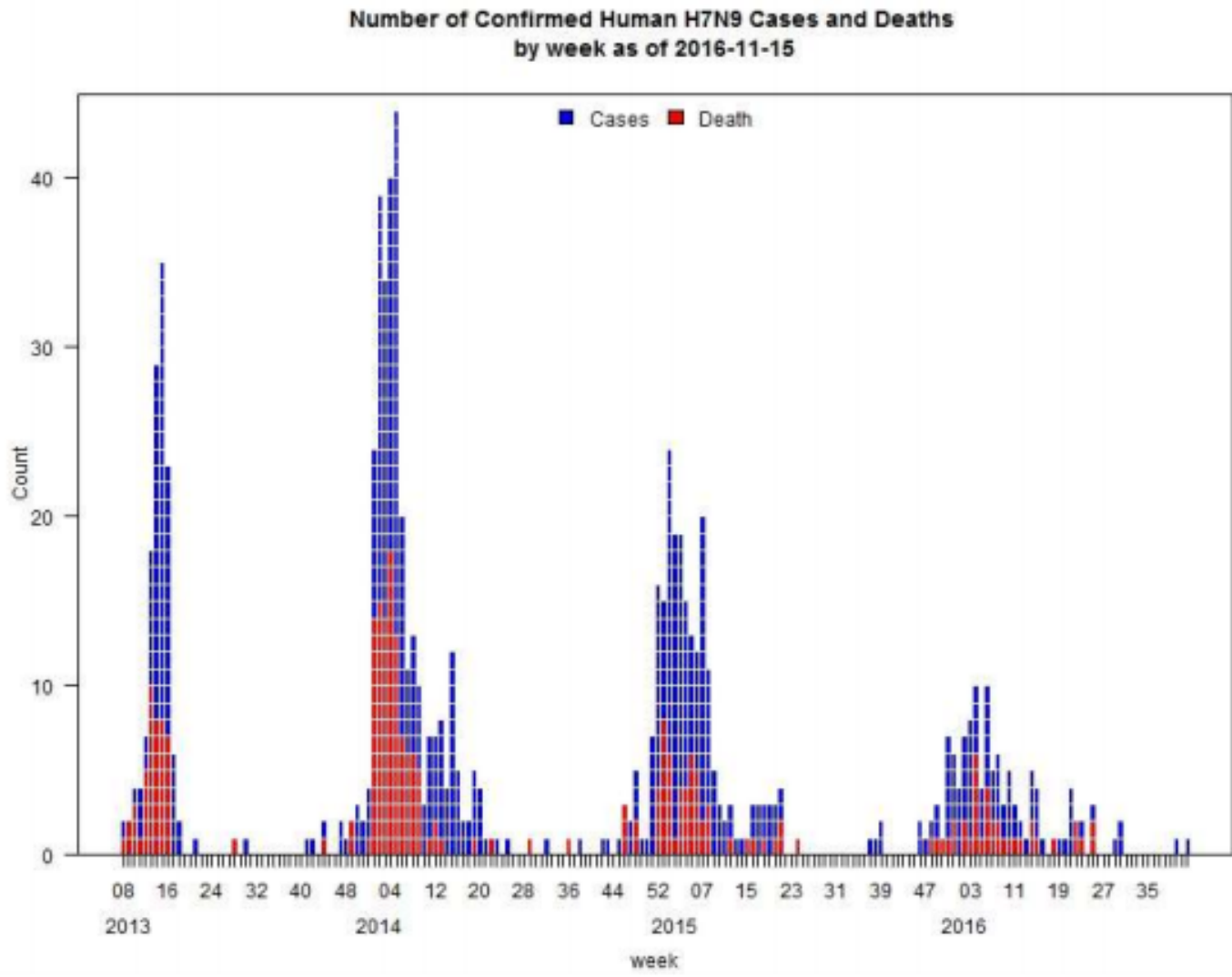
The largest outbreak, near Jinchang City in Gansu province, struck a farm of 95,172 birds on Oct 2. The virus caused 30,000 avian flu infections and 18,000 deaths.



kdlife / iStock

Great Wall in Gansu province. The province was home to the larger H5N6 outbreak.

Figure 2: Epidemiological curve of avian influenza A(H7N9) cases in humans by week of onset, 2013-2016



Distribution of confirmed cases of A(H7N9) by four periods of reporting (weeks 07/2013 to 46/2016)





Study: Flu vaccine doesn't prevent missed school days

Filed Under: **Influenza Vaccines**

Stephanie Soucheray | News Reporter | CIDRAP News | Nov 30, 2016



A new study published in *Influenza and Other Respiratory Viruses* shows that influenza vaccination does not reduce absenteeism, or the number of days of school that kids miss because of flu, casting some doubt about how often the vaccine prevents severe illness in children ages 5 to 17 years.

The study contradicts previous research that showed lower absenteeism in vaccinated school-age children. Those studies looked at children suffering from any acute respiratory illnesses (ARIs). This is the first study to look at absentee rates among children with lab-confirmed flu, not just nonspecific respiratory illnesses, the authors said.

Results across three flu seasons

From 2012 through 2015 children who came to the Marshfield Clinic Research Foundation (in Marshfield, Wisconsin) for ARIs were tested for flu. If they were positive for influenza, they were surveyed 1 week later about vaccination status and number of school days missed.



microgen / iStock

- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
 - Flu vaccine
- 3. Antimicrobial resistance**
- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

Antibiotic Resistance Is Prevalent in an Isolated Cave Microbiome

Kirandeep Bhullar¹, Nicholas Waglechner¹, Andrew Pawlowski¹, Kalinka Koteva¹, Eric D. Banks², Michael D. Johnston², Hazel A. Barton², Gerard D. Wright^{1*}

1 M.G. DeGroot Institute for Infectious Disease Research, Department of Biochemistry and Biomedical Sciences, McMaster University, Hamilton, Ontario, Canada, **2** Department of Biology, University of Akron, Akron, Ohio, United States of America

Abstract

Antibiotic resistance is a global challenge that impacts all pharmaceutically used antibiotics. The origin of the genes associated with this resistance is of significant importance to our understanding of the evolution and dissemination of antibiotic resistance in pathogens. A growing body of evidence implicates environmental organisms as reservoirs of these resistance genes; however, the role of anthropogenic use of antibiotics in the emergence of these genes is controversial. We report a screen of a sample of the culturable microbiome of Lechuguilla Cave, New Mexico, in a region of the cave that has been isolated for over 4 million years. We report that, like surface microbes, these bacteria were highly resistant to antibiotics; some strains were resistant to 14 different commercially available antibiotics. Resistance was detected to a wide range of structurally different antibiotics including daptomycin, an antibiotic of last resort in the treatment of drug resistant Gram-positive pathogens. Enzyme-mediated mechanisms of resistance were also discovered for natural and semi-synthetic macrolide antibiotics via glycosylation and through a kinase-mediated phosphorylation mechanism. Sequencing of the genome of one of the resistant bacteria identified a macrolide kinase encoding gene and characterization of its product revealed it to be related to a known family of kinases circulating in modern drug resistant pathogens. The implications of this study are significant to our understanding of the prevalence of resistance, even in microbiomes isolated from human use of antibiotics. This supports a growing understanding that antibiotic resistance is natural, ancient, and hard wired in the microbial pangenome.

Citation: Bhullar K, Waglechner N, Pawlowski A, Koteva K, Banks ED, et al. (2012) Antibiotic Resistance Is Prevalent in an Isolated Cave Microbiome. PLoS ONE 7(4): e34953. doi:10.1371/journal.pone.0034953

Editor: Ramy K. Aziz, Cairo University, Egypt

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Competing Interests: The authors have declared that no competing interests exist.

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Scientists find ancient, cave-dwelling resistant bacteria

Filed Under: [Antimicrobial Stewardship](#)

[Chris Dall](#) | [News Reporter](#) | [CIDRAP News](#) | [Dec 12, 2016](#)

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A thousand feet under the New Mexico soil, in the deepest limestone cave in the country, researchers have discovered an ancient bacterium that is resistant to many antibiotics used in human medicine today.

Researchers say the discovery not only provides new insight into the evolution of antibiotic resistance, but could also hold clues to combating it in the future.

The microbe, a non-pathogenic strain of bacteria called *Paenibacillus* sp LC231, was originally identified in 2012 in Lechuguilla Cave, a 136-plus-mile cave in New Mexico's Carlsbad Caverns National Park that's become an exploration site for cavers and scientists from around the world. Cavers are drawn by an array of unique formations and decorations; scientists by the chance to study microbes that have been sealed off from human or animal contact for more than 4 million of year.

In a new study published in *Nature Communications*, researchers describe what they found when they sequenced the genes of this ancient bacterium.


Finding resistance deep underground

For study author Gerry Wright, PhD, director of the



Max Wisshak

Researcher Hazel Barton, PhD, in New Mexico's Lechuguilla Cave.



TACKLING DRUG-RESISTANT INFECTIONS GLOBALLY: AN OVERVIEW OF OUR WORK

**THE REVIEW ON
ANTIMICROBIAL RESISTANCE**

*CHAIR*ED BY **JIM O'NEILL**

FEBRUARY 2016

Urgent Threats

- *Clostridium difficile*
- Carbapenem-resistant Enterobacteriaceae (CRE)
- Drug-resistant *Neisseria gonorrhoeae*

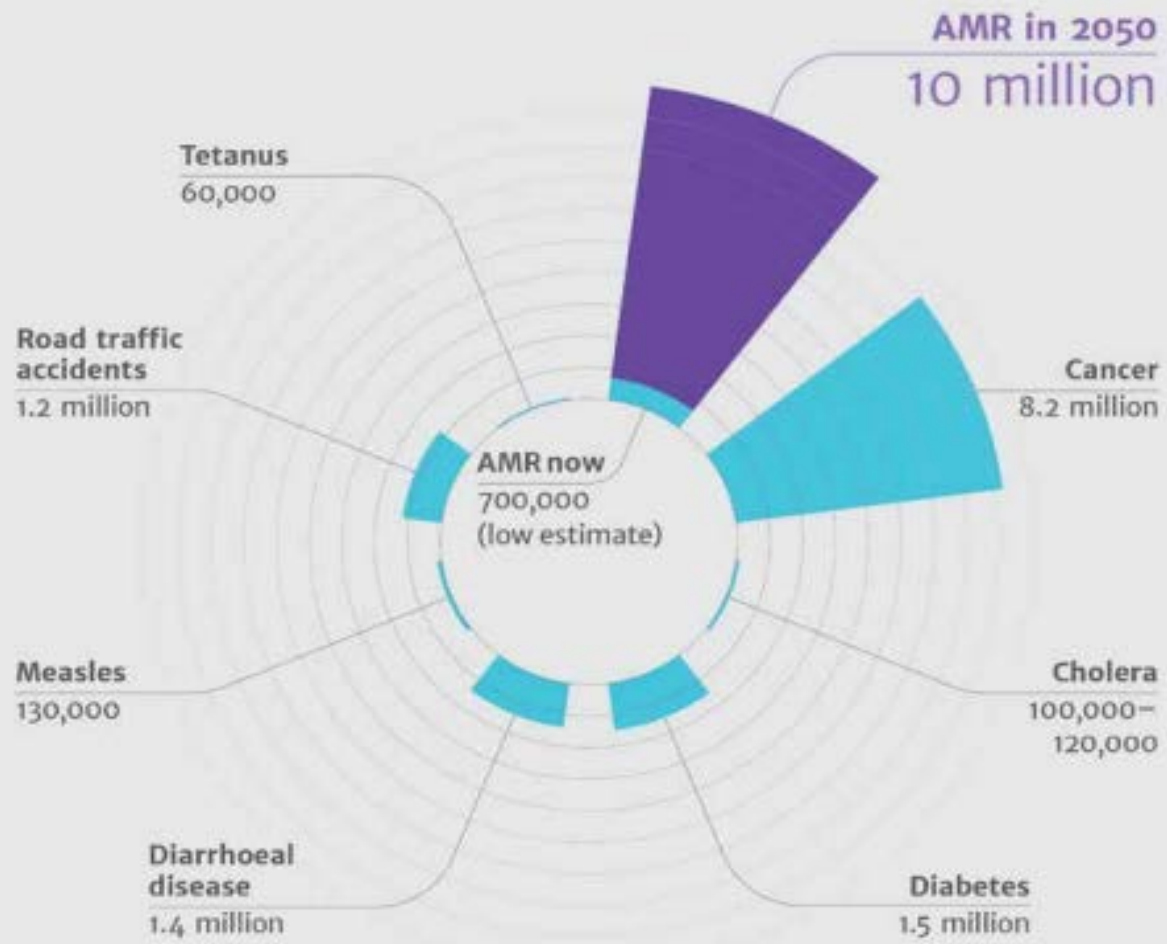
Serious Threats

- Multidrug-resistant *Acinetobacter*
- Drug-resistant *Campylobacter*
- Fluconazole-resistant *Candida* (a fungus)
- Extended spectrum β -lactamase producing Enterobacteriaceae (ESBLs)
- Vancomycin-resistant *Enterococcus* (VRE)
- Multidrug-resistant *Pseudomonas aeruginosa*
- Drug-resistant Non-typhoidal *Salmonella*
- Drug-resistant *Salmonella* Typhi
- Drug-resistant *Shigella*
- Methicillin-resistant *Staphylococcus aureus* (MRSA)
- Drug-resistant *Streptococcus pneumoniae*
- Drug-resistant tuberculosis

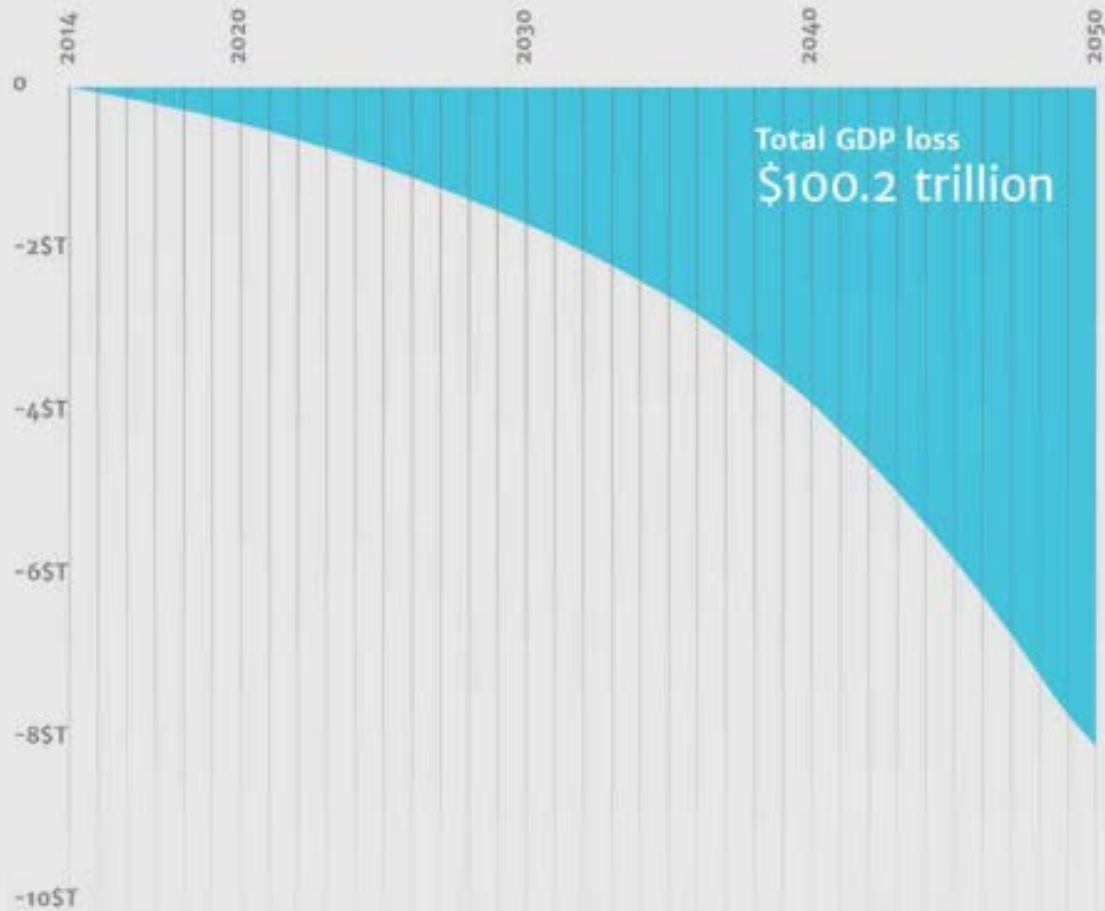
Concerning Threats

- Vancomycin-resistant *Staphylococcus aureus* (VRSA)
- Erythromycin-resistant Group A *Streptococcus*
- Clindamycin-resistant Group B *Streptococcus*

Deaths attributable to AMR every year compared to other major causes of death



AMR's impact on World GDP in trillions of USD



UN leaders pledge to fight antimicrobial resistance

Filed Under: [Antimicrobial Stewardship](#)

[Chris Dall](#) | News Reporter | [CIDRAP News](#) | Sep 21, 2016

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World leaders today made a commitment to work at national, regional, and global levels to address the growing threat of antimicrobial resistance (AMR).

The agreement came at the 71st meeting of the United Nations (UN) General Assembly, where delegates gathered today for a high-level meeting on AMR. It's only the fourth time the UN has held a General Assembly meeting to address a health issue, a fact that underscores how seriously world leaders take the threat of drug-resistant pathogens. Before the meeting, delegates agreed to a draft political declaration in which they committed to developing and implementing national action plans to address rising drug resistance.

"Antimicrobial resistance poses a fundamental, long-term threat to human health, sustainable food production and development," UN Secretary-General Ban Ki-moon told the assembled delegates. "We are losing our ability to protect both people and animals from life-threatening infections."



Nathan Reading / Flickr cc

Enterobacter cloacae with NDM-1 resistance gene growing in culture.



FAO advises nations on curbing ag antimicrobial use

Filed Under: [Antimicrobial Stewardship](#)

Lisa Schnirring | News Editor | CIDRAP News | Sep 16, 2016



Ahead of a high-level United Nations meeting on antimicrobial resistance (AMR) next week in New York, the group's Food and Agriculture Organization (FAO) this week unveiled an action plan to help countries build strategies to address the problem in their food and agricultural sectors by the middle of 2017.

Grappling with agricultural uses of antimicrobials is considered a key part of curbing the emergence of antimicrobial-resistant pathogens, preserving crucial antibiotics used for human health. The FAO said in a Sep 14 press release that livestock consumption of antimicrobials tops 60,000 metric tons each year, and that their use is likely to grow with the increasing demand for animal-sourced food products.



Cecilia Schubert / Flickr cc



Researchers find worrisome CRE on US swine farm

Filed Under: [Antimicrobial Stewardship](#)

Chris Dall | News Reporter | CIDRAP News | Dec 05, 2016



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Researchers today report identifying bacteria carrying a highly transmissible antibiotic-resistance gene in a US livestock operation, a finding that suggests a troubling new path for the spread of the drug-resistant pathogens.

In a study appearing in *Antimicrobial Agents and Chemotherapy*, investigators from The Ohio State University (OSU) say they recovered 18 isolates of multiple Enterobacteriaceae species harboring the beta-lactamase gene IMP-27, which confers resistance to carbapenem antibiotics, from the environment of an industrial US swine operation. All of the isolates carried the gene on what the researchers say is a highly mobile piece of DNA that can spread to a broad range of bacteria.

Carbapenems are a last line of defense against drug-resistant bacteria. While plasmid-mediated carbapenem-resistant Enterobacteriaceae (CRE) have been reported in European and Asian livestock and are known to cause life-threatening infections in US healthcare settings, this is the first time they have been identified in US livestock. The finding is surprising in part because carbapenem antibiotics are not approved for use in food animals in the United States.



Kadmy / iStock



EU report: Animal use of medically important antibiotics up

Filed Under: [Antimicrobial Stewardship](#)

Chris Dall | News Reporter | CIDRAP News | Oct 17, 2016



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New data on sales of veterinary antibiotics in Europe show a small drop in overall sales but a worrisome increase in the use of medically important antibiotics.

The data from the European Medicines Agency (EMA) show that, from 2011 to 2014, an overall 2.4% fall in total sales of veterinary antibiotics and a 2.9% reduction in the volume of tons sold was observed in 25 countries reporting to the European Surveillance of Veterinary Antibiotic Consumption. The report suggests implementation of responsible-use campaigns, restrictions on antibiotic use, and greater awareness of the threat of antimicrobial resistance could explain the decline in veterinary antibiotic use observed in some countries.



Oli / Flickr cc

"Despite low overall decrease in sales of veterinary antimicrobial products, data demonstrate that actions taken in the fight against antimicrobial resistance by the Member States are making a difference," the EMA said in a press release.

UK report finds drug-resistant *Campylobacter* rising in poultry

Filed Under: [Antimicrobial Stewardship](#); [Campylobacter](#); [Foodborne Disease](#)

Chris Dall | News Reporter | CIDRAP News | Nov 29, 2016

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A new report from the British government shows increasing antibiotic resistance in bacteria commonly found in retail poultry.

The report from the Food Standards Agency (FSA) found that resistance to fluoroquinolone antibiotics have increased steadily since 2001 in *Campylobacter jejuni* isolates from UK-produced poultry meat samples (especially chicken and turkey). While resistance to ciproflaxin and nalidixic acid were observed in 15% and 22% of poultry isolates in 2011, half of all isolates showed resistance to both drugs in 2014-2015.

But the FSA review, which aimed to assess the prevalence of antimicrobial resistant (AMR) bacteria in retail pork, poultry meat, dairy products, seafood, and fresh produce in the country, found the overall data for drug resistance levels in British-produced food were limited, a finding the report's authors say highlights the need for better AMR surveillance in the food chain. In particular, data were lacking for milk and dairy products, seafood, and fresh produce.



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- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
 - Flu vaccine
- 3. Antimicrobial resistance**
- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

The Ebola Vaccine Team B: a model for promoting the rapid development of medical countermeasures for emerging infectious disease threats



Michael Osterholm, Kristine Moore, Julie Ostrowsky, Kathleen Kimball-Baker, Jeremy Farrar, for the Wellcome Trust-CIDRAP Ebola Vaccine Team B*

In support of accelerated development of Ebola vaccines from preclinical research to clinical trials, in November, 2014, the Wellcome Trust and the Center for Infectious Disease Research and Policy (CIDRAP) at the University of Minnesota established the Wellcome Trust-CIDRAP Ebola Vaccine Team B initiative. This ongoing initiative includes experts with global experience in various phases of bringing new vaccines to market, such as funding, research and development, manufacturing, determination of safety and efficacy, regulatory approval, and vaccination delivery. It also includes experts in community engagement strategies and ethical issues germane to vaccination policies, including eight African scientists with direct experience in developing and implementing vaccination policies in Africa. Ebola Vaccine Team B members have worked on a range of vaccination programmes, such as polio eradication (Africa and globally), development of meningococcal A disease vaccination campaigns in Africa, and malaria and HIV/AIDS vaccine research. We also provide perspective on how this experience can inform future situations where urgent development of vaccines is needed, and we comment on the role that an independent, expert group such as Team B can have in support of national and international public health authorities toward addressing a public health crisis.

Introduction

On Aug 8, 2014, the Director-General of WHO declared that the Ebola virus disease (EVD) outbreak in parts of west Africa represented a Public Health Emergency of International Concern (PHEIC) under the 2005 International Health Regulations.¹ Also in August, 2014, WHO called for fast-track development of Ebola vaccines as part of the Ebola Response Roadmap² and in October, 2014,

development, to identify potentially overlooked aspects of the vaccine development process, and to synthesise information for distribution in the public domain as quickly as possible. To achieve these objectives, during the period from late November, 2014, to early February, 2015, working subgroups of Ebola Vaccine Team B experts met regularly via international conference calls to discuss and comment on various issues related to the development

Lancet Infect Dis 2015

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February 2015

Recommendations for Accelerating the Development of Ebola Vaccines

REPORT & ANALYSIS

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 **CIDRAP**
Center for Infectious Disease Research and Policy
Johns Hopkins University

March 2016

Ebola Vaccine Team B

Plotting the Course of Ebola Vaccines

CHALLENGES AND
UNANSWERED QUESTIONS

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UNIVERSITY OF MICHIGAN

Urbanization of African Countries of Potential Concern

- Kinshasa, DRC/Brazzaville, RC
 - 13.8 million (four other cities > 1 million)
- Lagos, Nigeria
 - 13.2 million (five other cities > 1 million)
- Nairobi, Kenya
 - 4.1 million
- Accra, Ghana
 - 2.8 million
- Monrovia/Freetown/Conakry
 - 4.2 million

Studies say mutation made West Africa's Ebola strain deadlier

Filed Under: [Ebola](#); [VHF](#)

Lisa Schnirring | News Editor | CIDRAP News | Nov 04, 2016

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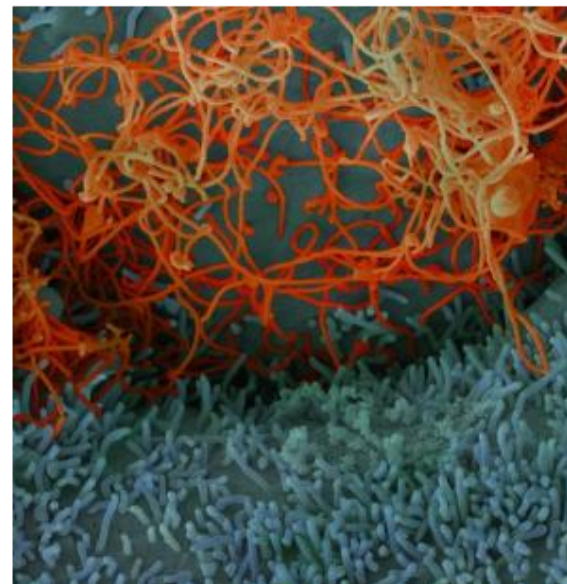
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In a development that may add a piece of the puzzle about why West Africa's Ebola outbreak was so much worse than others involving the virus, researchers yesterday described mutations that made it more capable of infecting humans.

Adding weight to the findings, two different groups reported similar discoveries involving the same mutation—A82V in the gene that encodes the Ebola virus glycoprotein—in the same issue of the journal *Cell*. One group was led by primarily by US researchers based at the University of Massachusetts Medical School and Harvard's Broad Institute, with the other a large international team that includes scientists from the University of Nottingham and the Pasteur Institute.

As the scope of the 2014-16 outbreak overwhelmed global health systems, experts worried that each new infection was adding more throws of the genetic dice, which could lead to changes enabling the virus to spread more quickly. By the time the outbreak wound down, more than 28,000 people were infected, including 11,000 people who died.



NIAID

Ebola Evolved Into Deadlier Enemy During the African Epidemic

Carl Zimmer

MATTER NOV. 3, 2016

The [Ebola](#) epidemic that tore through West Africa in 2014 claimed 11,310 lives, far more than any previous outbreak. A combination of factors [contributed to its savagery](#), among them a mobile population, crumbling public health systems, official neglect and hazardous burial practices.

But new research suggests another impetus: The virus may have evolved a new weapon against its human hosts. In studies published on Thursday in the journal *Cell*, two teams of scientists report that a genetic mutation may have made Ebola more deadly by improving the virus's ability to enter human cells.

The researchers do not yet understand exactly how it works, but several lines of evidence suggest it helped expand the scope of the epidemic. One alarming finding: Patients infected with the mutated version of Ebola were significantly more likely to die.



What We're Afraid to Say About Ebola

By MICHAEL T. OSTERHOLM SEPT. 11, 2014



Jonathon Rosen

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MINNEAPOLIS — THE [Ebola](#) epidemic in West Africa has the potential to alter history as much as any plague has ever done.

There have been more than 4,300 cases and 2,300 deaths over the past six months. Last week, the [World Health Organization](#) warned that, by early October, there may be thousands of new cases per week in Liberia, Sierra Leone, Guinea and Nigeria. What is not getting said publicly, despite briefings and discussions in the inner circles of the world's public health agencies, is that we are in totally uncharted waters and that Mother Nature is the only force in charge of the crisis at this time.

There are two possible future chapters to this story that should keep us up at night.

The first possibility is that the Ebola virus spreads from West Africa to megacities in other regions of the developing world. This outbreak is very different from the 19 that have occurred in Africa over the past 40 years. It is much easier to control Ebola infections in isolated villages. But there has been a 300 percent increase in Africa's population over the last four decades, much of it in large city slums. What happens when an infected person yet to become ill travels by plane to Lagos, Nairobi, Kinshasa or

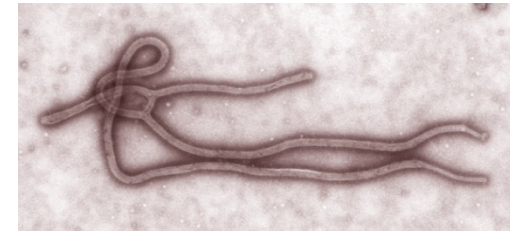
Is It Worth Imagining Airborne Ebola?

🕒 POSTED SUN, 02/22/2015

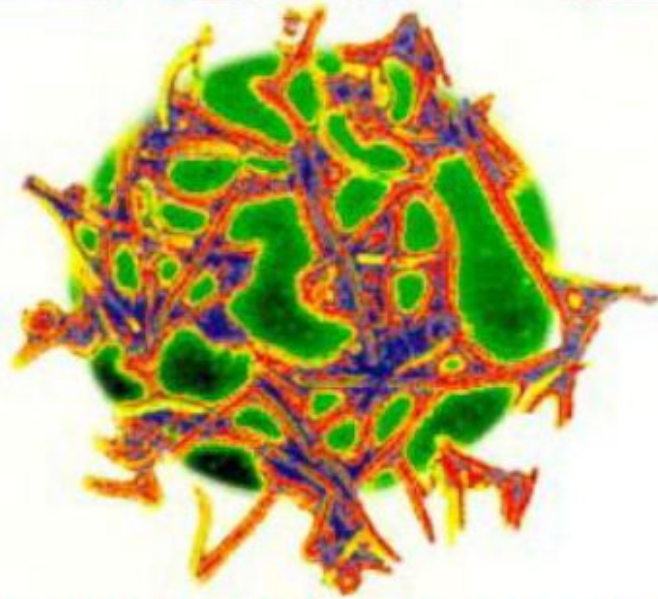
Back in September, when the West African Ebola outbreak was getting worse with every passing week, a lot of people began to worry that the virus could spread by air. And even if it couldn't spread by air yet, they worried that it might be on the verge of mutating into an airborne form.

When I talked to virus experts, they saw little ground for either concern. The epidemiology of the outbreak, like previous ones, had the sort of pattern you'd expect from a virus that spreads mainly through contact with body fluids. A look at the evolutionary history of viruses indicates that a fluid-adapted virus would be unlikely to switch to going airborne with just a couple mutations. (I wrote in the *New York Times* about these conversations [here](#) and [here](#).)

The anxiety over airborne Ebola has faded. The outbreak itself has dwindled down dramatically, although [driving it down to zero may prove hard](#). But a new “Opinion/Hypothesis” piece published in the journal *mBio*, called [“Transmission of Ebola Viruses: What We Know and Do Not Know,”](#) has breathed some new life into the old worry.



THE HOT ZONE



A TERRIFYING TRUE STORY
RICHARD PRESTON

SCIENTIFIC REPORTS

**OPEN**

Conserved differences in protein sequence determine the human pathogenicity of Ebolaviruses

Morena Pappalardo*, Miguel Juliá*, Mark J. Howard, Jeremy S. Rossman, Martin Michaelis & Mark N. Wass

Received: 08 July 2015

Accepted: 14 March 2016

Published: 24 March 2016

Reston viruses are the only Ebolaviruses that are not pathogenic in humans. We analyzed 196 Ebolavirus genomes and identified specificity determining positions (SDPs) in all nine Ebolavirus proteins that distinguish Reston viruses from the four human pathogenic Ebolaviruses. A subset of these SDPs will explain the differences in human pathogenicity between Reston and the other four ebolavirus species. Structural analysis was performed to identify those SDPs that are likely to have a functional effect. This analysis revealed novel functional insights in particular for Ebolavirus proteins VP40 and VP24. The VP40 SDP P85T interferes with VP40 function by altering octamer formation. The VP40 SDP Q245P affects the structure and hydrophobic core of the protein and consequently protein function. Three VP24 SDPs (T131S, M136L, Q139R) are likely to impair VP24 binding to human karyopherin alpha5 (KPNA5) and therefore inhibition of interferon signaling. Since VP24 is critical for Ebolavirus adaptation to novel hosts, and only a few SDPs distinguish Reston virus VP24 from VP24 of other Ebolaviruses, human pathogenic Reston viruses may emerge. This is of concern since Reston viruses circulate in domestic pigs and can infect humans, possibly via airborne transmission.

Scientists Rein In Fears of Ebola, a Virus Whose Mysteries Tend to Invite Speculation

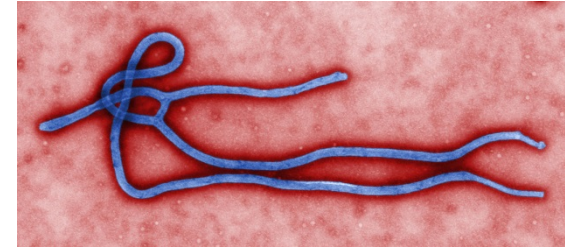
By CARL ZIMMER OCT. 13, 2014

News that a nurse in full protective gear had become infected with the Ebola virus raised some disturbing questions on Monday. Has the virus evolved into some kind of super-pathogen? Might it mutate into something even more terrifying in the months to come?

Evolutionary biologists who study viruses generally agree on the answers to those two questions: no, and probably not.

The Ebola viruses buffeting West Africa today are not fundamentally different from those in previous outbreaks, they say. And it is highly unlikely that natural selection will give the viruses the ability to spread more easily, particularly by becoming airborne.

“I’ve been dismayed by some of the nonsense speculation out there,” said Edward Holmes, a biologist at the University of Sydney in Australia. “I understand why people get nervous about this, but as scientists we need to be very careful we don’t scaremonger.”



News Scan for Dec 12, 2016

Breastmilk, semen carry Ebola virus for extended periods

An international group reporting in *Clinical Infectious Diseases* said a 9-month-old who died of Ebola in Guinea after her parents showed no signs of the illness likely contracted the virus through her mother's breastmilk. Both the mother's milk and the father's semen tested positive for Ebola virus.

The child represented the first case of Ebola in the area where she was living in 42 days, and no known epidemiologic contacts could be found. Genetic testing revealed that both parents carried the virus but reported being asymptomatic.

The authors note that, though rare, transmission of Ebola from asymptomatic mothers to children is possible via breastmilk.

Dec 10 *Clin Infect Dis* abstract

In related study published today in *The Lancet Global Health*, researchers studied 26 male Ebola survivors to measure how long Ebola stayed in their reproductive tracts post-infection.

They found Ebola virus RNA in semen samples up to 407 days after disease onset (median, 158 days). Using statistical analysis, they predicted that 90% of men will clear Ebola virus from their semen within 294 days of disease onset.

The men supplied seminal fluids every 3 to 6 weeks, with a median follow-up of 255 days. The authors said that the time to clearance of Ebola virus RNA from seminal fluid varied greatly. Previous studies showed Ebola virus RNA in semen for up to 9 months post-infection.

January *Lancet Glob Health* study


- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
 - Flu vaccine
- 3. Antimicrobial resistance**
- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

MERS infects 3 more in Saudi Arabia

Filed Under: **MERS-CoV**


Lisa Schnirring | News Editor | CIDRAP News | Nov 29, 2016

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Today Saudi Arabia's health ministry reported three new MERS-CoV infections in men who hail from different parts of the country, as the World Health Organization (WHO) provided more details on six cases reported earlier this month, two of whom had been exposed to camels or camel milk.

New cases from 3 different cities

In its daily update today, the Ministry of Health (MOH) said the patients are all Saudi citizens who have symptoms, including a 50-year-old from Riyadh who is in critical condition, a 78-year-old from Rejal Alma in the southwestern corner of the country who is also listed as critical, and a 59-year-old from Yanbua near the western border who is in stable condition.

None of the men are healthcare workers and all had primary sources of infection, meaning they likely weren't exposed to another patient infected with Middle East respiratory syndrome coronavirus (MERS-CoV).



Jon Connell / Flickr cc



Saudi officials announce 4 new MERS cases

Filed Under: [MERS-CoV](#)

[Lisa Schnirring](#) | [News Editor](#) | [CIDRAP News](#) | [Dec 05, 2016](#)

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Saudi Arabia's Ministry of Health (MOH) reported four new MERS-CoV cases in the past 3 days, including two from the holy city Medina, as the World Health Organization (WHO) today fleshed out more details about nine of the country's recently reported cases, four of which had a history of contact with camels or raw camel milk.

The new cases are part of a small but steady stream of cases from the country in which MERS-CoV (Middle East respiratory syndrome coronavirus) was first detected 4 years ago.

One of 4 new cases involved camel contact

All of the newly reported MERS cases involve men. On Dec 2 the MOH announced two cases, those of a 62-year-old Saudi from Sakaka in the northwestern part of the country and a 73-year-old Saudi from Medina, located in west central Saudi Arabia. Both of the patients are listed in stable condition and had primary sources of infection, meaning investigators found they weren't likely exposed to another sick patient.



Shabbir Siraj / Flickr cc

Prophet's Mosque in Medina, a city that has had 2 new MERS cases.



News Scan for Dec 06, 2016

3 new MERS cases reported in Saudi Arabia

The Saudi Arabian Ministry of Health (MOH) reported three new MERS-CoV cases today, and announced the death of a former patient. All three new patients are listed as having primary exposure to the virus, which means it is unlikely they contracted the disease from another person.

The new patients are all Saudi men: a 58-year-old from Afif, a 78-year-old from Riyadh, and a 24-year-old from Al Hofuf. All patients presented with symptoms of MERS-CoV (Middle East respiratory syndrome coronavirus) and remain in stable condition. There have been other recent cases announced in these cities, but no suggestion yet of a cluster of infections.

The MOH also said that a 62-year-old Saudi man from Sakaka whose case was reported earlier has died.

The new cases raises Saudi Arabia's total from the disease to 1,501 since the first human infections were detected in 2012. So far 621 people have died from MERS. Seventeen people are still being treated for their recently announced illnesses.

Dec 6 MOH report



News Scan for Dec 09, 2016

Three new cases of MERS confirmed in Saudi Arabia

The Saudi Arabian Ministry of Health (MOH) today confirmed three new cases of MERS-CoV, resulting in one death. The patient who died had direct contact with camels.

Two expatriate men, a 53-year-old from Riyadh and a 49-year-old from Jeddah, are in critical and stable condition after presenting with symptoms of MERS-CoV (Middle East respiratory syndrome coronavirus). The source of infection for both men is listed as primary, meaning they did not contract the respiratory virus from anyone else.

The Saudi man who died was 60 years old and from Mahayel Aseer.

The new cases raise Saudi Arabia's total from the disease to 1,505 since the first human infections were detected in 2012. So far 622 people have died from MERS. Eighteen people are still being treated for their recently announced illnesses.

Dec 9 MOH report



Saudi Arabia reports more MERS cases; WHO updates risk assessment

Filed Under: [MERS-CoV](#)

[Lisa Schnirring](#) | News Editor | [CIDRAP News](#) | Dec 12, 2016

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Saudi Arabia's ministry of health (MOH) reported two new MERS-CoV cases over the weekend, and the World Health Organization (WHO) issued an updated risk assessment for the virus, its first since July 2015, noting that experts are still deeply concerned about continuing healthcare spread, though the outbreaks are smaller and stopped relatively quickly.

In other Middle East respiratory syndrome coronavirus (MERS-CoV) developments, South Korean researchers recently published their analysis of transmission patterns during the country's large hospital outbreak, which showed a connection between super-spreading events, doctor shopping, and emergency department visits.

MERS sickens two more Saudis

One of the new cases involves a 59-year-old Saudi man from Mahayel Aseer, located in the southwestern corner of the country, who became ill after direct contact with camels, the MOH said on Dec 10. The man is listed in stable condition.



Lucia Lucci / iStock



News Scan for Dec 13, 2016

Saudi Arabia reports new MERS case

The Saudi Arabian Ministry of Health (MOH) announced one new case of MERS-CoV today. The patient had direct contact with camels.

The 72-year-old Saudi man from Taif is in critical condition because of his Middle East respiratory syndrome coronavirus (MERS-CoV) infection.

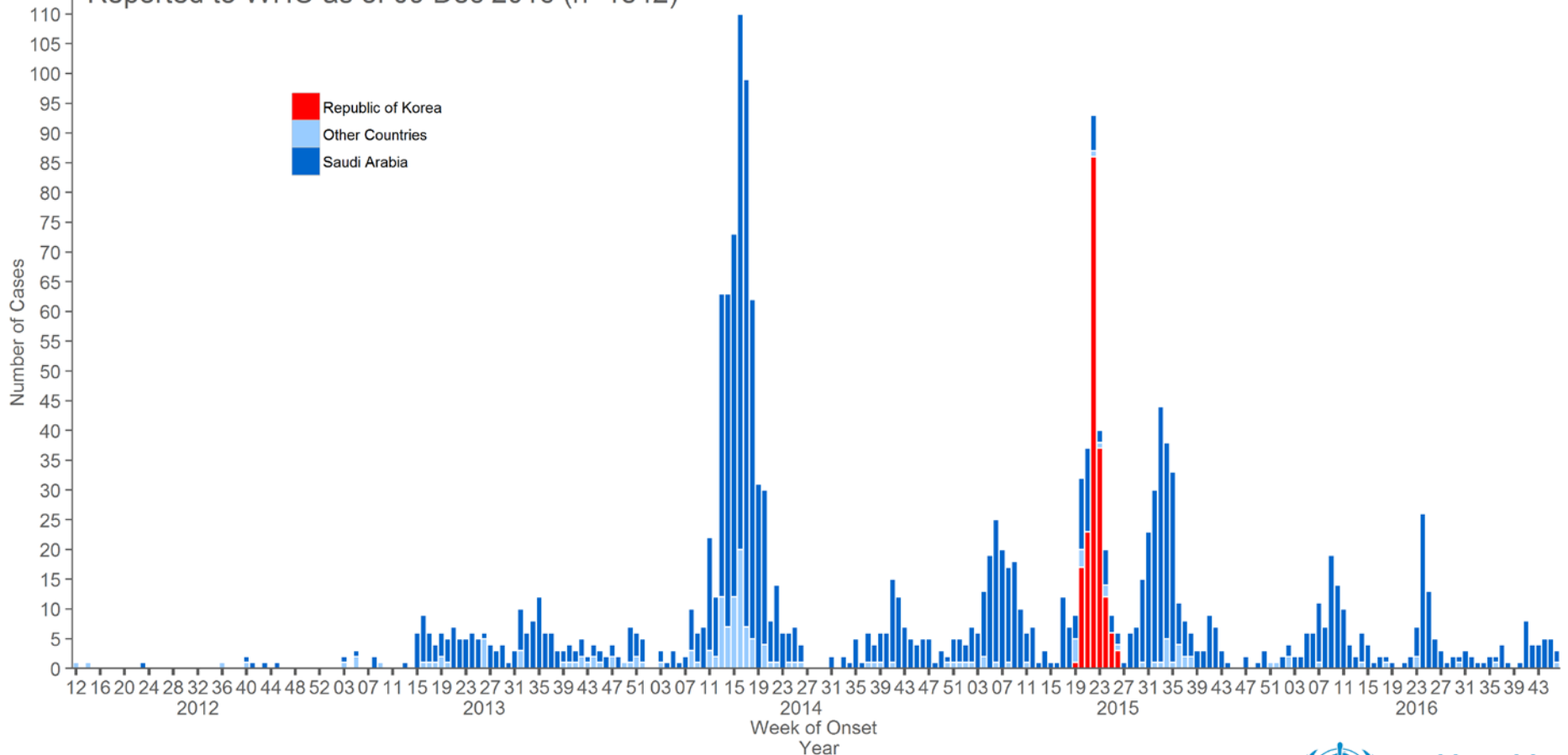
Contact with camels is a known risk factor for contracting the disease. Scientists do not yet understand how camels transmit the respiratory virus to humans, but drinking raw camel milk, raising camels, and eating their meat have all been linked to MERS cases.

The development raises Saudi Arabia's total number of MERS-CoV cases to 1,508 cases, 625 of them fatal. Fourteen people are currently recovering from infections.

Dec 13 MOH report

Confirmed global cases of MERS-CoV

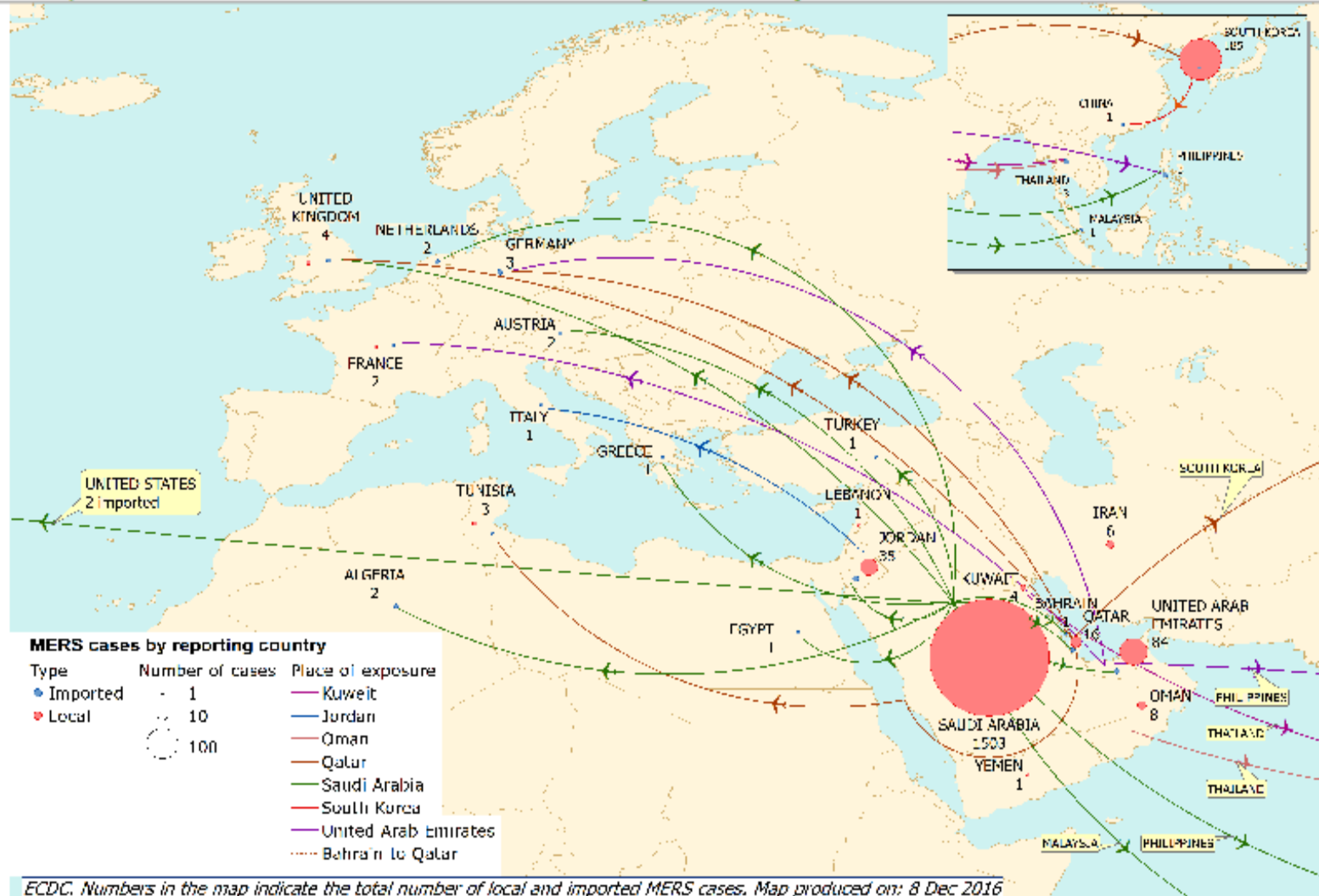
Reported to WHO as of 09 Dec 2016 (n=1842)



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.

Distribution of confirmed cases of MERS-CoV by place of reporting and probable place of infection, March 2012 – 8 December 2016 (n=1 875)





News Scan for Dec 01, 2016

Study says pigs, llamas susceptible to MERS-CoV infection

Pigs and llamas appear prone to infection with Middle East respiratory syndrome coronavirus (MERS-CoV), according to researchers who experimentally infected four animal species and reported their findings yesterday in *Emerging Infectious Diseases*.

Spanish and Dutch investigators inoculated 14 pigs, 8 llamas, 14 sheep, and 8 horses with MERS-CoV intranasally. They then collected nasal swabs at various times afterward.

Three each of the llamas, horses, and pigs excreted mucus after inoculation. Only pigs and llamas, however, excreted virus in the nose, as determined by polymerase chain reaction testing. Starting 2 days after inoculation, 7 of 14 pigs and 7 of 8 llamas tested positive for infectious virus for at least 1 day. Infectious MERS-CoV was found in pigs 4 days after inoculation and in llamas 7 days after inoculation, and viral titers were lower in the pigs.

A similar study last year in the journal *Viruses* found no MERS-CoV shedding in goats, sheep, and horses.

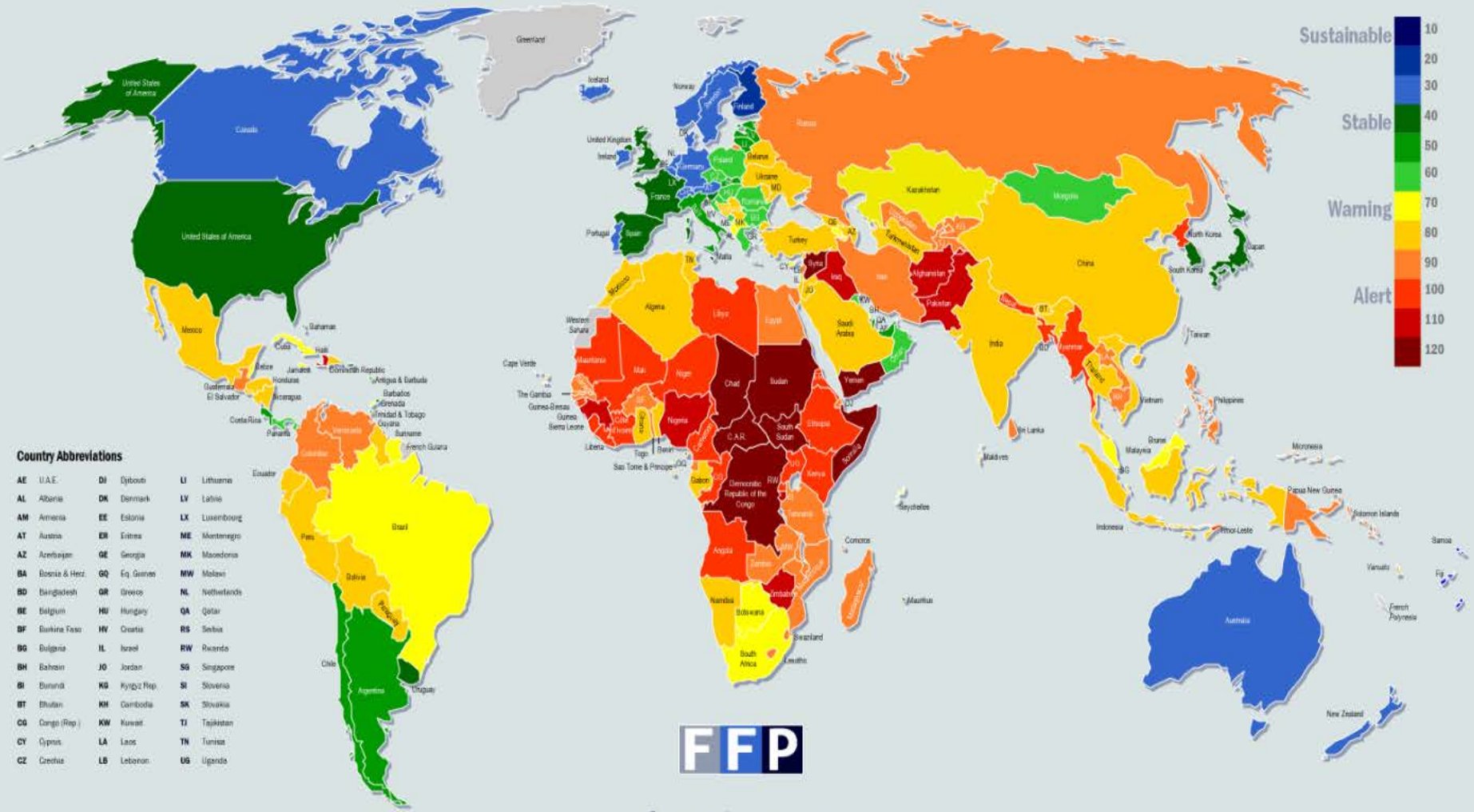
Regarding the results in pigs, the authors wrote, "The finding that pigs can be infected with MERS-CoV suggests that other members of the family Suidae could be susceptible to the virus, such as common warthogs (*Phacochoerus africanus*), bushpigs (*Potamochoerus larvatus*), and wild boars (*Sus scrofa scrofa*). Indeed, these animals are commonly found in the Greater Horn of Africa or the Middle East, sharing territories and water sources with dromedaries."

Nov 30 *Emerg Infect Dis* study

Aug 19, 2015 *Viruses* study

- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
 - Flu vaccine
- 3. Antimicrobial resistance**
- 4. Ebola**
- 5. MERS-CoV**
- 6. Potential impact of Trump Administration**
- 7. Other**

Fragile States Index: Fragility in the World 2016



Country Abbreviations

AE	UAE	DI	Djibouti	LI	Lithuania
AL	Albania	DK	Denmark	LV	Latvia
AM	Armenia	EE	Estonia	LX	Luxembourg
AT	Austria	ER	Eritrea	ME	Montenegro
AZ	Azerbaijan	GE	Georgia	MK	Macedonia
BA	Bosnia & Herz.	GQ	Eq. Guinea	MW	Malawi
BD	Bangladesh	GR	Greece	NL	Netherlands
BE	Belgium	HU	Hungary	QA	Qatar
BF	Burkina Faso	HR	Croatia	RS	Serbia
BG	Bulgaria	IL	Israel	RW	Rwanda
BH	Bahrain	JO	Jordan	SG	Singapore
BI	Burundi	KG	Kyrgyz Rep.	SI	Slovenia
BT	Bhutan	KH	Cambodia	SK	Slovakia
CG	Congo (Rep.)	KW	Kuwait	TJ	Tajikistan
CY	Cyprus	LA	Laos	TN	Tunisia
CZ	Czechia	LB	Lebanon	UG	Uganda



Trump names Rep. Tom Price as next HHS secretary


President-elect Donald Trump has chosen Rep. Tom Price (R-Ga.), a fierce critic of the Affordable Care Act and a proponent of overhauling the nation's entitlement programs, to lead the Department of Health and Human Services.

In a news release early Tuesday, Trump announced his selection of Price, a third-generation doctor who chairs the House Budget Committee and became a champion of Trump's candidacy. In naming him to join his Cabinet, the president-elect called Price "exceptionally qualified to shepherd our commitment to repeal and replace Obamacare and bring affordable and accessible health care to every American."

Trump also named Seema Verma, a health-care consultant who was the architect of Medicaid changes in Vice President-elect Mike Pence's home state of Indiana, to run a crucial section of HHS: the Centers for Medicare and Medicaid Services.

As HHS secretary, Price would be the nation's top health official and the incoming administration's point person for dismantling the sprawling 2010 health-care law, which Trump promised during his campaign to

Trump names Scott Pruitt, Oklahoma attorney general suing EPA on climate change, to head the EPA

By [Chris Mooney](#), [Brady Dennis](#) and [Steven Mufson](#) December 8 

President-elect Donald Trump on Thursday nominated Scott Pruitt, the attorney general of the oil and gas-intensive state of Oklahoma, to head the Environmental Protection Agency, a move signaling an assault on President Obama's climate change and environmental legacy.

Pruitt has spent much of his energy as attorney general fighting the very agency he is being nominated to lead.

He is the third of Trump's nominees who have key philosophical differences with the missions of the agencies they have been tapped to run. Ben Carson, named to head the Department of Housing and Urban Development, has expressed a deep aversion to the social safety net programs and fair housing initiatives that have been central to that agency's activities. Betsy DeVos, named education secretary, has a passion for private school vouchers that critics say undercut the public school systems at the core of the government's mission.

- 1. Vectorborne diseases**
 - Zika, Yellow Fever, Chikungunya
- 2. Avian Influenza**
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- 7. Other**

GLOBAL HEALTH

AIDS epidemic nears control in three African countries

Massive new surveys show stunning progress

By Jon Cohen

Amidst the reams of statistics that pour out on every World AIDS Day on 1 December came one surprising bit of good news this year. Three neighboring, cash-strapped countries in hard-hit southern Africa—Malawi, Zambia, and Zimbabwe—have had remarkable success against the virus, according to the most comprehensive study done to date.

The new study, coordinated out of the Columbia University Mailman School of Public Health and led by epidemiologist Wafaa El-Sadr, collected massive amounts of on-the-ground data by visiting 80,000 randomly selected households in the three countries. The upshot: HIV-infected people in the region are getting treated and sticking with their drug regimen in numbers that have surprised and delighted experts. The survey found that up to two-thirds of HIV-infected people in the three countries have fully suppressed the virus, slashing the rate of new infections. (In the United States, the comparable figure is 30%.) “We’re getting very close to the number that shuts down epidemics,” says Deborah Birx, who heads the U.S. President’s Emergency Plan for AIDS Relief (PEPFAR) in Washington, D.C.

Until now, the most authoritative estimates of new HIV infection rates, or incidence, and prevalence have come from the Joint United Nations Programme on HIV/

AIDS (UNAIDS). Those are based on mathematical models that largely extrapolate from clinics and nonrandomized surveys. The UNAIDS estimates do not include the level of virus in each infected person, a key indication of how well interventions are working.

The new population-based HIV impact assessments (PHIAs), which began in 2015 and are funded by PEPFAR, fill that gap. In addition to going door-to-door in cities, teams traveled to the remote countryside, often pulling up to thatch-roofed homes and erecting pop-up tents in which nurses did blood draws. Social scientists also interviewed participants about their health and lifestyle. Blood was assessed on the spot for HIV and syphilis, with counseling and treatment referrals made for anyone in need. Then the teams took the vials back to cities to analyze viral levels. “We have to reach people we haven’t reached and know exactly where the crusade is failing,” El-Sadr said during a survey in Zimbabwe.

The results, released in press releases and fact sheets, mostly confirm the UNAIDS estimates of HIV’s reach in the three countries—which each have a prevalence of more than 10% of the adult population. But they showed an annual rate of new infections in Zimba-

bwe and Zambia that was substantially lower than expected (see table, below). Peter Ghys, who directs strategic information and evaluation at UNAIDS in Geneva, Switzerland, says his team will incorporate the PHIA data in future modeling estimates.

Across the region, the PHIA results suggest, the rate of new infections has fallen by half since 2003. Data on viral levels point to one factor: At least 86% of people in each country receiving antiretroviral treatment had “fully suppressed” HIV. This means they had such low levels of virus in their blood that the drugs not only are staving off AIDS, but making it highly unlikely that they will infect others. “We were amazed when we saw this,” El-Sadr says.

The result helps assuage worries that many infected people in those countries are not

sticking with their treatment. PEPFAR surveys of clinics had suggested that more than 20% of people who started treatment ended up dropping it. “We were misled at the program level about retention,” Birx says. The PHIA data’s high level of viral suppression suggests that instead, “people were moving from one clinic to another and

it looked like they were lost to follow-up.”

All three countries have received substantial international assistance for HIV/AIDS prevention and treatment: Since 2004, PEPFAR has invested \$4 billion, and the Global Fund to Fight AIDS, Tuberculosis and Malaria has provided \$2 billion more. But funding alone does not explain the gains against the virus, Birx says. “These programs and the people implementing them have done an extraordinary job of working with the community and the individual clients.”

The new data have important implications for the global push to end HIV/AIDS epidemics by 2030. To achieve that, UNAIDS has set what is known as the 90-90-90 goal for 2020. UNAIDS modeling shows that epidemics will peter out if 90% of infected people know their HIV status, 90% of that group receives antiretrovirals, and 90% on treatment have undetectable viral levels. This translates to undetectable viral levels in 73% of all HIV-infected people in a population—including those who don’t know their status and have uncontrolled infections. The PHIA numbers suggest the goal is within reach: Malawi is

Vital statistics

A new study in southern Africa reveals a lower than expected annual rate of new HIV infections.

COUNTRY	PREVALENCE	NEW INFECTIONS
Malawi	10.6%	0.37%
Zambia	12.3%	0.66%
Zimbabwe	14.6%	0.45%




COLUMBIA UNIVERSITY

WHO marks malaria progress but worries about flat funding

Filed Under: **Malaria**

Lisa Schnirring | News Editor | CIDRAP News | Dec 13, 2016

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Though much progress has been made connecting people in malaria-endemic countries with key disease control interventions, significant gaps remain in some regions, with stagnant global funding that could slow progress on driving down the disease threat, according to an annual snapshot of the global malaria battle released today.

The assessment is detailed in a 186-page report from the World Health Organization (WHO) that lays out the latest global and regional malaria trends, highlights progress toward global targets, and describes success and challenges in controlling and eliminating the disease.



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STAT

What's the next global disease threat?

Some predictions

By HELEN BRANSWELL

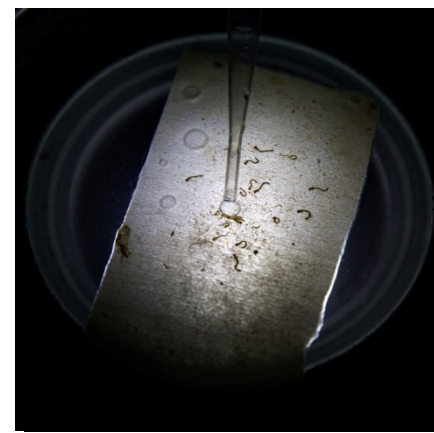
NOVEMBER 7, 2016

VIENNA — Wondering what the next [SARS](#) or Zika-like disease heading our way might be? At a conference this past weekend in the Austrian capital, a leading researcher made some predictions.

Kevin Olival, the associate vice president for research at the nonprofit EcoHealth Alliance, used a formula that takes into account the number of animal species a virus can infect and the number of vectors — think types of mosquitoes or ticks — that can transmit it.

Looking at flaviviruses — the family that includes [Zika](#), [dengue](#) and [yellow fever](#) — Olival rhymed off the top three on his “ones to watch” list at the International Meeting on Emerging Diseases and Surveillance.

They are hardly household names — the Usutu, Ilheus and Louping ill viruses. All three have on rare occasions infected people, but they also infect a number of other animal species, which suggests they may have what it takes to jump species. Virologists sometimes call viruses that can do this “promiscuous.”



Finding the world's unknown viruses — before they find us

By HELEN BRANSWELL [@HelenBranswell](#)

DECEMBER 13, 2016

One by one, the viruses have slipped from their hiding places in nature to threaten global populations — SARS, MERS, Zika.

In each case, scientists have scrambled to identify the viruses and to [develop vaccines](#) or drugs to stop their spread. After each crisis, the assessment has been the same: Countermeasures were not ready in time to help in the containment effort.

“Always too late,” said Jonna Mazet, a scientist at the University of California, Davis, who is keen to break the bugs’ winning streak. “We need to think about something different.”

Mazet is a key player in an ambitious endeavor called the [Global Virome Project](#), which has proposed cataloguing nearly all of the unknown viruses lurking in nature around the world. In a nutshell, Mazet and other experts want to search out mystery threats before they find us.

The idea has been around for a while and is supported by individual scientists and organizations including the US Agency for International Development, the nonprofit EcoHealth Alliance, HealthMap, ProMED, and the epidemic risk firm Metabiota.

This is the most dangerous time for our planet

Stephen Hawking

We can't go on ignoring inequality, because we have the means to destroy our world but not to escape it

As a theoretical physicist based in Cambridge, I have lived my life in an extraordinarily privileged bubble. Cambridge is an unusual town, centred around one of the world's great universities. Within that town, the scientific community that I became part of in my 20s is even more rarefied.

And within that scientific community, the small group of international theoretical physicists with whom I have spent my working life might sometimes be tempted to regard themselves as the pinnacle. In addition to this, with the celebrity that has come with my books, and the [isolation imposed by my illness](#), I feel as though my ivory tower is getting taller.

So the recent apparent rejection of the elites in both America and Britain is surely aimed at me, as much as anyone. Whatever we might think about the decision by the British electorate to [reject membership of the European Union and by the American public to embrace Donald Trump](#) as their next president, there is no doubt in the minds of commentators that this was a cry of anger by people who felt they had been abandoned by their leaders.

It was, everyone seems to agree, the moment when the forgotten spoke, finding their voices to reject the advice and guidance of experts and the elite everywhere.

DEADLIEST ENEMY

Michael T. Osterholm, PhD, MPH,
and Mark Olshaker



OUR WAR AGAINST KILLER GERMS



Questions, Comments and Discussion



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