Integrating Earth Observation and Satellite Telemetry of Wild Birds for Decision Support System of Avian Influenza

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This NASA Public Health project is built upon our previous projects, including NIH-funded Ecology-based risk assessment of avian influenza in Asia

NASA Land Use and Land Cover Change
National Institutes of Health
National Science Foundation
USGS
FAO

Many in-country collaborators
In China, Mongolia, Bangladesh and India

H5N1 has continued to infect poultry, birds and people.

As of August 9, 2011, A total of 564 human cases and 330 death

~ $20 billion of economic damage

New H5N1 clade 2.3.2.1 in China and Vietnam in 2011

From David Quammen, How animals and humans exchange disease -- Deadly Contact, National Geographic, 10/2007
Ecology and epidemiology of avian influenza

Weather / Climate

- Paddy rice fields
- Fish ponds
- Natural wetlands
- Water body

Migratory birds

Pig (swine flu)

Free-grazing ducks/geese

Poultry (AIV, H5N1)

Human (seasonal flu)

Production, market, trade, transport systems, Vaccine, movement control, culture, behavior
Mapping H5N1 highly pathogenic avian influenza risk in Southeast Asia

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The highly pathogenic avian influenza (HPAI) H5N1 virus that emerged in southern China in the mid-1990s has in recent years evolved into the first HPAI panzootic. In many countries where the virus was detected, the virus was successfully controlled, whereas established, spread, and persist everywhere equally. Virus establishment is influenced by the extent of surveillance and early detection, and therefore it is subject to an unknown degree of underreporting bias. Once established, HPAI H5N1 virus spread

Spatial Distribution and Risk Factors of Highly Pathogenic Avian Influenza (HPAI) H5N1 in China

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Abstract

Highly pathogenic avian influenza (HPAI) H5N1 was first encountered in 1996 in Guangdong province (China) and started spreading throughout Asia and the western Palearctic in 2004–2006. Compared to several other countries where the HPAI H5N1 distribution has been studied in some detail, little is known about the environmental correlates of the HPAI H5N1 distribution in China. HPAI H5N1 clinical disease outbreaks, and HPAI virus (HPAIV) H5N1 isolated from active risk-based surveillance sampling of domestic poultry (referred to as HPAIV). H5N1 surveillance positives in this manuscript) were
In China's Backcountry, Tracking Lethal Bird Flu

Five years after flu devastated wild birds in China, researchers have confirmed one likely transmission route

QINGHAI LAKE, CHINA—The lake glitters like a sapphire under a blue sky as birds circle near the shore. On the rocky beach, two researchers are tying a GPS transmitter to the back of a small gray duck. They will track its migration by satellite, part of a series of investigations that began after highly pathogenic avian influenza (H5N1 subtype) first swept the region in 2005.

The studies aim to pinpoint the viral reservoir and the role that wild birds play in transmission. “The lake has attracted the whole world’s researchers to keep a close eye on it,” says He Yubang, vice director of Administration of Qinghai Lake Chinese National Nature Reserve. No reservoir has yet been found, but transmission routes have come into clearer focus.

The emergence of H5N1 was a disaster for wildlife and humans alike. Since 2003, H5N1 has killed 300 people, including 18 so far this year, according to the World Health Organization. More than 250 million infected domestic poultry have been culled, and thousands of wild birds have been killed. In 2005 alone, more than 6000 wild birds at Qinghai Lake died. “the single largest H5N1 wild bird mortality event that has ever occurred,” says Scott Newman, an animal health officer for the UN Food and Agriculture Organization (FAO) in Rome.

H5N1 was first isolated in 1996 from a domestic goose in China’s Guangdong Province. The next year, the virus spread to people in Hong Kong. After laying low, H5N1 flared in 2004 in several Asian nations. It kills about 60% of those infected but does not spread easily from person to person. The virus has been held in check by poultry vaccination and better husbandry, but 16 countries, including China and Romania, have reported H5N1 outbreaks in poultry so far this year. A constant worry is that the virus will mutate into a more transmissible form among humans.

Because Qinghai Lake sits within the eastern portion of the Central Asian Flyway—which reaches from India and Bangladesh to Russia—some experts suspect it is a focal point of virus transmission. Others question whether wild birds play a major role in H5N1 dispersal, suggesting that the virus spreads primarily among poultry (Science, 21 October 2005, p. 426). To date, all human cases but one have been associated with exposure to poultry or found on farms. Researchers now believe that wild waterfowl on the eastern portion of the Central Asian Flyway help spread H5N1 into Mongolia each spring as they move across the Qinghai-Tibetan plateau to the north and east, says Newman. The role of wild waterfowl on the other major flyway is less certain.

Poultry production is on the rise in Asia, as are farming, trade, and the mixing of wild and domestic birds. “All of them are increasing the opportunities for viral transmission and persistence,” says Xiao Xiangming, a landscape ecologist and remote sensing expert at the University of Oklahoma, Norman.

Every summer, more than 100,000 migratory birds descend on Qinghai Lake, China’s largest inland body of water. Half the birds that died here in 2005 were bar-headed geese (Anser indicus), says Lei Fu-Min, an ornithologist at the Institute of Zoology of the Chinese Academy of Sciences. Yan Baopeng, chief engineer at the Computer Network Information Center in Beijing, led an academy team that set up a monitoring network after the die-off. The next year international scientists joined the effort. To date, the team led by FAO and the U.S. Geological Survey has tracked more than 525 waterfowl from 24 species in 11 countries.

In the past 5 years, the involvement of wild birds has become clearer, Lei says. “The H5N1 strains from wild birds that subsequently arrived in Asia and Eastern Europe were most like the H5N1 strains of Qinghai Lake,” far from large poultry farms, he says. GPS data on migration paths are now being used for the first time to explore the relationships between different groups of birds and their interactions with domestic fowl, says Diam Prosier, a biologist at USGS’s Patuxent Wildlife Research Center in Beltsville, Maryland. This year, she says, researchers learned that the majority of bar-headed geese tagged at Qinghai spend their winters in the Lhasa region of Tibet, south of the lake. These wintering grounds have domestic poultry and captive bar-headed goose farms—and H5N1 outbreaks have been reported there, suggesting a path for the virus to move from captive to wild birds.

Southeast of Lhasa, the ruddy shelduck may help explain the virus’s spread, says John Takekawa, an ecologist at USGS’s Western Ecological Research Center. In autumn and winter the ducks gather at Poyang Lake in the lower reaches of the Yangtze River within the East Asia Flyway (Science, 23 October 2009, p. 508). Qinghai strains can be traced to one early strain from Poyang based on the genomic analysis, Lei said. But recent work suggests that the viral reservoir may lie farther to the north, in Siberia—an area shared by both major Asian flyways—or that another as-yet-unstudied migratory bird may be carrying the virus from lake to lake. Since 2006, Xiao has led an international team to develop an early-warning system for H5N1 in Asia, focusing on agricultural and ecological risk factors.

Researchers need a better understanding of wild bird distribution, habitat use, and daily movements, Newman says. And the human role—including population growth and urbanization—must be better accounted for, says Takekawa. Why some people exposed to the virus become infected and others do not “is still an unsolved question,” says Shu Yue-long, director of the National Influenza Center of the Chinese Center for Disease Control and Prevention. China has launched a nationwide monitoring network to check poultry markets for H5N1. That’s a good start, but what’s needed is a global network, says Shu. It must get started now, he says, “without delay.”

Li Jiao is writer in Beijing.
Satellite observatories & telemetry

- cropping intensity & crop calendar
- wetlands, water bodies, irrigation
- land surface temperature, snow/ice
- human settlements

Wild birds
Local movement, migration distribution

AIV surveillance
Outbreak location & time
Control area, GenBank

- bird surveillance
- waterfowl migration time & flyway
- poultry, livestock, markets
- agricultural statistical data
- Interaction of human, bird, poultry, pig

In-situ observatories (field and lab)

Ecology of AIV
2003-2010
Patterns, dynamics, variables

Geospatial analysis

Species distribution models

Agent-based models

Spatial epidemiological models

Mathematical models

Nowcast & Early Warning
2011-
likely “hot spots” & “hot times”
Epidemic potential
Persistence and introduction

International
FAO
Decision Support Tools
EMPRES-i
- Risk assessment
- Decision-support
- Scenario tools
- Risk communication

National
Decision Support Tools

Citizens

A schematic diagram for ecology, epidemiology and decision support systems of avian influenza
Are wild birds a victim or vector?

Weather / Climate

- Paddy rice fields
- Fish ponds
- Water body

Natural wetlands

Migratory birds

Free-grazing ducks/geese

Pig (swine flu)

Poultry (AIV, H5N1)

Human (seasonal flu)

Production, market, trade, transport systems, Vaccine, movement control, culture, behavior
H5N1 outbreak in wild birds, Qinghai Lake, China

**BREVIA**

**Highly Pathogenic H5N1 Influenza Virus Infection in Migratory Birds**

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Asian influenza virus (AIV) involving at least three subtypes, H5, H7, and H9, has emerged as an important pathogen in the poultry industry and is of major current global health concern (1). The first case report of influenza in wild birds, H5N1, was confirmed in 1997 (2), since 2003, H5N1, a highly pathogenic AIV, has emerged in 10 Asian countries, including Thailand, Vietnam, and China (Fig. 1), and has claimed at least 53 human lives. Until recently, migratory waterfowl seemed to be exempt from widespread infection, although sporadic cases were recorded (3). Here we describe an outbreak of highly pathogenic H5N1 infection among waterfowl in Lake Qinghaihu, Qinghai Province, in eastern China (Fig. 1).

On 4 May 2005, a few birds were found dead on Bird Island, and by the end of the day, more than 100 birds had been affected. This lake is one of the most important breeding locations for migratory birds that overwinter in Southeast Asia, Tibet, and India (Fig. 1). Several species were infected, including the bar-headed goose (Anser indicus), great black-headed gull (Larus ichthyaetus), and brown-headed gull (Larus chroicocephalus). Two key symptoms were noticed: abnormal neurological signs (tremor and opisthotonos) and diarrhea. Among the gross lesions, pericarditis was obvious and was confirmed by tissue section with extensive areas of diffusely necrotic livers, consistent with pathology observed in domestic geese and ducks infected with HSN1 AIV (3). Brain sections revealed glial cell infiltration, perivascular cuffing, and congestion in the brain vessels. Serological tests (4) from one bar-headed goose and one brown-headed gull confirmed the presence of high-titer antibody against HSN1 AIV.

Several H5N1 viruses were isolated from the viremic, brain, and oropharyngal swabs of the geophagia and cloaca of sick and dead birds. Four of the isolates from different bird species were completely sequenced (4) and appeared to be closely related. None of the GenBank sequence data for known HSN1 AIV genome completely matched our sequences, implying the viruses are reassortants. Five of the eight genomic segments (M, PA, PB1, PB2, and NS) were closely related to the Hong Kong 2004 isolate (A/pigeon/ HK/0025/04) (5). We observed several characteristics in our four isolates: first, the sequence POQIEEDEEKEG, denoting multiple basic amino acids at the cleavage site of the barbellagulnase activity, a virulence island in the PB2 gene, PB2K, first seen in Hong Kong in 1997 (6), and third, a deletion of 20 amino acids in neuraminidase (amidase) position 49 to 69, also associated with high virulence.

To test virulence, mice and chickens were infected with the HSN1(Tai H8) (6) isolate. All eight infected chickens died within 20 hours, and seven of eight infected mice died within 72 hours; the last died 96 hours post-infection. Earlier isolates taken from ducks in China were less virulent in mice and chickens (6). Hence, we speculate that viruses might be emerging from reassortants that originate in birds overwintering in southeast Asia (7).

The occurrence of highly pathogenic H5N1 AIV infection in migratory waterfowl indicates that this virus has the potential to be a global threat. Lake Qinghaihu is a breeding center for migratory birds that congregate from Southeast Asia, Siberia, Australia, and New Zealand.

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References and Notes

4. Materials and methods are available in supporting material on Science Online.
10. Supported by the Ministry of Science and Technology of China. This study is an extension of the studies of D.J. B. of the Chinese Academy of Sciences (Beijing, China) and the China National Academy of Sciences (Beijing, China).

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**Fig. 1.** (A) The reported influenza virus prevalence sites during the 2004 outbreak in China are highlighted in yellow (B). Arrows indicate the migratory routes of the bar-headed goose (A. indicus) to Lake Qinghaihu. (B) A sick bar-headed goose showing typical symptoms before dying. (C) Bar-headed goose presenting with pericarditis lesions (arrows). (D) Necropsy lesions in bar-headed goose brain showing congestion in the blood vessels (white arrow) and glial cell infiltration (black arrow). Hematoxylin and eosin ×100 (scale bar, 50 μm).

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Supporting Online Material

www.sciencemag.org/cgi/content/full/1115273/DC1

Materials and Methods

Figs. 1 and 2.

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Capture and mark waterfowl to study their local movement, habitat use, and migration in relation to potential HAPI H5N1 spread

Qinghai Lake, China
Track migratory waterbirds through GPS-based satellite telemetry

524 transmitters
12 countries
24 species

from John Takekawa
Gilbert et al., 2011, Flying over an infected landscape: distribution of HPAI H5N1 risk in South Asia and satellite tracking of wild waterfowl, Ecohealth,
How to reduce spatial uncertainty in complex systems?

- Weather / Climate
  - Natural wetlands
  - Paddy rice fields
  - Fish ponds
  - Water body

- Migratory birds
  - AIV

- Pig (swine flu)
  - AIV

- Free-grazing ducks/geese
  - AIV

- Poultry (AIV, H5N1)
  - AIV

- Human (seasonal flu)

Production, market, trade, transport systems, Vaccine, movement control, culture, behavior

- Pig
  - AIV

- Human
  - AIV
The GeoPhoto Library
A community- and citizen- science data portal to share and archive geo-tagged field photos

www.eomf.ou.edu/photos
Geo-tagged field photos are ground reference data, and can be used for disease surveillance & epidemiology: poultry farms, free grazing, markets, virus samples.
Link geo-tagged field photos with satellite time series images
GeoPhoto library is used to support rapid and dynamic mapping of land use and land cover.
GeoHealth data portal

- Informatics approaches to integrate disparate sources of datasets
- Data mining and visualization

Disparate datasets
- Highly pathogenic avian influenza H5N1 data
- Human population
- Poultry, pigs,
- Satellite telemetry of wild birds - Wild bird migration
- Satellite-based mapping of agricultural land use - paddy rice
- AIV surveillance data (GenBank, OpenFlu)
- Market chain data
- Geo-tagged field photos
- Weather and climate
Data visualization and integration
Food and Agriculture Organization of the United Nations (FAO)

Animal Production and Health Division

Decision support system in FAO

The Emergency Prevention System (EMPRES) for Priority Animal and Plant Pest and Diseases

Crisis Management Center
Global Early Warning System (GLEWS) for animal diseases that are transmissible to humans

FAO, OIE and WHO established it in 7/2006.
To link FAO EMPRES-i data portal with OU EOMF GeoHealth data portal