Managing the matrix of influenza infections in line with the “One Health” vision

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Do we think that influenza pandemics are something we should worry about?
What do we know about the origin and emergence of pandemic influenza?
Influenza pandemics in last 100 years

• Spanish flu 1918-1819 – entirely of avian origin 20-40 million deaths (H1N1)

• “Asian flu” 1957, avian and swine origin (H2N2)

• “Hong Kong” 1968 – human and avian (H3N2)

• “H1N1 pdm 2009” – swine, human and avian (H1N1)

Always contained a novel “animal” component
Emergence of pandemic influenza

- Animal
  - Animal to human transmission (sporadic)
- Zoonotic
  - Adaptation/mutation
- Pandemic
  - Seasonal
  - Human to human transmission (pandemic/endemic)
Animal Health implications

Highly Pathogenic Avian Influenza, Italy 2000
One WHO Expert on SARS Finds Flu More Frightening

Grippe aviaire : l'épidémie devient extrêmement dangereuse

LOCK UP ALL OUR CHICKENS

Aviare, pericolo per l'umanità? Influenza killer

Gli esperti europei di influenza riuniti a Malta. Il nostro Paese deve aumentare le scorte di antivirali, pronto il piano di emergenza «Il virus dei polli colpirà 16 milioni di italiani»

Crovati: epidemia inevitabile. Le previsioni: 150 mila vittime. Un commissario in ogni Asl
H5N1 - where are we?

- H5N1 is still endemic in at least 5 countries
- The virus is able to infect approximately 50 avian species and 10 mammalian species, including human beings
- It causes a 50% fatality rate in infected individuals, but has not acquired human-to-human transmissibility
- Human beings are immunologically naive to the virus
- H5N1 is causing food security issues in developing countries
H5N1 is the first HPAI virus

- Which has persisted for over 13 years
- For which extensive vaccination has been applied
- Has spread to three continents
- Has infected an unpredictable number of animal species, including humans
- Is evolving into lineages and sublineages
- Has been mentioned by most political leaders of the world
Legacy of H5N1

- Investments in capacity building
- Increase of number of veterinary/human laboratories performing influenza surveillance
- Establishment of reliable contacts worldwide to provide information on local aspects
- Expansion of areas of research
- Availability of an unprecedented number of isolates containing valuable genetic information
- And above all has provided an opportunity
Contributing to
One World, One Health*

A Strategic Framework for Reducing Risks of Infectious Diseases at the Animal–Human–Ecosystems Interface

14 October 2008

Consultation Document

Produced by:

http://www.un-influenza.org/node/2341
H1N1 - Real pandemic?

- *Pandemic* – from the Greek
  - *pan*: all
  - *demos*: people
Gosh! From pigs...
Evolution of swine influenza viruses in North America

- 1997-1998

- 1998

- 2000+

2 genes of Eurasian lineage
First cases in San Luis Potosi, Mexico: 24 February 2009

April 15
First case Identified
A/California/4/2009

April 29
First Diagnostic Kits Shipped to State Labs

May 3
First Diagnostic Kits Shipped to WHO Network

May 23
Vaccine Strain Shipped to Manufacturers
Lessons learnt from H1N1pdm 2009

• The emergence (when and where and what subtype) of pandemic influenza cannot be predicted with current tools
• World-wide spread occurs within a few weeks of the index case
• The pathogenicity in the “new (human) host” including age or ethnic susceptibility was unknown
• Vaccine was available after the epidemic peak
• Pdm virus spills back into animals with unknown consequences
Two points of view: AH/PH

**Animal health**
- Fear of drop in consumption of pork/poultry meat
- Fear of trade restrictions
- Economic losses for the industry

**Public health**
- Understand epidemiology of infection in swine and other animal populations
- Understand reassortment dynamics with animal influenzavirus
- Evaluate PH aspects of H1N1pdm in animal populations
Pandemic H1N1 2009 events by country and affected species reported up to 31 January 2010
(Source: EMPRES-i FAO; [http://empres-i.fao.org/empres-i/home](http://empres-i.fao.org/empres-i/home))

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Confirmed animal cases with Pandemic H1N1 2009 Influenza virus
Situation as of 01 February 2010

Affected species:
- Swine
- Turkey
- Cat
- Dog
- Ferret
- Cheetah

(Source: EMPRES-i FAO; http://empres-i.fao.org/empres-i/home)
The emergence (when and where and what subtype) of pandemic influenza cannot be predicted with current tools.
Population size estimates (1950-1990) and projection (1990-2025), by regions show a drastic increase in Asia and Africa.
Forecast of meat consumption 1983-2020
High risk species for generation of pandemic influenza
THE PIG AS A ‘MIXING VESSEL’

α 2 - 3

α 2 - 6

α 2 - 6

α 2 - 6
Figure 27: Prices of selected meat products

- Ovine
- Beef
- Pigmeat
- Poultry
FIGURE 1
Per capita consumption of major food items in developing countries, 1961–2005

Index (1961 = 100)

Source: FAO, 2009b.
FIGURE 5
World production of main categories of meat, 1961–2007

Index (1961 = 100)

Source: FAO, 2009b.
Figure 43. Major poultry exporters

Source FAO Website:
http://www.fao.org/docrep/011/ai482e/ai482e08.htm#36
Challenges for the future

Is it appropriate to put influenza viruses in “boxes”? 
Genes originating from viruses of three animal species and two hemispheres

6 genes ↔ 2 genes

A/California/4/2009
Mars Weather Report
October 06 - 12, 2008:

“Throughout the week, clouds and dust were seen extending across Argyre and Hellas, while water-ice clouds continued to dominate the skies over all the large volcanoes”
Sharing of information
First appearance of H5N1 in Africa

- IZSVe was the first laboratory to isolate the H5N1 African strain
- Genetic characteristics of the first African isolates would shed light on H5N1 epidemiology and pathogenicity
- We declined offer to deposit sequence in password protected database (only 15 labs had access) and deposited the full sequence in GenBank
AVIAN INFLUENZA

As H5N1 Keeps Spreading, A Call to Release More Data

PARIS—An impassioned call by a prominent Italian influenza scientist has renewed the debate about how to balance global health against scientists’ needs to publish and countries’ demands for secrecy. On 16 February, Ilaria Capua of the Institute Zooprofilattico Blocco C in Rome, Italy, expressed deep concern at a press conference. "We need to know if these are multiple lineages of H5N1 virus, or just one," she said, referring to the H5N1 virus that has been spreading around the world. Capua countered that just isolating and sequencing a virus that comes in the mail does not give researchers the right to sit on the data—especially not at a government lab. "Most of us are paid to protect human and animal health," she says. "If publishing one more paper becomes more important, we have our priorities messed up." Governments can often be persuaded to release the sequences, adds Capua, who repeated her call at an OIE meeting in Paris on Monday and also plans to submit it to ProMED, an e-mail list about emerging infectious diseases.

WHO agrees that in an ideal world, scientists would share their data widely and voluntarily, says Wenqing Zhang of the agency’s Global Influenza Programme. But because that’s not happening, the agency created a special secured section at the Influenza Sequence Database at Los Alamos National Laboratory in New Mexico in 2004. Currently, some 15 labs have passwords to access these data, says Zhang, including WHO’s eight reference labs. The system is invaluable for WHO, she adds, as it helps the agency track the virus and adjust risk assessments if necessary.

Viruses at Yale Medical School of the University of
Ilaria Capua, a 39-year-old Italian veterinarian working on avian influenza in a government lab, last month received a sample of the virus in the mail from Nigerian health authorities. The virus had just attacked birds in Nigeria, the first confirmed case of the disease in Africa. The sample was something of a prize, a chance to study a specimen and explore how it spread from its stronghold in Asia.

Within days of isolating the virus, Dr. Capua says, she got an offer from a senior scientist at the WHO in Geneva, whom she declined to name, to enter her finding in the closed system. She could submit the virus’s genetic information, or sequence, to the database. In exchange, she would be given the password to the WHO’s massive stash of data. A spokesman for the WHO confirmed that the offer was made.

Instead, Dr. Capua posted the gene sequence in a public database accessible on the Internet. She also sent a letter on Feb. 16 to around 50 of her colleagues urging them to do the same with their bird flu samples. “If I had agreed” to the WHO’s request, she said in an interview, “it would have been another secret sequence.”

**Scientist Rebels Against WHO Over Bird Flu**

Scientists around the world, racing to discover how avian influenza is spreading and whether it is evolving toward a pandemic strain, face a dilemma: Should they share their interim findings widely, show them only to a select set of peers, or keep them to themselves until they can publish papers, often critical to their careers?

Now, a lone Italian researcher has cast a harsh spotlight on the WHO’s system, suggesting that it places academic pride over public health — and undermining it by posting prized bird-flu data in plain view.

**Editorial**

Secret Avian Flu Archive

At a time when health authorities are racing to head off a possible avian flu pandemic, it is distressing to learn that the World Health Organization is operating a secret database that holds the virus’s genetic information. A lone Italian scientist has challenged the system by refusing to send her own data to the password-protected archive. Instead, she released the information publicly and urged her colleagues to do the same. She is surely right. The limited-access archive should be opened or bypassed immediately to encourage research on this looming health menace.

The campaign by Ilaria Capua, an Italian veterinarian who works on avian influenza, was spotlighted in recent articles in the journal Science and The Wall Street Journal. The hidden data could be of immense value in determining how the virus is evolving and in developing effective vaccines or drugs. The possibility of breakthroughs can increase only if many more scientists can analyze the data.
RESOLUTION No. XXVI

Sharing of avian influenza viral material and information in support of global avian influenza prevention and control

1. OIE Members reporting outbreaks of avian influenza should agree to share animal avian influenza viral material and information about avian influenza viruses through OFFLU with the international scientific community.

2. OIE Reference Laboratories must actively encourage sharing of material and data with the international scientific community, and as a minimum deposit genetic data within 3 months of receiving an isolate into a public database designated by the OFFLU Steering Committee, which will manage scientific relations with the WHO.

3. To enhance cooperation and transparency, the actions taken by countries must be recognised in subsequent publications and other benefits arising from the use of biological material or data that they have submitted to OIE Reference Laboratories.
Pandemic influenza preparedness: sharing of influenza viruses and access to vaccines and other benefits

Outcome of the resumed Intergovernmental Meeting

Report by the Director-General

5.2 Genetic sequence data

5.2.1 Genetic sequence data, and analyses arising from that data, relating to H5N1 and other influenza viruses with human pandemic potential should be shared in a rapid, timely and systematic manner with the originating laboratory and among 
[WHO Network] laboratories. (Consensus)

5.2.2 Recognizing that greater transparency and access concerning influenza virus genetic sequence data is important to public health and there is a movement towards the use of public domain or public access databases such as Genbank and GISAID respectively; and (Consensus)
Avian flu: global sharing of virus samples

Another joint FAO/OIE initiative

1 August 2006, Rome - OFFLU, the OIE/FAO joint network of experts on avian influenza, will systematically make avian influenza virus sequences accessible to the entire scientific community. With this gesture OFFLU reiterates its call to the world’s scientists, international organisations and countries for a global sharing of virus strains and sequences.

Since its launch in April 2005, OFFLU has been mainly working on promoting the key objectives "to exchange scientific data and biological materials (including virus strains) within the network, and to share such information with the wider scientific community." Under this new impetus, strains will be sent to the U.S. National Institutes of Health for sequencing and deposited in full transparency on the free-access database, GenBank.

On 14 March 2006, the Scientific Committee of OFFLU, made up of the world’s leading veterinary experts on avian influenza, revised its terms of reference to put new emphasis on the need for further collection, characterization and exchange of avian influenza viruses, and for the expansion of the genomic database for animal influenza viruses.

Critical to surveillance and control efforts

Sharing virus strains, samples and sequences is a critical part of the global work on the surveillance and control of the highly pathogenic H5N1 virus, and supports the preparation of...
One Health, One Flu – Why?

- Need to improve our prediction capacity on pandemic potential and viral characteristics
- Established influenza surveillance capacity worldwide
- Increased awareness of the role of the animal reservoir in the generation of pandemic strains
- Sharing and transparency issues are being addressed
“One Flu” can improve prediction skills

- Understand how genes of influenza viruses migrate across species and continents, as one evolving gene pool
- Joint surveillance and research efforts between the human and the veterinary components of the equation
- Identify viral determinants for virulence and transmissibility in animals and humans
- Improve human and animal health as a collaborative effort
Develop and maintain a permanent influenza gene pool observatory

Capitalise on investments and networks established for H5N1

Perform harmonised and targeted surveillance in humans and animals

Improved human and animal health

- Preparedness
- Transdisciplinary collaboration
- Control and mitigation strategies
- Early warning systems
The FAO-OIE-WHO Collaboration

Sharing responsibilities and coordinating global activities to address health risks at the animal-human-ecosystems interfaces

A Tripartite Concept Note

April 2010

http://www.oie.int/downld/FINAL_CONCEPT_NOTE_Hanoi.pdf
Carpe diem