Emerging infectious diseases in a “One Health” context

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Emerging infectious diseases
Pathogens seeking the “right” opportunity, taking advantage of the globalised setting
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
Baby gets salmonella 'from snake'

A three-month-old baby contracted salmonella from her family's pet snake, her mother believes.

It took four days before Amanda Vry's daughter, Gabriella, was diagnosed with the potentially fatal bacterium and she said she feared she may lose her.

She said she found out from internet research that it could be contracted from reptiles.

Ms Vry, from Birmingham, said she thinks her son may have touched their pet snake then played with his sister.

The government's chief medical officer has previously warned that salmonella can be caught from exotic pets such as snakes and lizards.

Reg, a Colombian Rainbow Boa, was bought as a present for 18 month-old daughter Helena Strange.
Introduction of West Nile Virus into Italy

• Could we have predicted it?
• Can we control its spread more efficiently?
• Can we improve vector control?
• Can we accurately predict and control the emergence of other arbovirus infections (eg. Chikungunya, Dengue)?
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»
Crovari: epidemia inevitabile. Le previsioni: 150 mila vittime. Un commissario in ogni Asl
H5N1 epidemic - current situation

- H5N1 is still officially endemic in 5 countries (Egypt, China, Indonesia, Vietnam and Bangladesh)
- Still causes human deaths (mainly women and children)
- It represents a threat to food security in developing countries
- Control of infection is at least 10 years away
Highly Pathogenic Avian Influenza

H5N1 – a game changer
2005 - 2006: H5N1 spreads westward and reaches Europe, The Middle East and Africa
RIGHT LANE MUST TURN RIGHT
Investment in knowledge – tailored interventions, capacity building and diagnostic support
Legacy of H5N1

- Increase of number of human and veterinary laboratories diagnosing influenza virus infections
- Implementation of international training activities and capacity building
- Funding available for surveillance in wild and domestic bird populations
- Establishment of reliable contacts worldwide to provide information on local aspects
- Expansion of areas of research
- Availability of an unprecedented number of influenza isolates containing valuable genetic information
Do we think that influenza pandemics are something we should worry about?
What do we know about the origin and emergence of pandemic influenza?
Is it appropriate to put influenza viruses in "boxes"?
PB2, PA: ~ 1998
PB1: ~ 1968 → ~ 1998
HA, NP, NS: ~ 1918
NA, MA: ~ 1979

Triple reassortant
Classical swine
Eurasian swine

A/California/4/2009
PB2
PB1
PA
HA
NP
NA
MA
NA

Courtesy, Ron Fouchier, EMC
“One Flu”

• 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
• Improve human and animal health as a collaborative effort, capitalising on investments
Capitalise on investments and networks established for H5N1

Perform harmonised and targeted surveillance in humans and animals

Develop and maintain a permanent influenza gene pool observatory

Improved human and animal health
- Preparedness
- Transdisciplinary collaboration
- Control and mitigation strategies
- Early warning systems
Where are we with ‘One Flu’?

One Flu for One Health

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We invite donors and international agencies to invest in a novel approach to influenza virus infections, to abandon prefixed compartments linked to geographic origin or species of isolation, and to analyze the influenza gene pool as one entity. We propose capitalizing on existing achievements and investments to develop an international network and a permanent observatory, which will improve our understanding of the dynamics of the influenza virus gene pool in animals and humans. A greater understanding will generate important information to support both public and animal health.
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 Istituto Zooprofilattico tricky from the start. WHO, FAO, and OIE encourage countries to send virus samples to specialized reference labs that can confirm the outbreak and study the virus further. Some have been reluctant to do so because they worry about intellectual property rights or other issues. WHO, FAO, and OIE encourage countries to send virus samples to specialized reference labs that can confirm the outbreak and study the virus further. Some have been reluctant to do so because they worry about intellectual property rights or other issues.

Showing her cards, Ilaria Capua says she will submit H5N1 sequences from her lab to public databases immediately, dozens of individual governments, Brown says. Capua counters 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. Wiobisist Xi Fan of the University of
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?

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.

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 spokesperson 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."

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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.

Concern about the accessibility of data on flu strains remains an acute issue, which research administrators and political leaders should step forward and address. Indonesia has become the hot spot of avian flu, with the virus spreading quickly in animal populations, and human cases occurring more often than elsewhere. Yet from 51 reported human cases so far — 30 of them fatal — the genetic sequence of only one flu virus strain has been deposited in GenBank, the publicly accessible database for such information.

"H5N1 sequences should be promptly deposited in a publicly accessible database," David Brown, an editorial writer for The New York Times, wrote in an article published in the journal Nature. "Sharing data is key to beating threat from flu."

SIR — We fully support Ilaria Capua in her call for avian-influenza researchers to release data to the public, rather than store them in restricted databases, as reported in your Editorial "Dreams of the data" (Nature 440, 255–256; 2006). Keeping sequences secret, whatever the motivation, slows down scientific progress and hinders efforts to protect public health. The influenza genome sequencing project (www.rraid.nih.gov/ dmard/genome/ims/influenza.html) has, in the past year, sequenced more than 1,000 complete genomes of human influenza and...
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 - OIE/FAO, 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 OIE/FAO 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, OIEFLU 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 initiative, 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 OIEFLU, made up of the world's leading veterinarian 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...
Genetic evolution of H1N1p 2009
WHY is this so important

Because it can serve as a model for future epidemics threatening mankind – we would have a system in place to react promptly and maximise the outcome of research efforts
The REAL challenge of “One Health”

Open channels of information for improved public health worldwide
“Open One Health”