Coordinated surveillance of influenza viruses in European pigs: Enhanced Virological and Epidemiological analysis from the European Surveillance Network for Influenza in Pigs (ESNIP3)


SCFCAH, Brussels, 8/11/13

*Coordinator AHVLA-Weybridge, UK
OIE reference laboratory for swine influenza
EURL for Avian Influenza

ESNIP1 1999-2003
Coordinator
Guus Koch, CVI Lelystad, NL

ESNIP2 2005-2008
Coordinator Kristien Van Reeth, Ugent, BE

ESNIP3
Coordinator Ian Brown, AHVLA, UK
2010-2013
ESNIP3 objectives

• Expand knowledge of epidemiology and evolution of SIVs in Europe
  – Surveillance for influenza in pigs; harmonised
  – Contemporary data available at EU level
  – Service to pig industry
• Rapid virus characterisation
  – Harmonised diagnostics; new tools
• Use of new technologies/improvements linking datasets
  – Antigenic characterisation/mapping
  – Genetic characterisation
  – Phylogeography
  – Genotypic data
• Provide timely insights to veterinary public health risk
  – EFSA, ECDC
• EU SI Virus database and repository
• Global dissemination of information/exchange
  – Network interaction
Swine Influenza Viruses (SIV)

Influenza A viral subtypes in circulation in pigs: H1N1, H3N2, H1N2

Strain (origin and nature) different depending on 3 major geographic regions: North America, Europe, Asia

Several genetic lineages among a given subtype

Other subtypes isolated, but swine adaptation not demonstrated: avian H4N6, H3N3, H9N2, H5N1, (H7N7) H3N1, H2N3 > reassortants (sw/sw, sw/av, sw/hu) H1N7 (réass hu/eq), equine H3N8

European enzootic Swine Influenza Viruses (SIVs)

A/Sw/IleVilaine/1455/99
A/Sw/Finistere/2899/82
1979
1984
1973
1984
A/Sw/IleVilaine/1455/99
H1N1
H1N1
A/Port Chalmers/1/73
1973
1984
1983
1994
H3N2
Human-like swine H3N2

Reassortant human-like swine H3N2

European reassortant human-like swine H3N2

Human-like swine H3N2

A/Sw/Gent/1/84
A/Sw/Sw/Scotland/410440/94

Avian-like swine H1N1

A/England/80
A/USSR/90/77
A/Brazil/11/78

A/Port Chalmers/1/73

Simon, 2010
Pandemic virus A/H1N1 2009

North American triple réassortant virus

Swine H1-clade γ

H1N2 (1999)

or

rH1N1 (2007)

Eurasian avian-like swine H1N1 (1979)

Date, host, place?

Prevalence in European pigs?

Swine-Origin A/H1N1 H1N1pdm09

Classical swine H1N1

Human H3N2 (1998)

Avian H9N2 (1998)

Avian H1N1 (1979)

PB2

PB1

PA

HA

NP

M

NS

Slide courtesy of Galle Simon

Brookes et al., 2009, 2010; Lange et al., 2009; Simon, Virologie, 2010
Project consortia

• **25 partners:**
  – Veterinary institutes
    • Belgium, UK, The Netherlands, Italy, France, Germany, Denmark, Poland, Spain, Israel, Hungary, Finland, Greece, USA, China
  – Vaccine manufacturers
    • Merial (France), IDT (Germany) & Hipra (Spain)
Density of pig production in Europe
<table>
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<tr>
<th>Country</th>
<th>Partner</th>
<th>Number of herds investigated</th>
<th>Number of positive cases</th>
<th>Frequency of positive cases (%)</th>
<th>Number of subtyped viruses</th>
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**Total Nov10-Oct13** | **8810** | **2763** | **31,36** | **1671** |
Regional variation in the epidemiology of SI in Europe (ESNIP3)

- **H1avN1** (53%)
- **H3N2** (9%)
- **H1huN2** (16%)
- **rH1huN1 and rH1avN2** (8%)
- **H1N1pdm and reass.** (14%)
New diagnostics PCR harmonisation

• Validated tools for detection of all SIVs

• Specific detection of North American swine H3N2v confirmed

• New methods under evaluation for rapid serotyping
Mapping changes in the virus

- Why do we need to do?
  - Changes in virus spread, infectivity, & pathogenesis
  - Changes in virus host range
  - Veterinary Public Health Implications
  - Diagnostics
  - Intervention through vaccination

- Two approaches
  - Mapping antigenic changes
  - Identifying genetic mutations
  - Linking two datasets
Antigenic mapping

• Understand how the pigs immune response to infection with influenza will reduce infection and spread with other strains

• Probe combinations of virus and different flu antibodies to reveal relationships

• Cartography – visual tool for presenting datasets

• Applied in ESNIP3 for first time to European SIV’s
H1N1
H1N2
pdmH1
A/sw/Italy/71251/2005
A/sw/Scotland/410440/1994
A/sw/England/2008
A/swine/H1/
Genetic mapping/monitoring

• How are viruses mutating
• Determine the genetic code of SIV’s and compare between strains
• Identify trends/patterns
• Identify new virus genotypes from genetic reassortment

• ESNIP3 has contributed c400 new SIV genomes

• Inform veterinary public health risk
17 unique genotypes observed

- Green = Eurasian avian-like
- Red = pandemic
- Purple = Human H1/H3 N1/N2
- Blue = Classical swine
- Grey = Eurasian/Oceanic avian

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Genotype frequency throughout Europe

- EA EA/N2: 7%
- pdm H1/N2: 8%
- Singletons: 8%
- EA H3/N2: 18%
- EA H1/N2: 21%
- EA: 32%
Pandemic genotype observed in 5 European countries
Pandemic segments observed throughout European swine
SIV genotypes in Europe
Implications of genotypic variation

- Continual virus mixing in the pig
- New introductions primarily from humans
- Viruses that are best fitted to replicating and spreading pigs will be ‘selected’
- Contribute to virus change over time
- Importance of ongoing surveillance
- Implications for
  - control
  - economics
  - public health
Conclusions

• Surveillance approaches harmonised
• Four viruses cocirculating
• Significant regional variation
• Diagnostics fit for purpose
• Preliminary antigenic maps for H1 & H3
• Genomic data generated- genotypic evolution including with pdm09

• Data/knowledge exchanged with other networks, official bodies
The future?

- Project completion 31.10.13!
- Publication of work
- Continued engagement with stakeholders

- Future utility

- ESNIP4???
  - Lobbying & consultation

- No immediate prospect for continued funding of the network 😞
  - Horizon 2020??
Acknowledgements

- EU commission
- Competent authorities supporting surveillance programmes
- Industry: producers, PVS’s stakeholder groups etc
- Collaborating partners: WHO, OIE institutes
Thank you for your attention

Questions

Your views & comments welcome

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