

Integrated Surveillance for Animal and Human Influenza: A Challenge to be Overcome



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Concept Note: FAO-OIE-WHO Collaboration

Vision

A world capable of preventing, detecting, containing, eliminating, and responding to animal and public health risks attributable to zoonoses and animal diseases with an impact on food security through multi-sectoral cooperation and strong partnerships

The FAO - OIE - WHO Collaboration: A Tripartite Concept Note, April 2010

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The One Health Approach: Why Focus on One Flu?

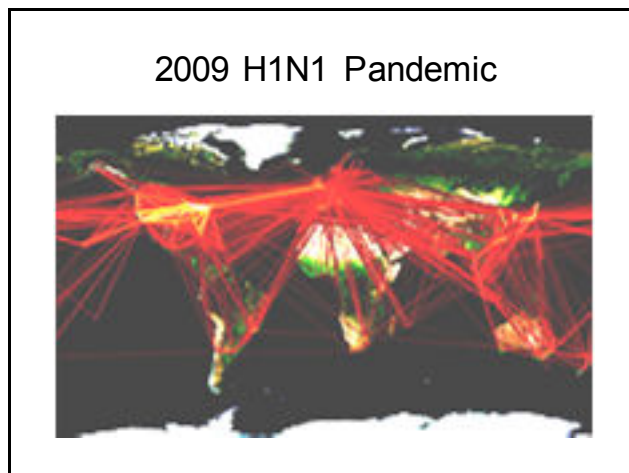
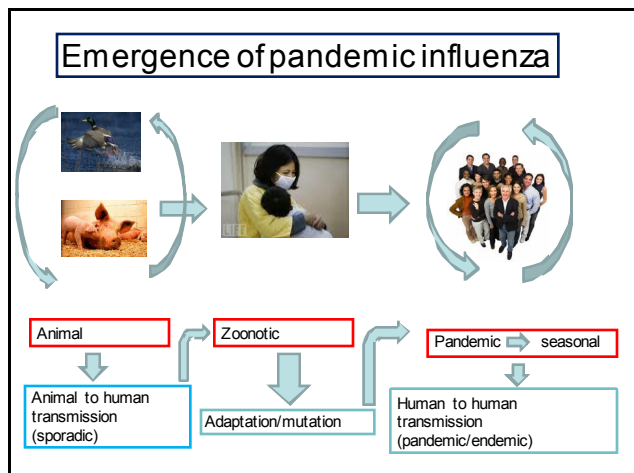
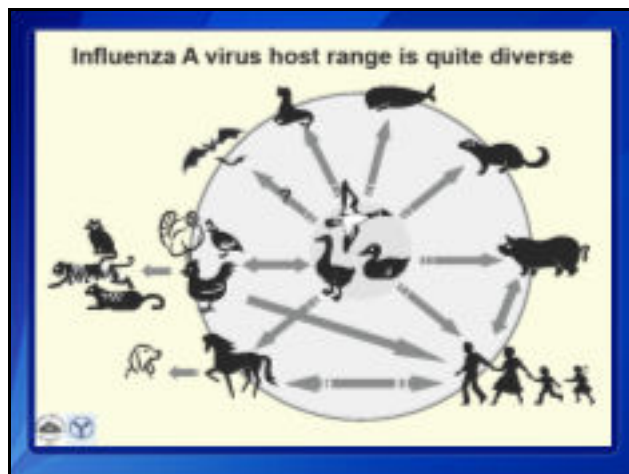
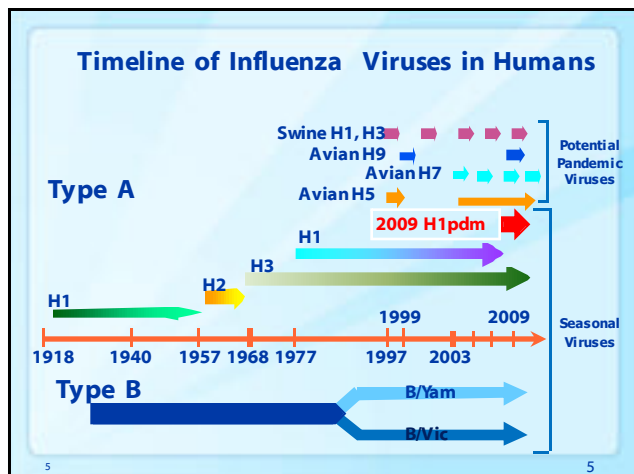
- We live with an ongoing risk of another influenza pandemic
 - HPAI H5N1 is enzootic in at least 6 countries
 - H9N2 & other avian influenza subtypes have infected mammals; widespread in birds in Asia and the Middle East; human-like receptor specificity
 - H1N1 pdm09 viruses are enzootic in swine around the world and genetic reassortment with other endemic swine viruses occurs frequently
 - Emergence of influenza A(H3N2) variant viruses in the U.S.

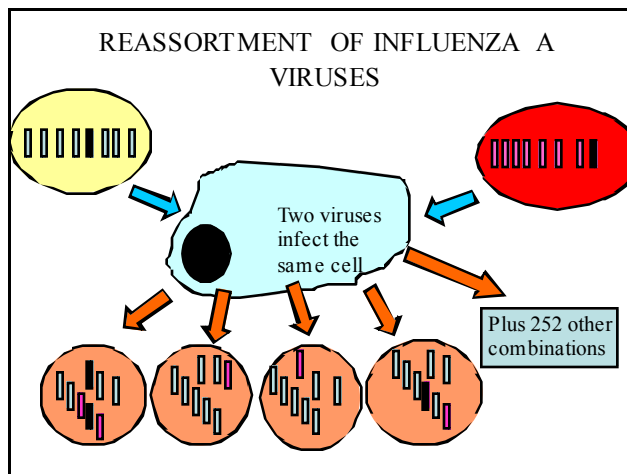
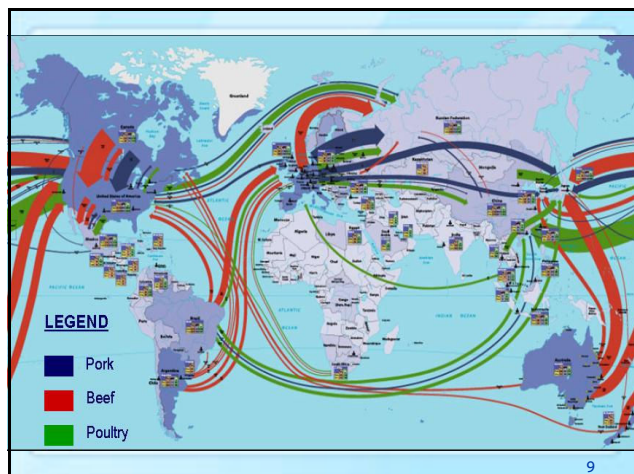
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One Health, One Flu: What Can We Do for Integrated Surveillance?

- Improve influenza surveillance capacity worldwide
- Increase awareness of the role of the animal reservoir in the generation of pandemic strains
- **Improve transparency and trust**
- Share surveillance data across human and animal health in real time
- Improve preparedness and 'prediction' for influenza viruses with pandemic potential and viral characteristics



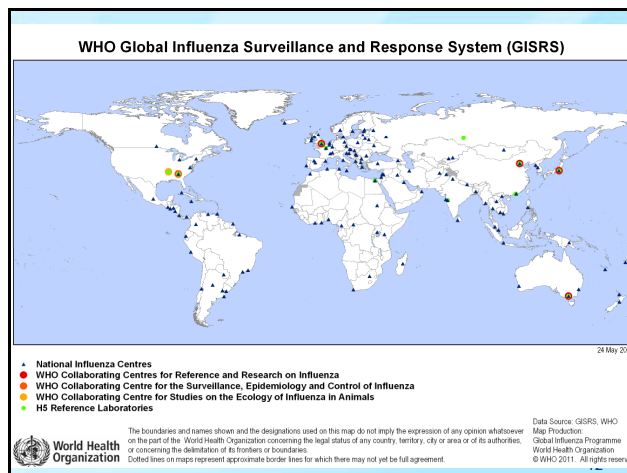


The Influenza Virus "Gene Pool"

- Historical literature and complex surveillance and gene sequence analysis of influenza viruses in nature suggests that gene segments of influenza A viruses are uniquely promiscuous within their primary aquatic bird reservoir - constant reassortment and transient gene constellations
- Much greater gene constellation stability appears to exist when a successful 8 segment gene constellation jumps from aquatic birds to infect a secondary host such as poultry, pigs, horses, humans etc.
- Adaption to a secondary host provides a "stabilized" 8 segment genome that then is transmitted onwards

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WHO Pandemic Vaccine Candidates, 2004 to Present

Virus	Clade	Institution	Availability
H5N1 reassortants with completed regulatory approval			
A/Vietnam/1203/2004 (CDC-RG; SRG-161053)	1	CDC and S/NIH	Yes
A/Vietnam/194/2004 (NBRG-14)	1	NBRG	Yes
A/Indonesia/05/2005 (CDC-RG)	2.1.3.2	CDC and S/NIH	Requires Indonesian government permission
A/Baharated grow/Quing/1/A/2005 (SRG-163222)	2.2	S/NIH	Yes
A/whooperawa/Mongilia/244/2005 (SRG-163243)	2.2	S/NIH	Yes
A/HongKong/1/2005 (NBRG-23)	2.2.1	NBRG	Yes
A/HongKong/1/2005 (IBCC-RG)	2.3.4	CDC	Yes
A/Japanese white-eye/HongKong/1038/2006 (SRG-164281)	2.3.4	S/NIH	Yes
A/Cambodia/040505/2007 (NBRG-88)	1.1	NBRG	Yes
A/India/03/2007 (IBCC-RG)	2.1	RIA	Yes
A/HongKong/795/2002 (SRG-166614)	2.1	S/NIH	Yes
A/HongKong/1/2007 (IBCC-RG)	2.1.1	CDC	Yes
A/HongKong/1/2007 (IBCC-RG)	4	S/NIH	Yes
A/HongKong/1/2007 (IBCC-RG)	7.1	CDC	Yes
A/HongKong/1/2007 (IBCC-RG)	2.2	CDC/NIH	Yes
A/HongKong/1/2007 (IBCC-RG)	2.2.1.1	CDC	Yes
A/HongKong/1/2007 (IBCC-RG)	2.3.2.1	S/NIH	Yes
A/HongKong/1/2007 (IBCC-RG)	2.2.1	CDC	Yes
A/HongKong/1/2007 (IBCC-RG)	2.3.4	S/NIH	Yes
A/HongKong/1/2007 (IBCC-RG)	2.3.2.1	CDC	Yes
H5N1 reassortants prepared and awaiting regulatory approval			
A/Indonesia/05/2005 (IBCC-RG25A)	7.1	CDC	Pending
A/Ban-Saewon/HK/010-1161/2010	2.3.2	S/NIH	Pending
H5N1 reassortants in development			
A/HongKong/1/2007 (IBCC-RG)	2.3.4.2		
H5N1 vaccine candidates			
A/HongKong/1/2007 (IBCC-RG)	G1-like	NBRG (wild type)	Yes
A/HongKong/1/2007 (IBCC-RG)	W80-like	NBRG (reverse genetic)	Yes
A/HongKong/1/2007 (IBCC-RG)	W80-like	CDC (reverse genetic)	Yes
A/HongKong/1/2007 (IBCC-RG)	G1-like	CDC (reverse genetic)	Yes
H5N1 reassortants in development			
A/HongKong/1/2007 (IBCC-RG)	G1-like	CDC	Pending

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Global Avian Influenza Surveillance at CDC (HPAI and LPAI)

- Diagnostics development and distribution
- Genetic analysis, complete genome sequencing and analysis for genetic markers from recent H5N1 papers
- Antigenic characterization
- Host range, transmissibility and pathogenicity studies
- Candidate vaccine virus development
- Tool development for the international Community
 - Influenza Risk Assessment Tool
 - Clade Designation Tool will be made available to IRD, GISAID and OFFLU
 - H5N1 Mutation Inventory

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Toward More Integrated Influenza Surveillance U.S. 2007 – 2012: Novel Influenza Virus Detection

- Risk assessment conducted for each case, nationally notifiable and reported through IHR channels to WHO

Communication and investigations by state, local, federal human and animal health officials

Ideally, each case investigated to determine if there is human to human transmission (and its extent)

Funding provided to USDA for SIV surveillance in 2008

- Laboratory testing included
 - Viral genome sequencing
 - Serologic studies
 - Other complex lab testing

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Collaboration with Industry and the USDA

Swine Influenza Virus Surveillance Program

- Allows producers to anonymously submit samples for influenza testing
- Allows for sharing of viruses and information between Public Health and Agriculture
- Began July 15, 2010

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CDC – USDA Collaboration

USDA-CDC teleconferences twice per month
> 360 swine influenza samples shared
Historical & contemporary isolates

Next Generation Sequencing (NGS) Platforms

Ion Torrent

Hosted USDA/NVSL laboratory staff member for Ion Torrent training at CDC (05/16-18/2012)

Technical protocols shared between agencies

CDC – DNA sequencing strategy

USDA/NVSL – RNA sequencing strategy

Compared results, merits and pitfalls of each strategy

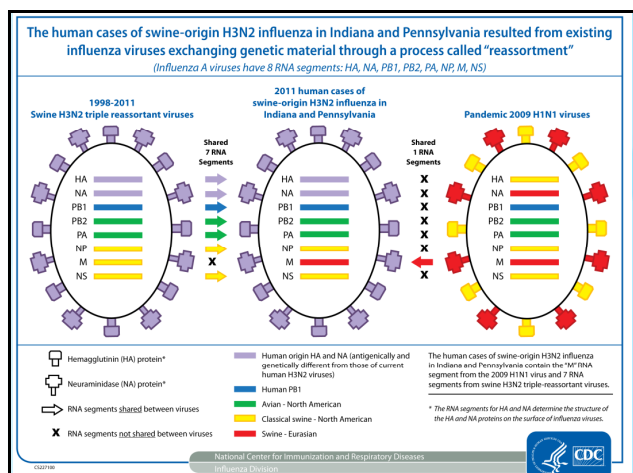
Explored bioinformatic strategies and tools for assembly and analysis of sequence data

Courtesy: C. Smith & J. Palmer

Human A(H3N2) Variant Triple Reassortant Infections



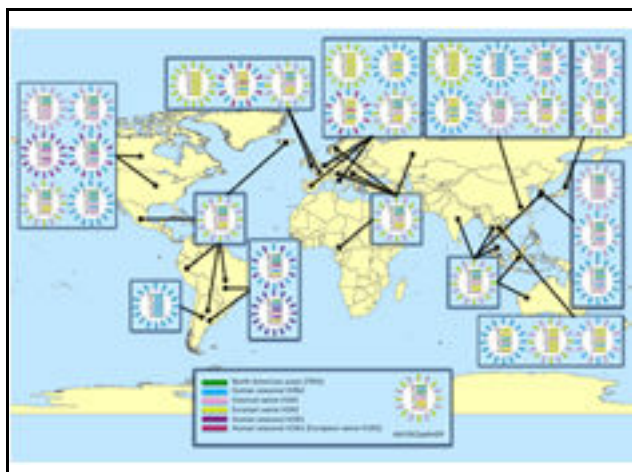
- 17 cases of human infection with swine-origin triple reassortant influenza A (H3N2) 2011-12
- All 17 cases with M gene segment from pH1N1* first detected in swine in 2010
- Most human cases with swine exposures at fairs



Toward Integrated Surveillance in the U.S.: Ongoing Investigation of H3N2(v) in Indiana, 2012

- 7/12 Veterinarian at local fair phoned Indiana Board of Animal Health (BOAH) to report febrile illness in swine. The following day was the final day of the fair and animals were scheduled to be sold (food)
- 7/13 All remaining ~250 pigs at Fair were examined and temperatures recorded; Identified ~40 pigs had temperatures > 104 (not allowed to be sold) and 12 pigs selected randomly for NP swabs
- Indiana Department of Health (DOH) was notified of ill people associated with pigs at the Fair
- 7/13–16 DOH gathered information regarding those exhibiting swine at the Fair and followed up reports of illness among 2 families

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Summary of Findings

- ❑ North American H3N2v viruses pose a risk to humans
- ❑ Younger populations susceptible, particularly young children; young adults have also been infected
- ❑ Limited H-2-H transmission documented (rare)
- ❑ Antigenic distance between HAs of SOIV H3 and seasonal H3 viruses is great
- ❑ Seasonal H3N2 virus not expected to protect against SOIV H3N2 viruses in young populations
- ❑ SOIV H3N2 viruses may pose a risk similar to “Russian Flu” in 1977 for the human population

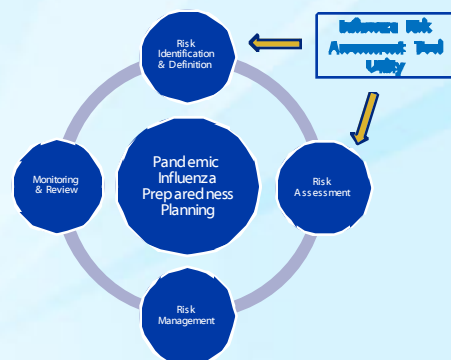
Need for Influenza Risk Assessment Framework

- Choose viruses to prioritize ongoing pandemic preparedness work
- Ongoing work for choosing influenza vaccine candidates for WHO and US global vaccine candidate library
- Nimble risk assessment and risk management for newly emerging threats e.g., H3N2v

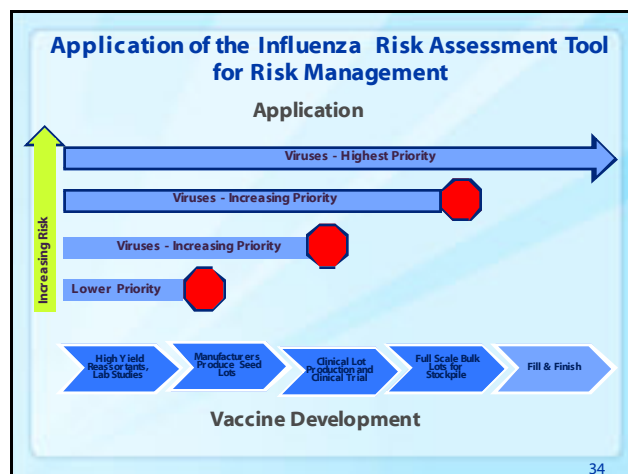
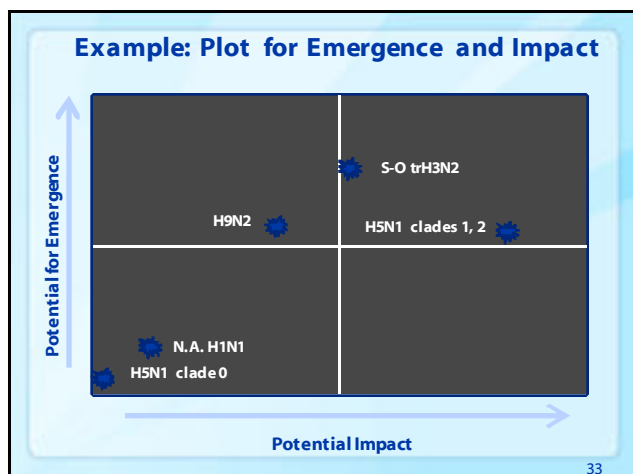


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Importance of Influenza Surveillance in Animals



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Saving Lives. Protecting People.

CDC 24/7

www.cdc.gov
1-800-CDC-INFO

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