Surveillance of swine influenza viruses: Hong Kong

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• 4000–5000 pigs are slaughtered each day.
• Only 5-20% of pigs are from Hong Kong.
• 1998-to date: 252 swabs (tracheal, nasal) and 100 sera collected monthly; increased to to 504 swabs monthly since May 2009.
• 668 viruses isolated: 573 H1, 93 H3, 2 H9 subtype viruses.
• Sequenced HA/NA of all viruses, full genome sequencing of 230 viruses (31.5%)
• MDCK cell culture: higher yield of isolates, especially so for human-like H3N2 viruses.

IDVET- ID Screen® Influenza A Antibody Competition test: Sensitivity (cf HI) - 70%

• Tracheal and nasal swabs gave comparable overall virus isolation rates (1.4%).
  - except with human-like H3N2 viruses where nasal swabs gave 4.8 fold higher isolation rates (0.17% vs. 0.036% respectively; p=0.002).
Viral lineages: 1998-present

Increased diversity and co-circulation of multiple SIV lineages since 2002

(a)
Evidence of inter-continental movement of virus lineages

EA monophyletic
(single introduction into China)

CS & TRIG NOT monophyletic
(multiple introductions into China)
Transient

H1 viral lineages, genotypes and reassortants

Seven gene segments “pandemic-like”. But phylogeny suggests NOT pandemic precursor

Pandemic virus and reassortants repeatedly detected in swine
# Swine viruses: Evidence of antigenic diversity

## Swine influenza A (H1) virus antigenic characterization as measured by hemagglutination inhibition

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Antigenically variant EA viruses: reassortants

Reassortment may play a role in generating SIV antigenic diversity?
Transmission risk to humans

Human infection
Serological and virological

Ex vivo models
Human respiratory tract

Transmission in ferrets
Replication in ex vivo cultures of human respiratory tract

- Classical swine virus
  - A/swine/HK/4167/99 (H1N1)
- Swine virus with 7 gene similar to H1N1pdm
  - A/swine/HK/915/04 (H1N2)
- Swine pandemic H1N1pdm Reassortant
  - A/swine/HK/201/10 (H1N1)
Respiratory transmission of swine influenza viruses in ex vivo human upper airways

Classical swine H1N1
A/Sw/HK/4167/99 (H1N1) Differed by PB2, PB1, PA, NA, M

No

A/Sw/HK/201/10 (H1N1) Differed by HA, M

No

A/Sw/HK/915/04 (H1N2) Differed by NA

Yes

Pandemic H1N1
A/HK/415742/09 A/CA/04/09

No

Seasonal influenza

Yes

M Chan & RWY Chan et al Unpublished
Respiratory transmission of swine influenza viruses in ferrets

- Classical swine H1N1
  - A/Sw/HK/4167/99 (H1N1)
  - Differed by PB2, PB1, PA, NA, M
- Triple reassortant
  - A/Sw/Arkansas/2976/02 (H1N2)
  - Differed by NA, M

- A/Sw/HK/201/10 (H1N1)
  - Differed by HA, M

- A/Sw/HK/915/04 (H1N2)
  - Differed by NA

- Pandemic H1N1
  - A/HK/415742/09
  - A/CA/04/09

- Seasonal influenza
  - A/Sw/HK/915/04 (H1N1)
  - Differed by NA

Yen HL et al Unpublished
Conclusions (1)

• Surveillance for swine influenza viruses in abattoirs is feasible
  – allows long term systematic surveillance to be carried out without causing significant impact on animal husbandry

• The epidemiology and evolution of SIV are strongly shaped by gene flow (among continents and among species) which facilitates reassortment and generation of diverse SIV lineages and occasionally results in substantial antigenic change.

• Need for a step-change in surveillance.
  – Systematic and frequent (to capture dynamics)
  – global (to capture gene flow)
  – whole genomic (to capture reassortment)
Conclusions (2)

Combine surveillance in pigs with assessment of potential of transmission to humans

- **Zoonotic transmission to humans**

- **Ferret transmission**
  - While majority of SIV do not have capacity for aerosol transmission in ferrets, one of them (transient reassortant A/Sw/HK/915/04) appears to have capacity for partial transmission. Investigation of the viral genetic determinants of transmission?

- **Virus tropism in ex vivo cultures of human respiratory tract**
  - Of swine viruses tested, only A/Sw/Hk/915/04 had capacity to infect the human upper respiratory tract.

- **Human sero-epidemiology** (gaps in herd immunity)
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Evolution
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Justin Bahl

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Samir Bhatt

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