



Advancing global health since 1903

AMERICAN SOCIETY OF TROPICAL MEDICINE AND HYGIENE

111 Deer Lake Road, Suite 100
Deerfield, IL 60015 USA
+1-847-480-9592
FAX +1-847-480-9282
info@astmh.org
www.astmh.org

**EMBARGOED UNTIL WEDNESDAY, NOVEMBER 2, 2011
4:00 PM US CENTRAL/5:00 PM US EASTERN/2100 Hours GMT**

Contact:

**Bridget DeSimone, +1 301.280.5735, bdesimone@burnesscommunications.com
Preeti Singh, +1 301.280.5722, psingh@burnesscommunications.com**

FLU WATCH:

**Scientists in Global Flu Hot-Spot Report Rare Occurrence of Humans
Harboring Two Strains of the Disease at the Same Time**

While dual infections in Cambodia did not produce new strain, study cites need for continuous tracking against risk of different influenza viruses combining to create a new pandemic

(Deerfield, Ill., USA – November 2, 2011) Researchers conducting influenza-like illness surveillance in Cambodia have confirmed a rare incidence of individuals becoming infected with a seasonal influenza and the pandemic strain at the same time, a reminder of the ongoing risk of distinct flu viruses combining in human hosts to produce a more lethal strain, according to a report in the November issue of the *American Journal of Tropical Medicine and Hygiene*. A pandemic strain is a type of flu against which people have little or no natural immunity.

While the individuals recovered and the two strains did not recombine into a new and different virus, experts say coinfections in Southeast Asia deserve particularly close scrutiny given the ongoing transmission of the deadly avian influenza virus H5N1 and circulation of the pandemic H1N1 influenza that first emerged in 2009. The report comes as flu season gets underway in the United States, and while Cambodia and other tropical parts of Asia are reporting continued flu activity.

As of October 10, 2011, the World Health Organization (WHO) had tallied 566 known human infections with H5N1 and 332 deaths for a fatality rate of over 60 percent. In Cambodia, 16 of 18 infected individuals have died, with the most recent case reported in August. Thus far the virus has shown a very limited ability to pass from human to human—almost all the infections have been traced to contact with sick poultry and other diseased birds. But in the scientific community, fears remain that under the right conditions avian flu could acquire far greater human virulence through a co-mingling—or reassortment—with a human strain.

“Influenza viruses are continually changing,” said Patrick Blair, PhD, director of respiratory diseases at the US Naval Health Research Center in San Diego, California. “Finding a coinfection in an area where there is considerable seasonal flu, pandemic flu and H5N1 avian flu shows there is an opportunity for co-mingling in swine or human hosts that could create an ominous global health problem.” Blair co-authored the study with colleagues from the Cambodia National Institute of Public Health, US Navy Medical Research Unit-2-Phnom Penh, and the US (Maryland)-based J. Craig Venter Institute.

The scientists identified the coinfection from viruses isolated from a young Cambodian boy and his teacher in October of 2009, several months after the pandemic H1N1 influenza strain began circulating around the world. Tests revealed the two viruses to be H1N1 and a human seasonal flu variety known as H3N2. When the researchers conducted a complete sequencing of both virus genomes, they were able to determine there had been no “genetic recombination.”

“This kind of thorough surveillance and scientific investigation is the result of a commitment and collaboration of health authorities around the world—and particularly the US Department of Defense—to invest the resources required to remain vigilant against one of the biggest biological threats of our time,” said Peter J. Hotez, MD, PhD, noted infectious disease expert and president of the American Society of Tropical Medicine and Hygiene (ASTMH), which publishes the journal. “Highly infectious strains of the virus against which humans have little defense can spread from one continent to another with 24 hours.”

Staying Vigilant Against Worst-case Scenario

Blair said the mere existence of coinfection is of interest to disease experts for a number of reasons. First, as the study notes, coinfections are relatively rare. In one study conducted in 2010, scientists examined over 2,000 influenza samples without turning up a single coinfection. Other studies pinpointed a relatively small number of co-infections involving the pandemic H1N1 virus: one in Singapore, six in China, and 11 in New Zealand.

Researchers are keenly interested in identifying any coinfections because, regardless of their immediate risk, there is an urgent need to learn more about the human role in the “genetic reshuffling” that allows different influenza strains to interact and create a pandemic strain.

For example, researchers probing the dual infections in New Zealand found that the H1N1 pandemic strain was co-inhabiting with a strain that was resistant to the anti-viral oseltamivir (sold under the brand name Tamiflu). Such coinfections, they said, “raise the potential of an oseltamivir-resistant pandemic strain.”

As bad as that would be, Blair said the worst-case scenario for many disease experts is one in which a coinfection with avian flu and a human strain results in a highly lethal virus that easily jumps from person to person.

As the study on the Cambodian coinfection notes, the prevalence of H5N1 “in poultry in many areas of Southeast Asia provides increased opportunity for human exposure and adaptation of a lethal virus suitable for sustained human transmission.” The researchers point out that several

pandemic flu strains, including the 2009 H1N1 outbreak, have displayed a mix of genetic material from human and animal influenza.

For example, they note that H1N1 virus samples isolated in Southern California in April of 2009 “contained genetic elements from four different sources, including North American swine influenza viruses, North American avian influenza viruses, human influenza viruses, and a Eurasian swine influenza viruses.” Similarly, the flu pandemics of 1957 and 1968 have both been traced to a “reassortment between human and avian strains.”

Blair said it’s hard to predict the chances of H5N1 providing the genetic platform for the next pandemic. “Even though there may be a very small chance of this occurring, avian flu is still percolating in Southeast Asia and it continues to exhibit an extraordinarily high fatality rate in humans,” he said.

###

About ASTMH

[American Society of Tropical Medicine and Hygiene](#), founded in 1903, is a worldwide organization of scientists, clinicians and program professionals whose mission is to promote global health through the prevention and control of infectious and other diseases that disproportionately afflict the global poor.