Novel Pathogen Research at Human-Animal Nexus

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Plane passengers behaving badly are you guilty of these annoying habits?


http://www.eastbysoutheast.com/china-maritime-silk-road-africa/


Emerging Infectious Disease Problems

Avian influenza

MERS-coronavirus

Ebola virus

H3N2 variant influenza

https://www.smithsonianmag.com
Selection of AMR pathogens

From http://essays.biochemistry.org/content/61/1/11
E. Coli outbreak knows where it

Frozen tuna recall
Salmonella risk

By Kelsey M. Mackin on April 17, 2020

Jensen Tuna of Louisiana is recalling their products because it may potentially be contaminated with Salmonella, confirmed to date in some of their products. The recall is in response to the Centers for Disease Control and Prevention outbreak that has now infected 96 people.

The recall notice posted on the FDA's website says the recall is in response to an outbreak of Salmonella. The recall involves several products from March 26 to April 3, 2020, including but not limited to:

- 20 oz. can of Frozen Tuna in Water
- 20 oz. can of Frozen Tuna in Water with Jalapenos
- 20 oz. can of Frozen Tuna in Water with Mango
- 20 oz. can of Frozen Tuna in Water with Pineapple

The recall notice states that some of the products may be contaminated with Salmonella. The recall notice also includes a list of codes and lot numbers that are affected by the recall.

The recall notice states that consumers should not consume the affected products and should return them to the place of purchase for a full refund. Consumers are also advised to wash their hands with soap and water after handling the affected products.

The recall notice also includes information on how to contact Jensen Tuna for more information.

By Michael Brice-Saddler
April 8

The Centers for Disease Control and Prevention is investigating a multi-year Listeria outbreak linked to sliced deli meat or cheese contaminated with the bacteria Listeria monocytogenes that has hospitalized eight people, one of whom died.

All of the people sickened were exposed to the same strain of listeria.

The CDC's announcement Wednesday also comes as Consumer Reports is analyzing the results of our own testing of counter-sliced deli meat. One of our samples of turkey, purchased from a deli in New York City, contained a strain of listeria similar to the one involved in this current outbreak.
In a nutshell

• No one person or discipline is trained to engage such complex problems
• No one agency or organization has authority to control such complex problems
Such Complex Problems Require Collaborative Interdisciplinary Partnerships
One Health Defined

“One Health is the collaborative effort of multiple disciplines - working locally, nationally, and globally - to attain optimal health for people, animals, and our environment.”

AVMA One Health Initiative Task Force 2008
A One Health approach gains cooperation from all parties involved and employs public health, veterinary health, and environmental health approaches to bring balance to solving difficult public health problems.
Interest in One Health is Increasing

Known academic institutions and organizations with some type of One Health activity

Aug 2016

Sept 2018

70% increase

New programs since 2016

_Infection Ecology & Epidemiology. 2016 Jan 1;6(1):33680._
From PLOS Biology | DOI:10.1371/journal.pbio.1002448 April 21, 2016. Number of papers captured by our search through time. Blue = veterinary community; gold = ecology community; red = group 3. Numbers are the annual percent growth rate within each community.

...."The number of publications fulfilling our search criteria increased by 14.6% per year, which is faster than growth rates for life sciences as a whole and for most biology subdisciplines."
One Health has now been mentioned as a approach in more than 100 active or archived requests for proposals (RFPs) since 2007 on www.grants.gov. On 9/8/18, we extracted summary data from 96 of these RFP records (HHS, USAID, USDA, DoD, EPA) and found grant funding to total $4,885,519,322.
CHAPTER 2

Value of Investing in One Health

Given the high cost of emerging diseases as well as the persistent burden of endemic diseases (see Figure 2.1 and Table 2.1), One Health should be considered to assist client countries in strengthening their ability to address known and potential disease threats at the human-animal-environment interface. For a One Health approach to be warranted, it must provide added value. Fundamentally, strong sectoral health systems (e.g., human health, animal health, environmental health) must be in place—or existing systems strengthened—to support effective coordination and collaboration. Relevant metrics for value generation depend on the goal of an investment or client country, but in general, One Health offers synergies among these sectoral systems, providing expanded capacity and effectiveness in prevention of damages and/or control of disease, efficiency, and ultimately financial savings.

Figure 2.1: Examples of economic impacts of disease outbreaks (see also Table 2.1): icons represent examples of highly-affected sectors.
G20 nations pledge to strengthen health systems, combat antimicrobial resistance

HAMBURG: The G20 nations, including India, today pledged to strengthen health systems and also combat the menace of antimicrobial resistance, which the grouping termed as a "growing threat" to public health and economic growth.

The declaration adopted by the nations said they would aim to tackle the spread of AMR through the implementation of their respective national action plans based on "one health" approach.

"We call on the UN to keep global health high on the political agenda and we strive for cooperative action to strengthen health systems worldwide, including through developing the health workforce," the declaration said.
Duke One Health Research & Training Network

>30 Partners  |  >30 pathogens  |  ~30 projects  |  13 countries

Website: [https://sites.globalhealth.duke.edu/dukeonehealth/](https://sites.globalhealth.duke.edu/dukeonehealth/)
Address complex health problems through the One Health approach, microbiology, and epidemiology methods.

What We Do?

Pathogen Discovery
- Non-invasive Environmental Sampling Techniques for the Detection of Novel Pathogens
  - Bioaerosol Sampling
  - Molecular and Culture Techniques

Epidemiology
- Epidemiology Studies Among Humans & Animals with a Focus on Zoonotic Pathogens
  - Livestock Production
  - New Disease Hotspots
  - Live Animal Markets

Diagnostic Evaluations
- Field Evaluations of Diagnostic Assays and Platforms
  - Diagnostic Platforms
  - Diagnostic Kits

Training & Capacity Building
- Workshops in Conducting Molecular Surveillance for Biological Threats
  - On-site or On-campus Training
Working Closely with Veterinarians
Studying Places Where Humans and Animals Mix
We publish our research! In 2019 we have already published 19 papers in peer-reviewed journals (9 with impact factor > 5), with 11 more under review.
Recent One Health team members who have been offered faculty positions

Laura Pulscher, MSc
Nguyen Thi Tham, MPH
Sarah Philo, MSc
Jane Fieldhouse, MSc
Laura Borkenhagen, MSc
Ben D. Anderson, MPH, PhD
Michael von Fricken, MPH, PhD
Amber N. Barnes, MPH, PhD
Emily S. Bailey, PhD
Kristen K. Coleman, PhD

Recent One Health team members who are pursuing PhDs
Which pathogen threats should we be most concerned about?
Bill Gates thinks a coming disease could kill 30 million people within 6 months — and says we should prepare for it as we do for war

Kevin Loria  Apr 27, 2018, 5:38 PM

• The next deadly disease that will cause a global pandemic is coming, Bill Gates said on Friday at a discussion of epidemics.

• We're not ready.
Our One Health Laboratory’s Focus - Novel Respiratory Virus Detection & Epidemiological Study

More Cases of Rare 'Polio-Like' Illness Pop Up Around the US
By Rachael Rettner, Senior Writer  |  October 11, 2018 07:19am ET

Enterovirus D68 found in 4 patients who have died, including 10-year-old girl
By Joseph Wilson and Greg Brannon, CMMI
Updated 5:50 AM ET, Thu, October 2, 2014

CDC: Deadly Mutation of Common Cold Kills 10, Sickens 140 in Past 18 Months
Friday, November 16, 2007

Severe pediatric enterovirus 71 infection investigated in Hong Kong
Posted by Staff on November 25, 2015 // 1 Comment

Emerging Killer Virus Starts Like a Cold, But Kills Many
Saturday, July 19, 2008 by David Gutierrez, staff writer

2 Swine Flu Cases Among 3 Fever Deaths in Tiruchi
By Express News Service  |  Published: 21st November 2015 06:12 AM
Last Updated: 21st November 2015 06:12 AM
A Mini Review of the Zoonotic Threat Potential of Influenza Viruses, Coronaviruses, Adenoviruses, and Enteroviruses

A systematic review of evidence that enteroviruses may be zoonotic

Jane K. Fieldhouse, Xinye Wang, Kerry A. Mallinson, Rick W. Tsao, and Gregory C. Gray

The continual threat of influenza virus infections at the human–animal interface

What is new from a one health perspective?

Detecting Novel Respiratory Viruses that Emerge from the Human-Animal Interface

Molecular Detection Algorithms

Routine Assessment

Pathogen Discovery

Influenza Virus

Adenovirus

Coronavirus

Revealing Patterns in Genomes

Flu and Throat swab

Early detection

Pooled testing

Cluster analysis

Identifying human

Virion analysis

Pathogen Discovery

Routine Assessment

Pathogen Discovery

Revealing Patterns in Genomes

Flu and Throat swab

Early detection

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Early detection

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Cluster analysis

Identifying human

Virion analysis

Revealing Patterns in Genomes

Flu and Throat swab

Early detection

Pooled testing

Cluster analysis

Identifying human

Virion analysis
Recent One Health Pathogen Detection Workshops

1. Hanoi, Vietnam
2. Erbil, Iraq
3. Tbilisi, Georgia
4. Singapore
5. Sibu, Malaysia
6. Hanoi, Vietnam
Horse Influenza A Viruses

- EIV 2nd most important respiratory tract disease in adult horses
- EIV epizootics are common among equine species
- Equine mortality as high as 20%
- Chiefly H3N8 viruses today
Serological evidence of equine influenza infections among persons with horse exposure, Iowa

Kerry R. Leedom Larson\textsuperscript{a}, Gary L. Heil\textsuperscript{b}, Thomas M. Chambers\textsuperscript{c}, Ana Capuano\textsuperscript{d}, Sarah K. White\textsuperscript{b}, Gregory C. Gray\textsuperscript{b,\textasteriskcentered}

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\textsuperscript{c} Gluck Equine Research Center, Department of Veterinary Science, University of Kentucky, Lexington, KY, USA
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H3N8 subtype
Occupational exposure
Seroepidemiologic study
Veterinarians

ABSTRACT

Background: Equine influenza virus (EIV) is considered enzootic in North America and experimental studies have documented human EIV infections.

Study design: This cross-sectional study examined 94 horse-exposed and 34 non-exposed controls for serological evidence of EIV infection. Sera were evaluated for antibodies against three EIV and two human H3N2 viruses using microneutralization (MN), neuraminidase inhibition (NI), enzyme-linked lectin (ELLA), and hemagglutination inhibition (HI) serological assays. Risk factor analyses were conducted using logistic regression and proportional odds modeling.

Results: There was evidence of previous infection by MN assay against A/equine/Ohio/2003 (H3N8) but not the other 2 EIVs. Eleven (11.7%, maximum titer 1:320) horse-exposed and 2 (5.9%, maximum titer 1:160) control subjects had MN titers $\geq$ 1:80. Among the horse-exposed, 18 (19.1%) were positive by NI assay and 8 (8.5%) had elevated ELLA titers $\geq$ 1:10. Logistic regression modeling among horse-exposed revealed that having an elevated MN or ELLA titer ($\leq$ 1:10) was associated with having a positive NI titer (OR = 4.9; 95% CI = 1.3–18.7, and OR = 53.2; 95% CI = 5.9–478.5, respectively). Upon proportional odds modeling, having worked as an equine veterinarian (OR = 14.0; 95% CI = 2.6–75.9), having a history of smoking (OR = 3.1; 95% CI = 1.2–7.7), and receipt of seasonal influenza vaccine between 2000 and 2005 (OR = 2.7; 95% CI = 1.0–5.0) were important independent risk factors for elevations in MN assay.

Conclusions: While we cannot rule out confounding exposures, these data support the premise that occupational exposure to EIV may lead to human infection.
A Review of Evidence that Equine Influenza Viruses Are Zoonotic

Tai Xie 1,2, Benjamin D. Anderson 1, Ulziimaa Daramragchaa 3, Maitsetset Chuluunbaatar 3 and Gregory C. Gray 1,*

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2 Faculty of Health Service, Second Military Medical University, Shanghai 200433, China
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Academic Editor: Janet M. Daly
Received: 14 May 2016; Accepted: 8 July 2016; Published: 12 July 2016

Abstract: Among scientists, there exist mixed opinions whether equine influenza viruses infect man. In this report, we summarize a 2016 systematic and comprehensive review of the English, Chinese, and Mongolian scientific literature regarding evidence for equine influenza virus infections in man. Searches of PubMed, Web of Knowledge, ProQuest, CNKI, Chongqing VIP Database, Wanfang Data and MongolMed yielded 2831 articles, of which 16 met the inclusion criteria for this review. Considering these 16 publications, there was considerable experimental and observational evidence that at least H3N8 equine influenza viruses have occasionally infected man. In this review we summarize the most salient scientific reports.

Keywords: equine influenza; influenza A; epidemiology; zoonotic diseases; H3N8
Historical Review

Equine Influenza Virus—A Neglected, Reemergent Disease Threat

Alexandra Sack, Ann Cullinane, Ulziimaa Daramragchaa, Maitsetseg Chuluunbaatar, Battsetseg Gonchigoo, and Gregory C. Gray

Author affiliations: Institute of Veterinary Medicine, Ulaanbaatar, Mongolia (A. Sack, U. Daramragchaa, M. Chuluunbaatar, B. Gonchigoo); Duke University, Durham, North Carolina, USA (A. Sack, G.C. Gray); Irish Equine Centre, Johnstown, Ireland (A. Cullinane); Duke-NUS Medical School, Singapore, Singapore (G.C. Gray); Duke-Kunshan University, Kunshan, China (G.C. Gray)

Abstract

Equine influenza virus (EIV) is a common, highly contagious equid respiratory disease. Historically, EIV outbreaks have caused high levels of equine illness and economic damage. Outbreaks have occurred worldwide in the past decade. The risk for EIV infection is not limited to equids; dogs, cats, and humans are susceptible. In addition, equids are at risk from infection with avian influenza viruses, which can increase mortality rates. EIV is spread by direct and indirect contact, and recent epizootics also suggest wind-aided aerosol transmission. Increased international transport and commerce in horses, along with difficulties in controlling EIV with vaccination, could lead to emergent EIV strains and potential global spread. We review the history and epidemiology of EIV infections, describe neglected aspects of EIV surveillance, and discuss the potential for novel EIV strains to cause substantial disease burden and subsequent economic distress.
Dog Influenza A Viruses

- H3N8 variant was first detected in Florida racing grey-hounds in 2004
- Dog farming may have contributed to canine adapted strains

https://barkpost.com/good/korean-dog-meat-farms/
WHO WE ARE

The Parrish laboratory
We are at the Eber Institute for Animal Health, College of Veterinary Medicine, Cornell University. We study viral diseases of animals, including dogs, cats, and horses, as well as wild animals like raccoons, mink, and other carnivores. The main viruses we have been studying include Canine and Feline Parvoviruses and Equine and Canine Influenza viruses, where we seek to understand the ways in which their host ranges can vary. We are also interested in the interactions of those as well as Adeno-Associated viruses and their interactions with antibodies.
No evidence for zoonotic transmission of H3N8 canine influenza virus among US adults occupationally exposed to dogs

Whitney S. Krueger, Gary L. Heil, Kyoung-Jin Yoon, Gregory C. Gray

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Correspondence: Whitney S. Krueger, College of Public Health & Health Professions, and Emerging Pathogens Institute, University of Florida, 2005 Mowry Road, PO Box 10009 Gainesville, FL 32611, USA. E-mail: wksk@phhp.ufl.edu

Accepted 26 September 2013. Published Online 14 November 2013.

Objectives. The zoonotic potential of H3N8 canine influenza virus (CIV) has not been previously examined; yet considering the popularity of dogs as a companion animal and the zoonotic capabilities of other influenza viruses, the public health implications are great. This study aimed to determine the seroprevalence of antibodies against CIV among a US cohort.

Design. A cross-sectional seroepidemiological study was conducted between 2007 and 2010.

Setting. Recruitment primarily occurred in Iowa and Florida. Participants were enrolled at dog shows, or at their home or place of employment.

Sample. Three hundred and four adults occupationally exposed to dogs and 101 non-canine-exposed participants completed a questionnaire and provided a blood sample.

Main outcome measures. Microneutralization and neuraminidase inhibition assays were performed to detect human sera antibodies against A/Canine/Iowa/13628/2005(H3N8). An enzyme-linked lectin assay (ELA) was adapted to detect antibodies against a recombinant N8 neuraminidase protein from A/Equine/Pennsylvania/1/2007(H3N8).

Results. For all assays, no significant difference in detectable antibodies was observed when comparing the canine-exposed subjects to the non-canine-exposed subjects.

Conclusion. While these results do not provide evidence for cross-species CIV transmission, influenza is predictably unpredictable. People frequently exposed to ill dogs should continually be monitored for novel zoonotic CIV infections.

Keywords. Communicable diseases, emerging, Dog diseases, influenza A virus, occupational exposure, seroepidemiologic studies, zoonoses.
Avian Influenza

Avian Influenza A Viruses

- In May 1997, investigations revealed 18 (H5N1) human cases (6 deaths) by the end of 1997, all of them in Hong Kong. Exposure to birds the major risk factor
- This led to the culling of 1.2 million birds and cost the government 245 million in Hong Kong dollars in compensation.
## Recent Avian Influenza Outbreaks that have Infected Man

<table>
<thead>
<tr>
<th>Years</th>
<th>Avian Influenza A</th>
<th>Country</th>
<th>Number of humans</th>
<th>Number of deaths</th>
</tr>
</thead>
<tbody>
<tr>
<td>1997</td>
<td>H5N1</td>
<td>Hong Kong</td>
<td>18</td>
<td>6</td>
</tr>
<tr>
<td>1999</td>
<td>H9N2</td>
<td>Hong Kong</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>2002</td>
<td>H7N2</td>
<td>Virginia</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>2003</td>
<td>H5N1</td>
<td>Hong Kong</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>2003</td>
<td>H7N7</td>
<td>The Netherlands</td>
<td>89</td>
<td>1</td>
</tr>
<tr>
<td>2003+</td>
<td>H9N2</td>
<td>Various</td>
<td>?</td>
<td>?</td>
</tr>
<tr>
<td>2003</td>
<td>H7N2</td>
<td>New York</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2004</td>
<td>H7N3</td>
<td>Canada</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>2004</td>
<td>H10N7</td>
<td>Egypt</td>
<td>2</td>
<td></td>
</tr>
<tr>
<td>2004-</td>
<td>H5N1</td>
<td>Numerous</td>
<td>&gt;650</td>
<td>&gt;386</td>
</tr>
<tr>
<td>2013+</td>
<td>H7N9</td>
<td>China+</td>
<td>&gt;407</td>
<td>&gt;115</td>
</tr>
<tr>
<td>2013</td>
<td>H6N1</td>
<td>Taiwan</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2014</td>
<td>H10N8</td>
<td>China</td>
<td>3</td>
<td>1</td>
</tr>
<tr>
<td>2014</td>
<td>H5N6</td>
<td>China</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

Data derived from various CDC and WHO reports
Cross-Sectional Studies of Avian-exposed for Avian Influenza Infections

DISPATCHES

Avian Influenza among Waterfowl Hunters and Wildlife Professionals

James S. Gill,* Richard Webby,† Mary J.R. Gilchrist,* and Gregory C. Gray‡

We report serologic evidence of avian influenza infection in 1 duck hunter and 2 wildlife professionals with extensive histories of wild waterfowl and game bird exposure. Two laboratory methods showed evidence of past infection with influenza A/H1N9, a less common virus strain in wild ducks, in these 3 persons.

### Results Zoonotic Influenza Study: Avian Viruses

<table>
<thead>
<tr>
<th>Variable</th>
<th>Avian H5 Unadjusted OR (95% CI)</th>
<th>Avian H5 Adjusted OR (95% CI)</th>
<th>Avian H6 Unadjusted OR (95% CI)</th>
<th>Avian H6 Adjusted OR (95% CI)</th>
<th>Avian H7 Unadjusted OR (95% CI)</th>
<th>Avian H7 Adjusted OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age continuous</td>
<td>1.01 (0.99-1.03)</td>
<td>1.01 (0.99-1.03)</td>
<td>1.02 (0.98-1.06)</td>
<td>1 (0.96-1.04)</td>
<td>0.99 (0.97-1.02)</td>
<td>0.99 (0.96-1.02)</td>
</tr>
<tr>
<td>Hunt wild birds</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>1.7 (0.9-3.1)</td>
<td>---</td>
<td>2.1 (1-4.7)</td>
<td>---</td>
<td>2.3 (1-5)</td>
<td>2.8 (1.2-6.5)</td>
</tr>
<tr>
<td>No</td>
<td>reference</td>
<td>---</td>
<td>reference</td>
<td>---</td>
<td>reference</td>
<td>reference</td>
</tr>
<tr>
<td>Worked with poultry from 2000 on*</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>1.4 (0.8-2.7)</td>
<td>---</td>
<td>3.6 (1.5-8.7)</td>
<td>3.4 (1.4-8.5)</td>
<td>2.5 (1.1-5.5)</td>
<td>2.5 (1.1-5.7)</td>
</tr>
<tr>
<td>No</td>
<td>reference</td>
<td>---</td>
<td>reference</td>
<td>---</td>
<td>reference</td>
<td>reference</td>
</tr>
<tr>
<td>Score for frequency to touch live poultry or game birds §</td>
<td>1.2 (1.01-1.5)</td>
<td>1.2 (1.02-1.5)</td>
<td>1.3 (1.1-1.7)</td>
<td>---</td>
<td>1.3 (0.99-1.7)</td>
<td>---</td>
</tr>
<tr>
<td>Human H1N1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Positive</td>
<td>2 (1.2-3.3)</td>
<td>2 (1.2-3.4)</td>
<td>2.3 (1.2-4.8)</td>
<td>---</td>
<td>2.2 (1.1-4.6)</td>
<td>3.1 (1.4-7)</td>
</tr>
<tr>
<td>Negative</td>
<td>reference</td>
<td>reference</td>
<td>reference</td>
<td>---</td>
<td>reference</td>
<td>reference</td>
</tr>
</tbody>
</table>

Gray GC, McCarthy T, Capuano AW, Setterquist SF, Alavanja MC, Lynch CF Evidence for Avian Influenza A Infections Iowa’s Agricultural Workers. Influenza & Resp Vir 2008; available on line 4/07/08

•44
Table 4. Odds ratios for a positive serologic response against avian influenza viruses among growers with fewer than 1000 turkeys using logistic regression.

<table>
<thead>
<tr>
<th>Avian influenza virus subtype</th>
<th>Unadjusted OR (95% CI)</th>
<th>Adjusted OR (95% CI)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Avian H4†</td>
<td>4.4 (1.4-13.6)</td>
<td>3.9 (1.2-12.8)</td>
</tr>
<tr>
<td>Avian H5†</td>
<td>5.7 (1.9-17.2)</td>
<td>6.2 (2.0-19.6)</td>
</tr>
<tr>
<td>Avian H6‡</td>
<td>4.4 (1.4-13.6)</td>
<td>15.3 (2.0-115.2)</td>
</tr>
<tr>
<td>Avian H9†</td>
<td>4.4 (1.4-13.6)</td>
<td>3.9 (1.2-12.8)</td>
</tr>
<tr>
<td>Avian H10§</td>
<td>3.6 (1.5-8.5)</td>
<td>5.8 (1.2-27.7)</td>
</tr>
</tbody>
</table>

*: Saturated model included age, gender, race, current use of tobacco, reporting an influenza-like illness in the previous year, antibody titers against human influenza H1N1 and H3N2 viruses, and exposure to chicken, wild birds, and swine, titers ≥ 1:10 were considered positive
†: Adjusted for antibody titers against human influenza H1N1 virus
‡: Adjusted for antibody titers against human influenza H1N1 virus and age
§: Adjusted for antibody titers against human influenza H1N1 virus and exposure to chickens or swine
Kamphaeng Phet Province, Thailand
Evidence for Subclinical Avian Influenza Virus Infections Among Rural Thai Villagers


1Department of Virology, US Armed Forces Research Institute of Medical Sciences, Bangkok, Thailand; 2Naval Medical Research Unit #2/National Institute of Public Health, Phnom Penh, Cambodia; 3Emerging Pathogens Institute and 4Department of Environmental and Global Health, College of Public Health and Health Professions, University of Florida, Gainesville, Florida; 5National Institute of Health, Ministry of Public Health, Nonthaburi, Thailand; and 6Department of Epidemiology, College of Public Health, University of Iowa, Iowa City, Iowa


Methods. In 2008, we enrolled a cohort of 800 rural Thai adults living in 8 sites within Kamphaeng Phet Province in a prospective study of zoonotic influenza transmission. We studied participants’ sera with serologic assays against 16 avian, 2 swine, and 8 human influenza viruses.

Results. Among participants (mean age 49.6 years and 58% female) 65% reported lifetime poultry exposure of at least 30 consecutive minutes. Enrollees had elevated antibodies by microneutralization assay against 3 avian viruses: A/Hong Kong/1073/1999(H9N2), A/Thailand/676/2005(H5N1), and A/Thailand/384/2006(H5N1). Bivariate risk factor modeling demonstrated that male gender, lack of an indoor water source, and tobacco use were associated with elevated titers against avian H9N2 virus. Multivariate modeling suggested that increasing age, lack of an indoor water source, and chronic breathing problems were associated with infection with 1 or both HPAI H5N1 strains. Poultry exposure was not associated with positive serologic findings.

Conclusions. These data suggest that people in rural central Thailand may have experienced subclinical avian influenza infections as a result of yet unidentified environmental exposures. Lack of an indoor water source may play a role in transmission.
<table>
<thead>
<tr>
<th>Variables</th>
<th>Total N</th>
<th>A/Thailand/676/2005(H5N1)</th>
<th>A/Thailand/384/2006(H5N1)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Unadjusted OR (95% CI)</td>
<td>Adjusted OR (95% CI)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Age (yrs)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≥60</td>
<td>184</td>
<td>32.1 (5.2-infinity)*†</td>
<td>31.2 (5.0-infinity)*†</td>
</tr>
<tr>
<td>40-59</td>
<td>427</td>
<td>7.8 (1.2-327.5)*†</td>
<td>8.4 (1.3-354.8)*</td>
</tr>
<tr>
<td>20-39</td>
<td>189</td>
<td>Reference</td>
<td>Reference</td>
</tr>
<tr>
<td>Indoor water</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No</td>
<td>257</td>
<td>3.1 (1.7-5.7)*†</td>
<td>3.2 (1.7-6.1)*</td>
</tr>
<tr>
<td>Yes</td>
<td>543</td>
<td>Reference</td>
<td>Reference</td>
</tr>
<tr>
<td>Chronic breathing problems</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes</td>
<td>37</td>
<td>2.9 (1.1-7.8)*†</td>
<td>---</td>
</tr>
<tr>
<td>No</td>
<td>763</td>
<td>Reference</td>
<td>Reference</td>
</tr>
</tbody>
</table>

* Binary logistic regression (Negative = titer <1:10, Positive = titer ≥1:10). †Exact conditional method used. ‡Proportional odds model used. §Negative = titer <1:40, Positive = titer ≥1:40. These covariates have missing data.
Bioaerosol Sampling to Detect Avian Influenza Virus in Hanoi’s Largest Live Poultry Market

Vuong N. Bui, Tham T. Nguyen, Hung Nguyen-Viet, Anh N. Bui, Katie A. McCallion, Hu Suk Lee, Son T. Tham, Kristen K. Coleman, and Gregory C. Gray

Virology Department, National Institute of Veterinary Research, Hanoi, Vietnam; Program in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore; International Livestock Research Institute, Hanoi, Vietnam, and Center for Public Health and Ecosystem Research, Hanoi University of Public Health, Vietnam; College of Veterinary Medicine, North Carolina State University, Raleigh, North Carolina, and Division of Infectious Diseases, Global Health Institute, and Nicholas School of the Environment, Duke University, Durham, North Carolina; and Global Health Research Center, Duke-Kunshan University, China

**Background.** Newly emergent and virulent strains of H7N9 avian influenza virus are rapidly spreading in China and threaten to invade Vietnam. We sought to introduce aerosol sampling for avian influenza viruses in Vietnam.

**Methods.** During October 2017, National Institute for Occupational Safety and Health 2-stage aerosol samplers were assembled on a tripod and run for 4 hours. Concomitantly, up to 20 oropharyngeal (OP) swab samples were collected from chickens and ducks, which were then tested with 0.2–1.5 m from each sampler.

**Results.** The 3 weeks of sampling yielded 30 aerosol samples that were 90% positive for influenza A, by quantitative reverse-transcription polymerase chain reaction, and 119 OP swab sample pools (5 samples per pool) that were 47% positive. Egg cultures yielded 1 influenza A virus (not H5 or H7) from aerosol and 25 influenza A viruses from OP swab sample pools (5 were H5 positive). The association between positive sample types (over time and position) was strong, with 91.7% of positive OP pooled swab samples confirmed by positive aerosol samples and 81% of influenza A positive aerosol samples confirmed by positive OP swab samples.

**Conclusions.** We posit that aerosol sampling might be used for early warning screening of poultry markets for novel influenza virus detection, such as H7N9. Markets with positive aerosol samples might be followed up with more focused individual bird or cage swabbing, and back-tracing could be performed later to locate specific farms harboring novel virus. Culling birds in such farms could reduce highly pathogenic avian influenza virus spread among poultry and humans.

**Keywords.** avian influenza; influenza A virus; Vietnam; poultry; epidemiology.

<table>
<thead>
<tr>
<th>Country</th>
<th>Timepoint</th>
<th>Seroreactivity to Avian influenza virus strain</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>H5N1*</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A/Water fowl/Hong Kong/ Mpb127/2005(H7N7)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>A/Hong Kong/ 1073/1999(H9N2)</td>
</tr>
<tr>
<td>Thailand</td>
<td>Enrollment</td>
<td>28/800 (3.5%) (384)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>45/800 (5.6%) (676)</td>
</tr>
<tr>
<td></td>
<td>12 months</td>
<td>-- --</td>
</tr>
<tr>
<td></td>
<td>24 months</td>
<td>1/790 (0.1%) (676)</td>
</tr>
<tr>
<td>Cambodia</td>
<td>Enrollment</td>
<td>--</td>
</tr>
<tr>
<td></td>
<td>12 months</td>
<td>--</td>
</tr>
<tr>
<td></td>
<td>24 months</td>
<td>--</td>
</tr>
<tr>
<td>Nigeria</td>
<td>Enrollment</td>
<td>1/369 (0.3%)</td>
</tr>
<tr>
<td></td>
<td>12 months</td>
<td>5/326 (1.5%)</td>
</tr>
<tr>
<td></td>
<td>24 months</td>
<td>5/379 (1.3%)</td>
</tr>
<tr>
<td>Romania</td>
<td>Enrollment</td>
<td>--</td>
</tr>
<tr>
<td></td>
<td>12 months</td>
<td>--</td>
</tr>
<tr>
<td></td>
<td>24 months</td>
<td>--</td>
</tr>
<tr>
<td>Mongolia</td>
<td>Enrollment</td>
<td>1/349 (0.3%)</td>
</tr>
<tr>
<td></td>
<td>12 months</td>
<td>1/363 (0.3%)</td>
</tr>
<tr>
<td></td>
<td>24 months</td>
<td>--</td>
</tr>
</tbody>
</table>

Thailand: A/Thailand/384/2006(H5N1) and A/Thailand/676/2005(H5N1)  
Cambodia: A/Cambodia/R0404050/2007(H5N1)  
Nigeria: A/Chicken/Nigeria/2007/1132123(H5N1)  
Romania: A/Chicken/Romania/6059-1TS/2008(H5N1)  
Mongolia: A/Cygnus/Mongolia/3/2009(H5N1)  

*50
Swine Influenza A Viruses
The Great Spanish Flu Pandemic of 1918-1919

- Sept 30- Oct 5th, Iowa’s Cedar Rapids Swine Show – a flu-like illness spread to millions of swine across Iowa
- JS Koen, an inspector, Division of Hog Cholera Control of the Bureau of Animal Industry-
  - Rapidly spread through herds
  - Swine developed high temperatures, heavy coughs, drippy noses and eyes, many died
Table 1. Adjusted odds ratios of antibody against swine influenza virus, proportional odds model.

<table>
<thead>
<tr>
<th>Risk factors</th>
<th>Swine H1N1</th>
<th>Swine H1N2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Occupation</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Farmers/controls</td>
<td><strong>35.3 (7.7-161.8)</strong></td>
<td><strong>13.8 (5.4-35.4)</strong></td>
</tr>
<tr>
<td>Meat processing workers/controls</td>
<td><strong>6.5 (1.4-29.5)</strong></td>
<td><strong>2.7 (1.1-6.7)</strong></td>
</tr>
<tr>
<td>Veterinarian workers/controls</td>
<td><strong>17.8 (3.8-82.7)</strong></td>
<td><strong>9.5 (3.6-24.6)</strong></td>
</tr>
<tr>
<td>Age</td>
<td>1 (1-1)</td>
<td>1 (1-1)</td>
</tr>
<tr>
<td>Gender</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male/Female</td>
<td><strong>2.9 (1.6-5.2)</strong></td>
<td><strong>2.3 (1.4-3.7)</strong></td>
</tr>
<tr>
<td>Antibody to human virus</td>
<td></td>
<td></td>
</tr>
<tr>
<td>H1N1</td>
<td><strong>2.8 (1.6-5)</strong></td>
<td><strong>2.7 (1.6-4.5)</strong></td>
</tr>
</tbody>
</table>

It seems rather tragic that after the 2009 H1N1 pandemic .....we still do not have a clear view of the dynamic ecology of SIV-like viruses... Instead we must often wait for humans to serve as sentinels through their infection with such novel viruses.
Influenza A(H1N1) pdm09 Virus among Healthy Show Pigs, United States

Gregory C. Gray, Jeffrey B. Bender, Carolyn B. Bridges, Russell F. Daly, Whitney S. Krueger, Michael J. Male, Gary L. Heil, John A. Friary, Robin B. Derby, and Nancy J. Cox

Within 5 months after the earliest detection of human influenza A(H1N1)pdm09 virus, we found molecular and culture evidence of the virus in healthy US show pigs. The mixing of humans and pigs at swine shows possibly could further the geographic and cross-species spread of influenza A viruses.

PCR (rRT-PCR) (6) to screen for influenza A virus. Swab specimens (run in duplicate) with cycle threshold (C_t) values <35 were considered positive for influenza Avirus; specimens with C_t values of 35 to <40 were suspected to be positive; and specimens with C_t values >40 were considered negative. In a blinded fashion, aliquots of swab specimens from pigs were shared with the Minnesota Veterinary Diagnostic Laboratory (St. Paul, MN, USA), where rRT-PCRs for matrix, hemagglutinin (HA), and neuraminidase (NA) genes were performed. Specimens were then shared with the National Veterinary Services Laboratory (Ames, IA, USA) and later with CDC for further molecular and sequencing studies.

Positive and suspected-positive rRT-PCR specimens were cultured in shell vials on MDCK cells by using standard techniques. Sequence-based analyses of the influenza A virus isolates were performed by the CDC influenza division, using full or partial genome sequencing approaches for all 8 gene segments. Sequences were compared by using BLASTn alignment search techniques (http://blast.ncbi.nlm.nih.gov).

*Count difference reflect missing data. % rRT-PCR+ = percentage positive for influenza A
## 2009 Pandemic H1N1 Influenza Presumptive and Confirmed Results

**December 23, 2009**

<table>
<thead>
<tr>
<th>Date Sample Collected</th>
<th>Specie(s)</th>
<th>Sample Information</th>
<th>No. of Samples</th>
<th>State</th>
<th>Positive Matrix PCR</th>
<th>Positive N1 PCR</th>
<th>VIRUS ISOLATION</th>
<th>GENETIC SEQUENCING</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aug/Sept 2009</td>
<td>Swine</td>
<td>CDC-funded research project at State Fairs; clinically healthy swine</td>
<td>6</td>
<td>MN</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>Aug/Sept 2009</td>
<td>Swine</td>
<td>CDC-funded research project at State Fairs; clinically healthy swine</td>
<td>5</td>
<td>MN</td>
<td>3/5 Positive</td>
<td>2/5 Negative</td>
<td>YES-1, NO-4</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>Aug/Sept 2009</td>
<td>Swine</td>
<td>CDC-funded research project at State Fairs; clinically healthy swine</td>
<td>1</td>
<td>SD</td>
<td>YES</td>
<td></td>
<td>NO</td>
<td>N/A</td>
</tr>
<tr>
<td>10/5/09</td>
<td>Ferret</td>
<td>Clinically ill pet ferret following exposure to human with influenza-like illness</td>
<td>1</td>
<td>OR</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>10/22/09</td>
<td>Swine</td>
<td>USDA swine surveillance</td>
<td>4</td>
<td>IN</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>10/30/09</td>
<td>Cat</td>
<td>Clinically ill cat following exposure to human with influenza-like illness</td>
<td>1</td>
<td>IA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>10/30/09</td>
<td>Ferret</td>
<td>Clinically ill pet ferret following exposure to human with influenza-like illness</td>
<td>1</td>
<td>NE</td>
<td>YES</td>
<td></td>
<td>NO</td>
<td>N/A</td>
</tr>
<tr>
<td>10/23/09</td>
<td>Ferret</td>
<td>Clinically ill pet ferrets following exposure to human with influenza-like illness</td>
<td>3</td>
<td>OR</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/9/09</td>
<td>Cat</td>
<td>Clinically ill cat following exposure to human with influenza-like illness</td>
<td>1</td>
<td>OR</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/7/09</td>
<td>Cat</td>
<td>Clinically ill cat following exposure to human with influenza-like illness</td>
<td>1</td>
<td>PA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/17/09</td>
<td>Cheetah</td>
<td>Clinically ill cheetah</td>
<td>1</td>
<td>CA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/20/09</td>
<td>Turkey</td>
<td>Clinically ill turkeys (drop in egg production), possible exposure to human with influenza-like illness</td>
<td>4</td>
<td>VA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/23/09</td>
<td>Turkey</td>
<td>Clinically ill turkeys (drop in egg production), possible exposure to human with influenza-like illness</td>
<td>1</td>
<td>VA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>12/2/09</td>
<td>Turkey</td>
<td>Clinically ill turkeys (drop in egg production), possible exposure to human with influenza-like illness</td>
<td>2</td>
<td>VA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>No seq performed-same premises as 11/20</td>
</tr>
<tr>
<td>Same premises as 11/20</td>
<td>Turkey</td>
<td>Clinically ill turkeys (drop in egg production), possible exposure to human with influenza-like illness</td>
<td>2</td>
<td>VA</td>
<td>YES</td>
<td>YES</td>
<td>YES</td>
<td>No seq performed-same premises as 11/20</td>
</tr>
<tr>
<td>11/11/09</td>
<td>Swine</td>
<td>USDA swine surveillance</td>
<td>5</td>
<td>IL</td>
<td>Isolate rec'd-YES</td>
<td>Isolate rec'd-YES</td>
<td>N/A</td>
<td>2009 Pandemic H1N1</td>
</tr>
<tr>
<td>11/24/09</td>
<td>Swine</td>
<td>Mild clinical signs; possible exposure to humans with influenza-like illness</td>
<td>3</td>
<td>NC</td>
<td>Pending</td>
<td>YES</td>
<td>YES</td>
<td>2009 Pandemic H1N1</td>
</tr>
</tbody>
</table>
pH1N1 in pigs by country

Generated from OIE data available from World Animal Health Information Database & sequences deposited in GenBank, August 2010…Courtesy of Dr. Amy Vincent of National Animal Disease Center, Ames, IA
Novel H1N2 swine influenza reassortant strain in pigs derived from the pandemic H1N1/2009 virus

Ana Moreno\textsuperscript{a,*}, Livia Di Trani\textsuperscript{b}, Silvia Faccini\textsuperscript{a}, Gabriele Vaccari\textsuperscript{b}, Daniele Nigrelli\textsuperscript{a}, M. Beatrice Boniotti\textsuperscript{a}, Emiliana Falcone\textsuperscript{b}, Arianna Boni\textsuperscript{b}, Chiara Chiapponi\textsuperscript{a}, Enrica Sozzi\textsuperscript{a}, Paolo Cordioli\textsuperscript{a}

\textsuperscript{a}Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLEI), Via Bianchi, 9, 25124 Brescia, Italy
\textsuperscript{b}Department of Veterinary Public Health and Food Safety, Istituto Superiore di Sanità, Vle Regina Elena, 299, 0016 Rome, Italy

Multiple Reassortment between Pandemic (H1N1) 2009 and Endemic Influenza Viruses in Pigs, United States

Mariette F. Ducatez, Ben Hause, Evelyn Stigger-Rosser, Daniel Darnell, Cesar Corzo, Kevin Juleen, Randy Simonson, Christy Brockwell-Staats, Adam Rubrum, David Wang, Ashley Webb, Jeri-Carol Crumpton, James Lowe, Marie Gramer, and Richard J. Webby

Emerging Infectious Diseases • www.cdc.gov/eid • Vol. 17, No. 9, September 2011
2017 – 10 or more unique clades/clusters of H1 and H3 subtypes in US Midwestern farms!
Notably, swine in the United Kingdom have largely had a replacement of the endemic Eurasian avian virus-like ("avian like") genotypes with A(H1N1)pdm09-derived genotypes.

23 unique genotypes are described!
Genotypic diversity

>70 genotypes with 27 persistent types

Unpublished data: Maria Huachen Zhu
Joint Institute of Virology (STU-HKU) Shantou University
State Key Laboratory of Emerging Infectious Diseases The University of Hong Kong
This is a qualitative, graphical depiction of the authors’ assessment of the current risk of influenza A viruses crossing from various domestic animals to infect man. The graphic is composite or gestalt of case reports, sero-epidemiological studies, archeo-epidemiological studies, environmental studies, and historical observations. The authors’ intent with this graphic is to illustrate the high relative probability of continued movement of influenza A viruses between pigs and man, contrasting that with the knowledge that swine viruses have been associated with at least four recent pandemics, yet worldwide we continue to have relatively sparse surveillance for novel influenza A virus detections among pigs.

**Figure by L. Borkenhagen**

Influenza A viruses in swine were associated with the 1918, 1957, 1968 and 2009 pandemics

Surveillance for novel viruses in pigs is sparse

Through limited study we know there are multiple unique influenza A viral strains circulating in pigs which could generate new pandemic viruses

Modern Farming Has Contributed to the Movement of Swine Influenza Viruses (SIV)

Spatial Dynamics of Human-Origin H1 Influenza A Virus in North American Swine

Introductions and Evolution of Human-Origin Seasonal Influenza A Viruses in Multinational Swine Populations

Abstract

The capacity of influenza A virus to evolve and spread presents a continued threat to human and animal health. Knowledge of the human-swine interface is particularly important for understanding viruses with pandemic potential in other hosts. The sequence of genome of 141 influenza viruses collected from North American swine during 2011 to 2017 and 810 full-length swine viruses that possessed all eight genes suggest that human-origin A(H1N1) viruses are a moderate clue to some that this virus...
Enrollment questionnaire & sera from 300 exposed and 100 nonexposed workers (6 farms)
Annual serum sampling
Annual risk factor questionnaire
Weekly monitoring for ILI & influenza A
ILI questionnaire
ILI sera and swabs

Monthly rope swab sampling of 50 pigs
Sample various ages (sows, boars, and production pigs)
50 pens x 6 farms per month = 300 rope swabs per month

CAFO questionnaire
Multiple CAFOs in separate provinces
Monthly environmental studies of CAFO environment for influenza A
144 total aerosol, fecal, environmental swab, and water samples/per month
When visiting the farms in China our research teams noted a frequent lack of biosecurity and sparse use of personal protective equipment, especially in the older and smaller farms. In at least three farms, ducks, geese, chickens, or dogs were housed very near or found comingling with pigs. Often there were no barriers to separate pigs from birds or rodents.
Clin Infect Dis; 2018;66:533-40. PMID: 29401271
Prospective surveillance for influenza A virus in Chinese swine farms

Benjamin D. Anderson, Mai-Juan Mai, Guo-Lin Wang, Zhen-Qiang Bi, Bing Lu, Xian-Jun Wang, Chuang-Xin Wang, Shan-Hui Chen, Yan-Hua Qian, Shao-Xia Song, Min Li, Teng Zhao, Meng-Na Wu, Laura K. Borkenhagen, Wu-Chun Cao and Gregory C. Gray

Abstract

Pork production in China is rapidly increasing and swine production operations are expanding in size and number. However, the biosecurity measures necessary to prevent swine disease transmission, particularly influenza A viruses (IAV) that can be zoonotic, are often inadequate. Despite this risk, few studies have attempted to comprehensively study IAV ecology in swine production settings. Here, we present environmental and animal sampling data collected in the first year of an ongoing five-year prospective epidemiological study to assess IAV ecology as it relates to swine workers, their pigs, and the farm environment. From March 2015 to February 2016, we collected 396 each of environmental swab, water, bioaerosol, and fecal/slurry samples, as well as 3300 pig oral secretion samples from six farms in China. The specimens were tested with molecular assays for IAV. Of these, 46 (11.6%) environmental swab, 235 (7.1%) pig oral secretion, 23 (5.8%) water, 20 (5.1%) bioaerosol, and 19 (4.8%) fecal/slurry specimens were positive for influenza A by qRT-PCR. Risk factors for IAV detection among collected samples were identified using bivariate logistic regression. Overall, these first year data suggest that IAV is quite ubiquitous in the swine production environment and demonstrate an association between the different types of environmental sampling used. Given the mounting evidence that some of these viruses freely move between pigs and swine workers, and that mixing of these viruses can yield progeny viruses with pandemic potential, it seems imperative that routine surveillance for novel IAVs be conducted in commercial swine farms.
High Risk of Influenza Virus Infection Among Swine Workers: Examining a Dynamic Cohort in China

Laura K. Borkenhagen, Guo-Lin Wang, Ryan A. Simmons, Zhen-Di Bie, Bing Li, Xian-Jun Wang, Chuang-Xin Wang, Shan-Hui Chen, Shao-Xia Song, Min Li, Teng Zhao, Meng-Na Wu, Lawrence P. Park, Wu-Chun Cao, Mai-Juan Ma, and Gregory C. Gray

1Division of Infectious Diseases, School of Medicine, Global Health Institute, Duke University, Durham, North Carolina; 2State Key Laboratory of Pathogen and Biosecurity, Beijing Institute of Microbiology and Epidemiology; 3Shandong Provincial Center for Disease Control and Prevention, and 4Shandong Provincial Key Laboratory of Disease Control and Prevention, Jinan, 5Wuxi Center for Disease Control and Prevention, 6Licheng District Center for Disease Control and Prevention, Jinan, and 7Global Health Research Center, Duke Kunshan University, China; and 8Program in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

Background. China is thought to be a hotspot for zoonotic influenza virus emergence, yet there have been few prospective studies examining the occupational risks of such infections.

Methods. We present the first 2 years of data collected from a 5-year, prospective, cohort study of swine-exposed and non-exposed participants at 6 swine farms in China. We conducted serological and virological surveillance to examine evidence for swine influenza A virus infection in humans.

Results. Of the 658 participants (521 swine-exposed and 137 swine-unexposed), 207 (31.5%) seroconverted against at least 1 swine influenza virus subtype (swine H1N1 or H3N2). Swine-exposed participants’ microneutralization titers, especially those enrolled at confined animal feeding operations (CAFOs), were higher against the swine H1N1 virus than were other participants at 12 and 24 months. Despite elevated titers, among the 187 study subjects for whom we had complete follow-up, participants working at swine CAFOs had significantly greater odds of seroconverting against both the swine H1N1 (odds ratio [OR] 19.16, 95% confidence interval [CI] 3.55–358.65) and swine H3N2 (OR 2.97, 95% CI 1.16–8.01) viruses, compared to unexposed and non-CAFO swine workers with less intense swine exposure.

Conclusions. While some of the observed increased risk against swine viruses may have been explained by exposure to human influenza strains, study data suggest that even with elevated preexisting antibodies, swine-exposed workers were at high risk of infection with enzootic swine influenza A viruses.

Keywords. influenza A virus; swine influenza; zoonoses; epidemiology.
To Succeed, One Health Must Win Animal Agriculture’s Stronger Collaboration

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The One Health approach has received widespread international endorsements from professional, academic, and governmental organizations as the way forward in tackling complex interdisciplinary problems, such as emerging zoonotic diseases, antimicrobial resistance, and food safety. Yet conspicuously absent from US One Health training or research activities are the animal agricultural industries. Their absence is likely due to multiple factors, including the lack of appreciation for their potential problem-solving roles, as well as the industries’ business-oriented fears that such engagement could cause them to suffer economic damage. As demands on the swine, poultry, egg, beef, and dairy production industries are closely linked to the above-mentioned complex problems, we must find new, nonthreatening ways to better engage and win animal agriculture’s collaboration into One Health training and research partnerships for successful health problem solving. Without animal agricultural industries’ improved cooperation, One Health’s efforts to control these complex problems are not likely to succeed.

Keywords. biosecurity; One Health; zoonotic diseases; antimicrobial resistance, animal agriculture.
Which Way to the National Institute of Veterinary Medicine?
Estimated UC San Francisco College of Medicine vs. University of California Davis College of Veterinary Medicine Research Funding 2013
New Study Says Bird Flu Spread By Wind, Humans, Fowl

By PEGGY LOWE • JUN 16, 2015

Research shows airborne transmission of avian flu a possibility

By TOM CHABOT on Jun 16, 2015 at 8:30 p.m.

ST. PAUL, Minn. -- Scientists do not yet know whether spring winds carried the highly pathogenic avian influenza into barns and infected turkey or egg-laying flocks.

But they now consider airborne transmission a possibility in some of the cases of infected barns, according to the United States Department of Agriculture. It recently reported that "a preliminary analysis of wind data showed a relationship between sustained high winds and an increase in the number of infected farms approximately five days later."

Signs of airborne H5N2 found; outbreaks

Filed Under: Avian Influenza (Bird Flu)  
Robert Roos | News Editor | CIDRAP News | May 08, 2015

Evidence of the H5N2 avian influenza virus has been found in air samples collected in and near infected Minnesota poultry barns, a researcher said today, supporting the suspicion that the virus may go airborne for short distances, while Iowa reported seven new H5 outbreaks involving 4 million chickens and an unknown number of turkeys.

In addition, Wisconsin authorities today reported finding H5N2 in an owl along Green Bay, while hard-hit Minnesota had its second day this week without any new poultry outbreaks.
InDevR FluChip-8G Multiplexed, Multipurpose Influenza Diagnostic System

Diagnostic results in eight hours instead of two weeks
A Feasibility Study of Conducting Surveillance for Swine Pathogens in Swine Slurry in North Carolina Swine Farms

Collaborating Institutions:
• Duke University
• NC Agromedicine Institute

Objectives:
• Establish non-invasive slurry sampling as a means of routine surveillance for the detection of pathogens of zoonotic and economic concern
• Train farm owners/managers to collect slurry samples and to implement surveillance of their swine herds

Overall Goal: To determine if slurry sampling was a viable alternative non-invasive method for virus surveillance on swine farms.
Chan Zuckerberg Biohub and Chan Zuckerberg Initiative Announce First-of-its-Kind “IDseq” Platform And Service To Enable Real-time Global Disease Surveillance and Prevention

Posted on October 16, 2018

- New open-source cloud-based tool rapidly interprets terabytes of data to detect disease-causing pathogens
- In an ongoing pilot project and partnership with the Bill & Melinda Gates Foundation, IDseq is helping to identify mystery infections at a hospital in Dhaka, Bangladesh
- New funding from the Bill & Melinda Gates Foundation to expand the pilot by providing next-generation genome consumers and IDseq training for labs and clinics throughout the world
### Sample Details

Min Contig Size: 4

12243 rows passing filters, out of 12243 total rows. Randomly subsampled to 2000000 out of 22378364 non-host reads.

<table>
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<th>Taxon</th>
<th>Score</th>
<th>Z^2</th>
<th>rPM</th>
<th>r^2</th>
<th>contig r</th>
<th>contig r</th>
<th>%ID</th>
<th>log(1/E)</th>
<th>NT</th>
<th>NR</th>
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<tr>
<td>All taxa with neither family nor genus classification (952 species)</td>
<td>361,575,635</td>
<td>64.6</td>
<td>74,340.2</td>
<td>627,142</td>
<td>684</td>
<td>544,119</td>
<td>92.3</td>
<td>65.8</td>
<td>182</td>
<td>NR</td>
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<td>Thermostoga (9 bacterial species)</td>
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<td>62</td>
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<td>Bacteroides (128 bacterial species)</td>
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<td>16,804.3</td>
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<td>Oscillibacter (14 bacterial species)</td>
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<td>75,603</td>
<td>42</td>
<td>60,833</td>
<td>90.5</td>
<td>75.0</td>
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<td>Blautia (11 bacterial species)</td>
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<td>88.8</td>
<td>7,497</td>
<td>8</td>
<td>5,012</td>
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<tr>
<td>Muribaculum (3 bacterial species)</td>
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<td>Clostridium (147 bacterial species)</td>
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<td>Non-genus-specific reads in family Ruminococcaceae (16 bacterial species)</td>
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<td>90.3</td>
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*Note: NT and NR columns indicate non-template and non-reference reads.*
Viral breakdown

Fanning shape hints at new viral strain
Influenza A Virus in Pigs

The available data suggest that influenza A viruses in pigs…

• May move back and forth between humans and pigs. Often these infections are subclinical.
• Modern influenza A strains which are reservoired in pigs occasionally cause outbreaks and severe disease in humans
• Historically influenza A viruses circulating in pigs have been associated with four recent pandemics and have great potential to play a role in generating pandemic strains.
Duke One Health Web Site

Are agriculture workers at increased risk for emerging pathogen infections?

http://sites.globalhealth.duke.edu/dukeonehealth/