



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









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Do we think that influenza pademics are something we should worry about?



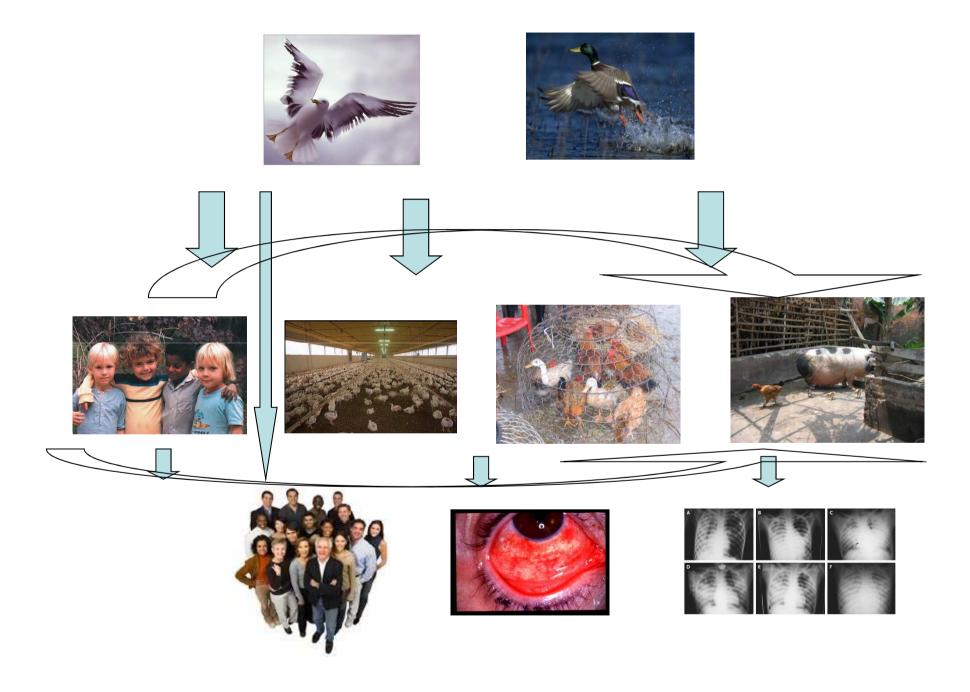
What do we know about the origin and emergence of pandemic influenza?











Influenza pandemics in last 100 years

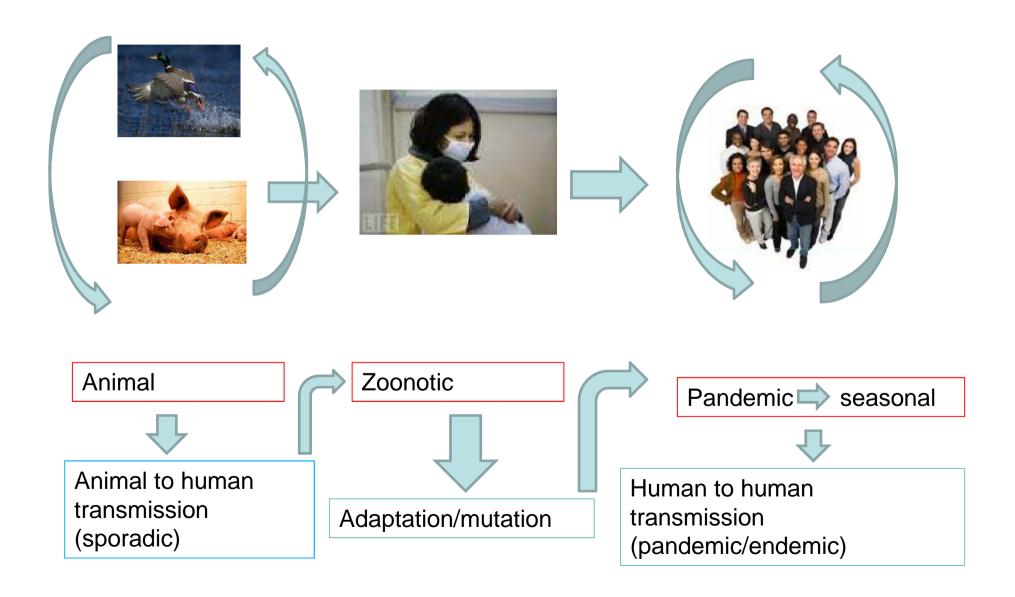


- •Spanish flu 1918-1819 entirely of avian origin 20-40 million deaths (H1N1)
- •"Asian flu" 1957, avian and swine origin (H2N2)
- •"Hong Kong" 1968 human and avian (H3N2)
- "H1N1 pdm 2009" swine, human and avian (H1N1)

Always contained a novel "animal" component



Emergence of pandemic influenza



Animal Health implications





Highly Pathogenic Avian Influenza, Italy 2000



One WHO Expert on SARS Finds Flu More Frightening

Doctor Deems World Unprepared na-Awaited Pandemic

By GAUTAM NAIR



Juppé fait face à sol la droite critique le

devient extrêmement dangereuse





Documento riservato della Casa Bianca pubblicato dal «New York Times»

milioni di morti, ospedali in tilt

L'influenza aviaria in Europa: duemila tacchini colpiti in Turchia





Gli esperti europei di influenza riuniti a Malta. Il nostro Paese deve aumentare le scorte di antivirali, pronto il piano di emergenza

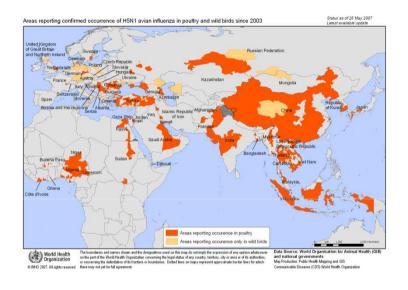
Grippe aviaire : l'épidémie

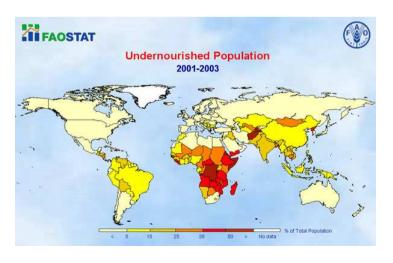
«Il virus dei polli colpirà 16 milioni di italiani»

Crovari: 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:













UN System Influenza Coordination

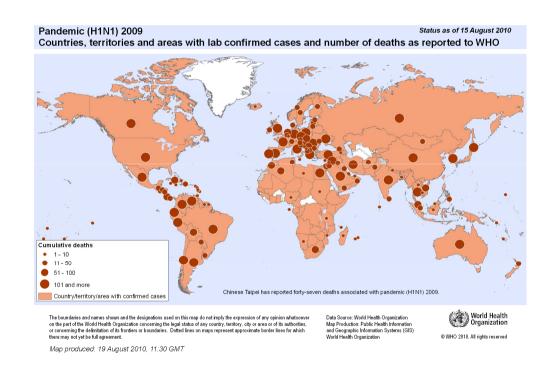


H1N1 - Real pandemic?

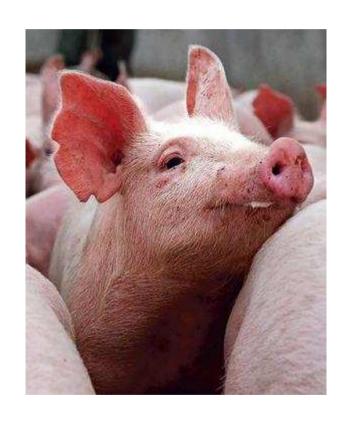
• Pandemic – from the Greek

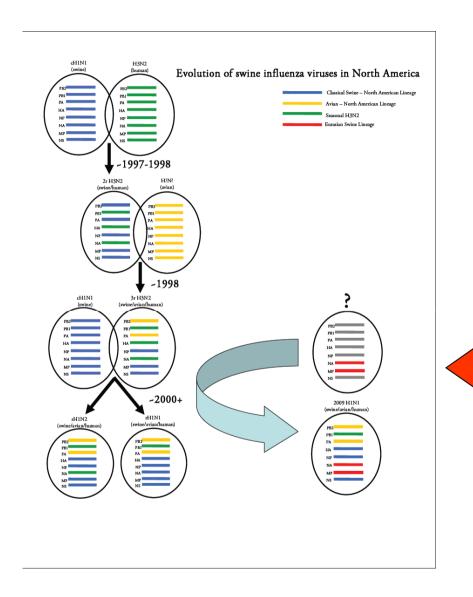
-pan: all

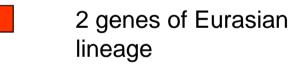
-demos: people



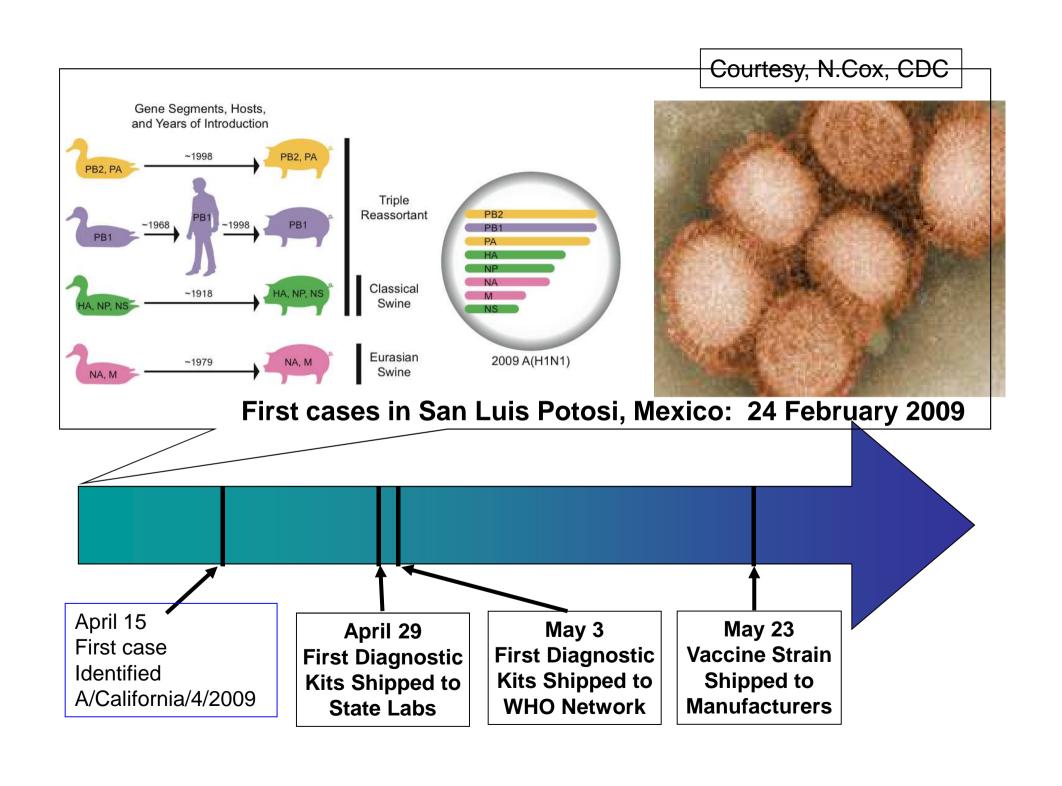
Gosh! From pigs...











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

Istituto Zooprofilattico Sperimentale delle Venezie

Public health

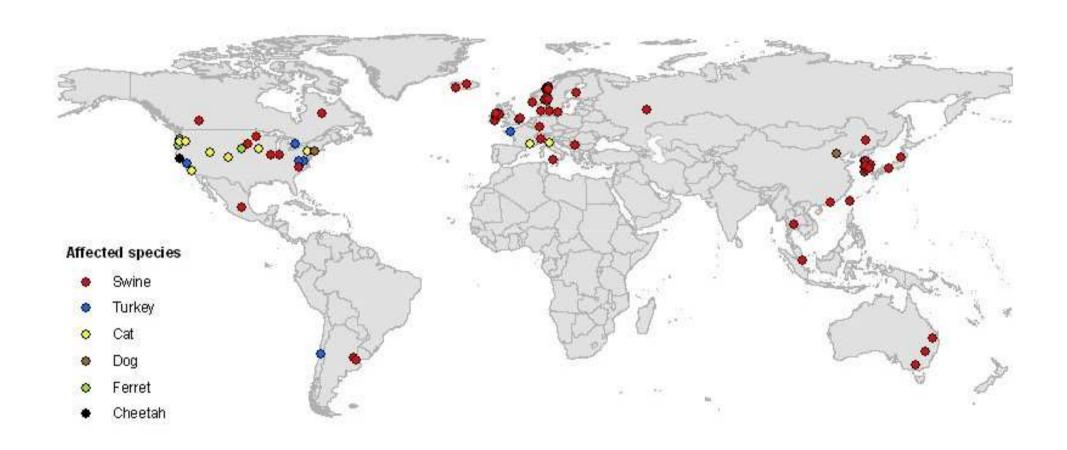
- Understand epidemiology of infection in swine and other animal populations
- Understand reassortment dynamics with animal influenzaviruses
- Evaluate PH aspects of H1N1pdm in animal populations

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)

Country	Cats	Cheetah	Dogs	Ferrets	Swine	Turkeys	Grand Total
Argentina					2		2
Australia					3		3
Canada					2	1	3
Chile						2	2
China			1		5		6
Denmark					4		4
Finland					1		1
France	1					1	2
Germany					1		1
Iceland					2		2
Indonesia					1		1
Ireland					2		2
Italy	1				2		3
Japan					2		2
Mexico					1		1
Norway					39		39
Rep. of Korea					18		18
Rep. of Serbia					1		1
Russian Fed.					1		1
Singapore					1		1
Thailand					1		1
U.K.					6		6
U.S.A.	9	1	1	3	9	4	27
Grand Total	11	1	2	3	104	8	129

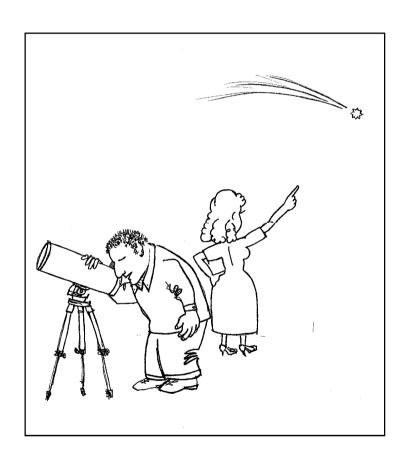
Confirmed animal cases with Pandemic H1N1 2009 Influenza virus Situation as of 01 February 2010



(Source: EMPRES-i FAO; http://empres-i.fao.org/empres-i/home)

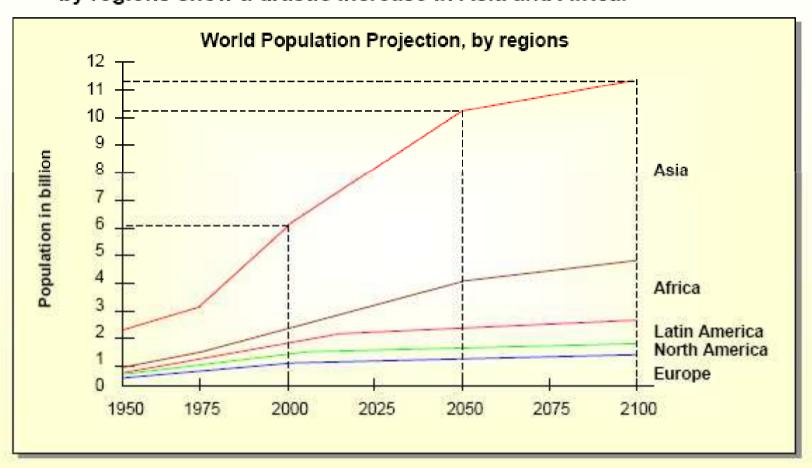
Predicting the 3 W's

The emergence (when and where and what subtype) of pandemic influenza cannot be predicted with current tools

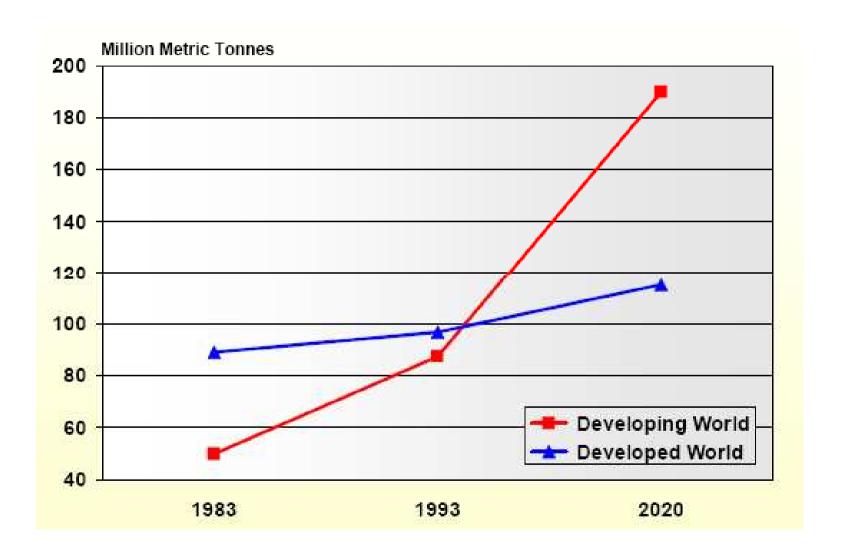




Population size estimates (1950-1990) and projection (1990-2025), by regions show a drastic increase in Asia and Africa.



Forecast of meat consumption 1983-2020



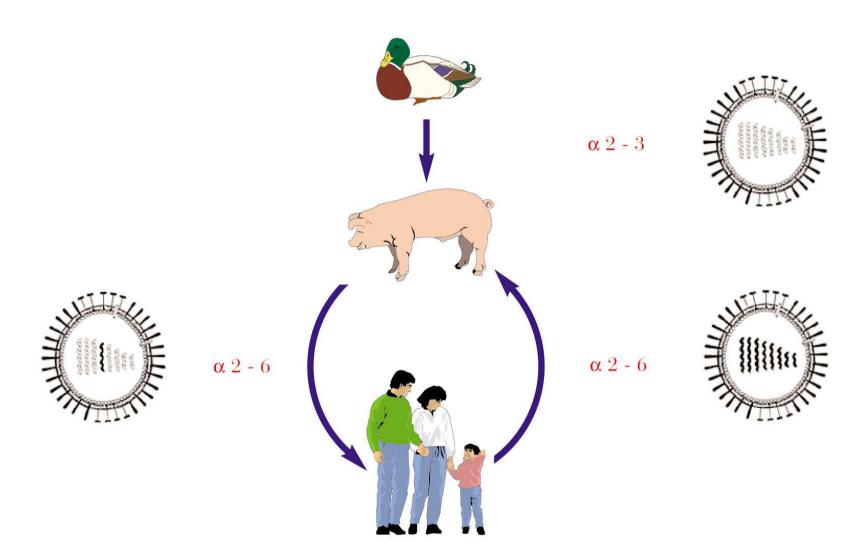


High risk species for generation of pandemic influenza





THE PIG AS A 'MIXING VESSEL'





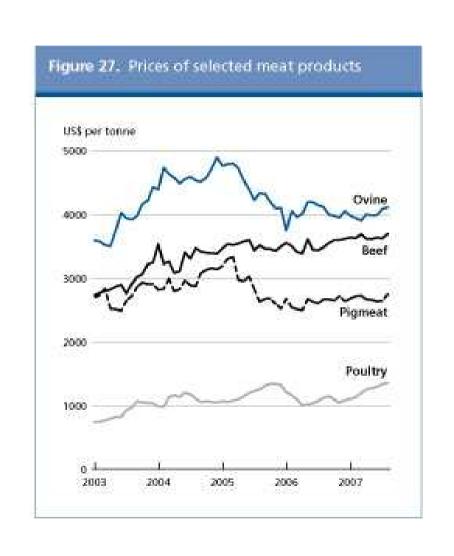
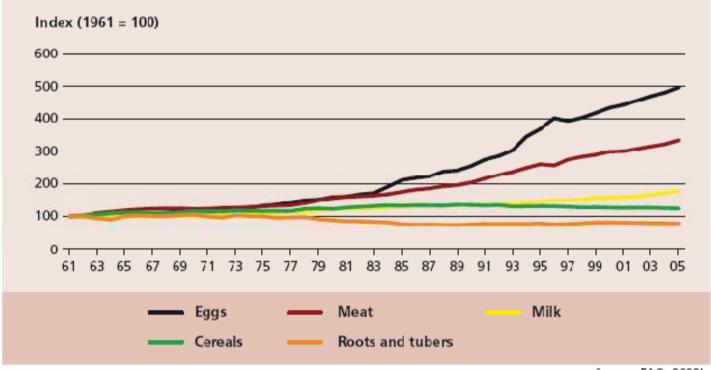
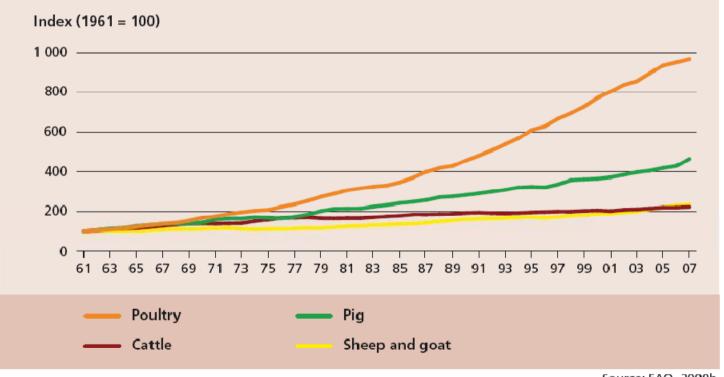


FIGURE 1
Per capita consumption of major food items in developing countries, 1961–2005

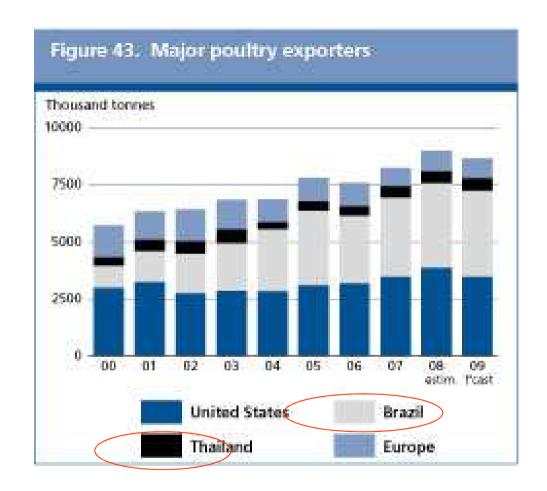


Source: FAO, 2009b.

FIGURE 5
World production of main categories of meat, 1961–2007



Source: FAO, 2009b.



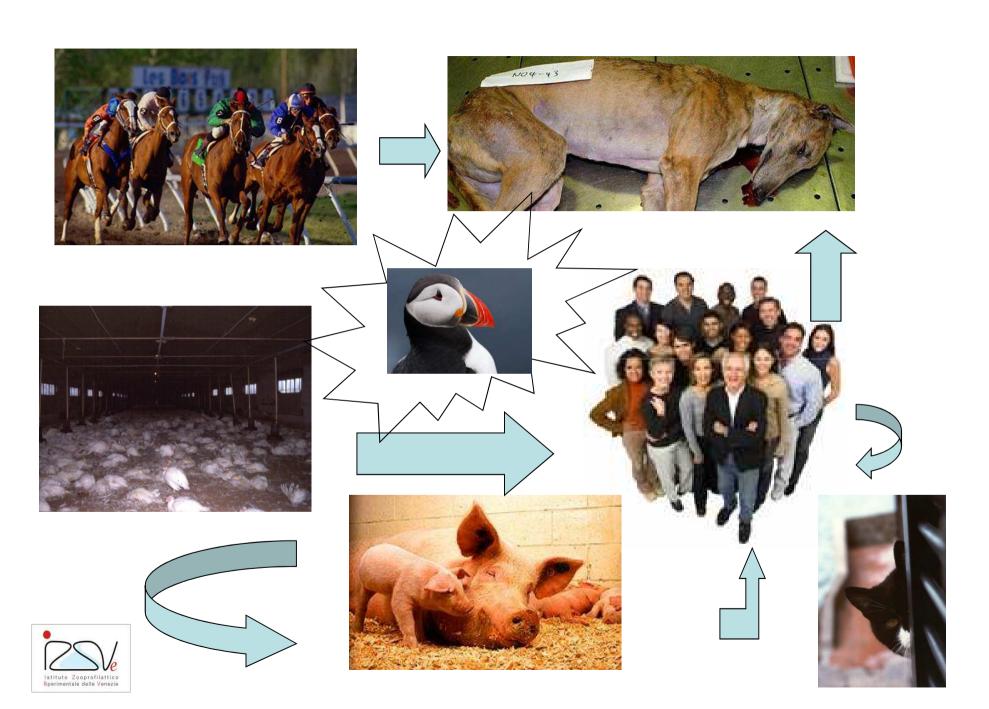
Source FAO Website: http://www.fao.org/docrep/011/ai482e/ai482e08.htm#36

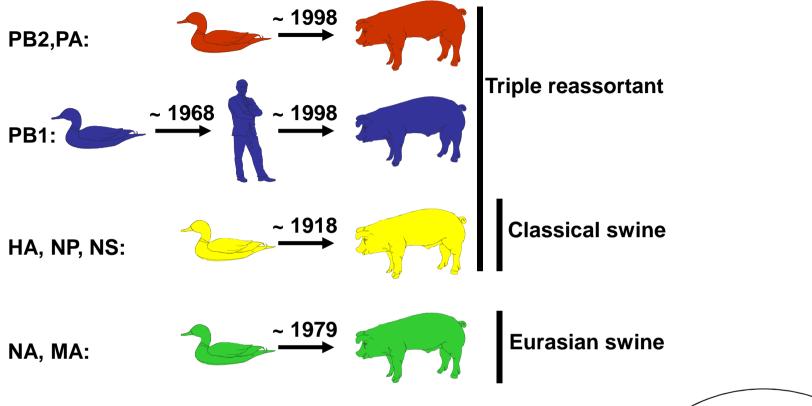
Challenges for the future



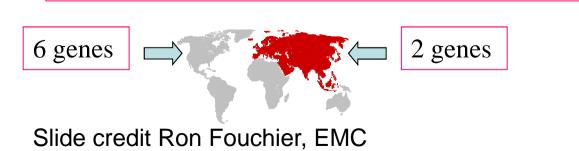
Is it appropriate to put influenzaviruses in "boxes"?

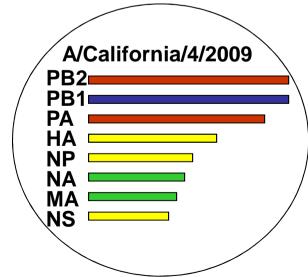


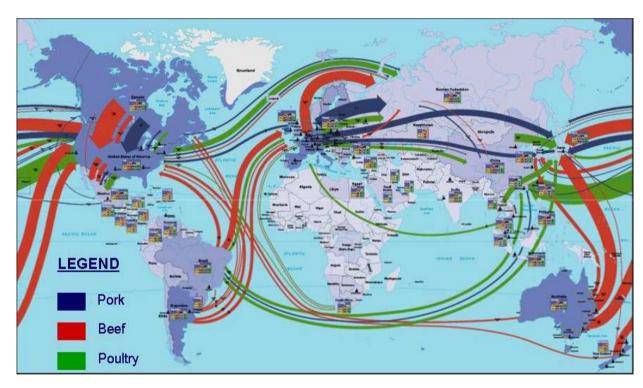


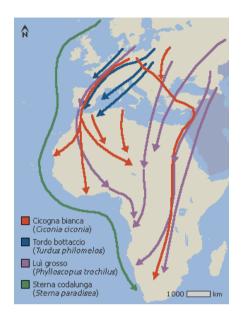


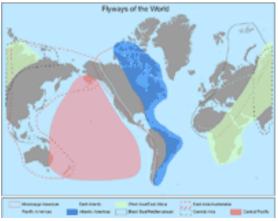
Genes originating from viruses of three animal species and two hemispheres



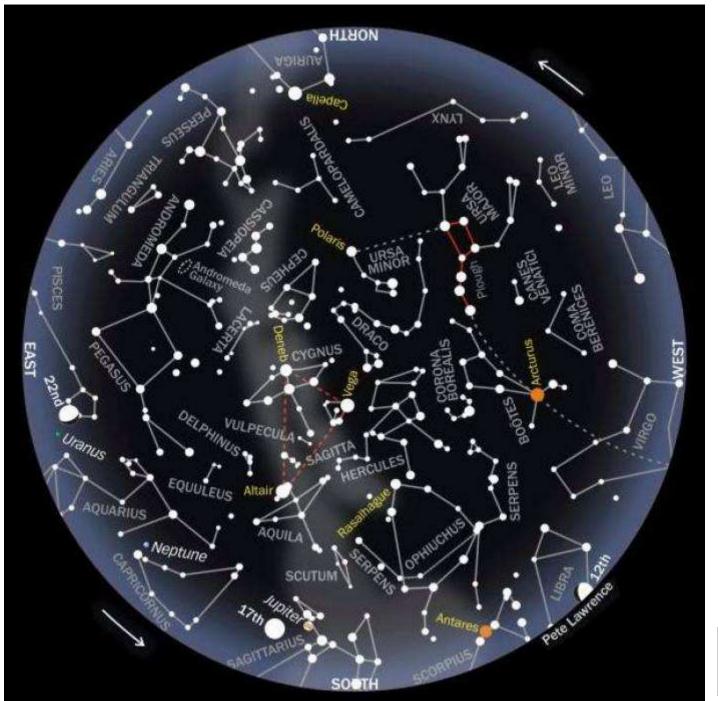










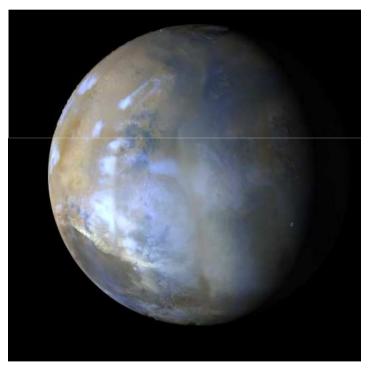




FROM EART 100005 TO MAR 1100005 an interactive timeline 10015



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







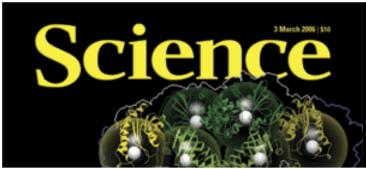
First appearance of H5N1 in Africa

- 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 Canna of the Istitute Zeoprofilattica.

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 not

NEWS>>

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.

Virologist Vi Guan of the University of

THE WALL STREET JOURNAL

MONDAY, MARCH 13, 2006

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 snubbing it by posting prized bird-flu data in plain view.



taria Capua

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 its pread 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-fu samples.

"If I had agreed" to the WHO's request, she said in an interview, "it would have been another secret sequence."

The New Hork Times

EDITORIAL

Secret Avian Flu Archive

Published: March 15, 2006

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.

washingtonpost.com

Bird Flu Fears Ignite Debate on Scientists' Sharing of Data

By David Brown Washington Post Staff Writer Thursday, May 25, 2006; A20

The issue gained public attention in February when Ilaria Capua, a 40-year-old virologist at the Tri-Veneto Region Experimental Animal Health Care Institute in Italy, sequenced the first H5N1 sample from Africa, isolated from a chicken farm in northern Nigeria. Someone at WHO invited her to contribute it to the Los Alamos data, but she declined and instead filed it in GenBank.

nature

Action stations

The time for sitting on flu data is over.

oncern 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 there than elsewhere. Yet from 51 reported human cases so far — 39 of the m fatal — the genetic sequence of only one flu virus strain has been deposited in GenBank, the publicly accessible database for such information.

And last week in China, researchers belatedly published details of

EDITORIALS

NATUREIVol 441l 29 June 2006

the appearance of human-to-human transmission. In the Sumatra event, the transmission did not spread beyond the family.

Yet scientists outside the WHO networks have no access to these data. The problem last year spurred the US National Institutes of

"H5N1 sequences should be promptly deposited in a publicly accessible database."

Health (NIH) to create a consortium to sequence and make public thousands of flu strains from humans and birds. Very quickly, this more open approach led to the useful discovery that viruses swap genes with each other more

frequently than had been previously thought.

Some political leaders are drawing the appro-

Some political leaders are drawing the appropriate conclusions. Dennis Kucinich (Democrat, Ohio) and Wayne Gilchrest (Republican, Maryland) are circulating a letter in the House of Representatives

nature

CORRESPONDENCE

NATUREI Vol 440 | 30 March 2006

Shared data are 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 flu 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.niaid.nih.gov/dmid/genomes/mscs/influenza.htm) 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

- 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.



SIXTY-SECOND WORLD HEALTH ASSEMBLY Provisional agenda item 12.1

A62/5 Add.1 18 May 2009

Pandemic influenza preparedness: sharing of influenza viruses and access to vaccines and other benefits

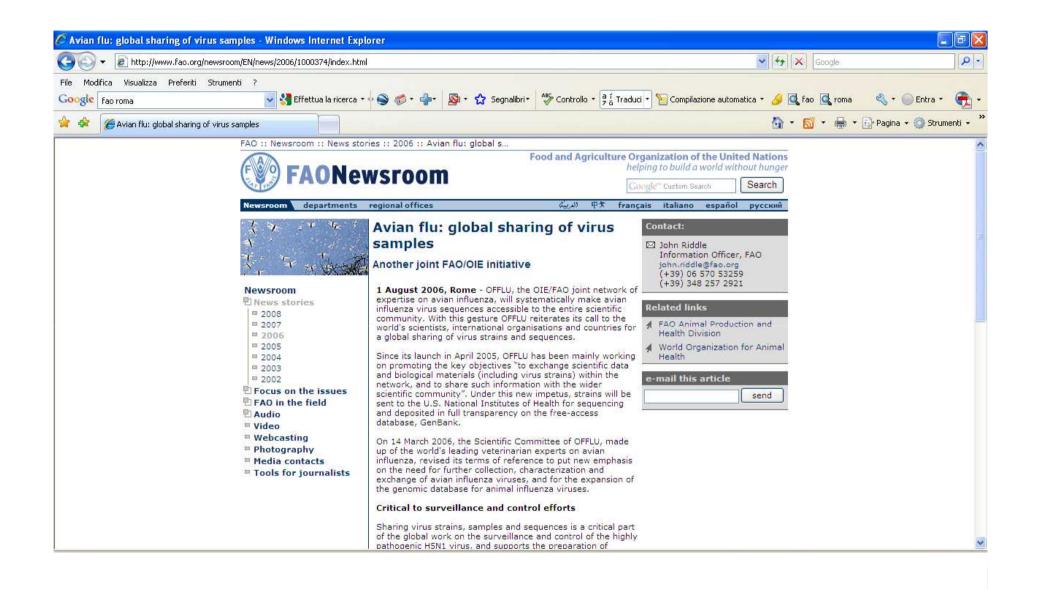
Outcome of the resumed Intergovernmental Meeting

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)

http://apps.who.int/gb/ebwha/pdf_files/A62/A62_5Add1-en.pdf



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 influenzaviruses 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 mantain 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

