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


OFFLU SIV group meeting, Univ Minnesota, Minneapolis
19-20 March 2014

*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 (SIVs)

- 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

European enzootic Swine Influenza Viruses (SIVs)

- European enzootic Swine Influenza Viruses:
  - A/Sw/IleVilaine/1455/99
  - A/Sw/Finistere/2899/82
  - H1N1 1979
  - Avian-like swine H1N1
  - A/England/80 1983
  - Reassortant human-like swine H3N2

- Avian-like swine H1N1
  - A/Sw/Scotland/410440/94
  - Human-like swine H3N2
  - A/Sw/Gent/1/84
  - European reassortant human-like swine H3N2

- Simon, 2010
Pandemic virus A/H1N1 2009

North American triple réassortant virus

SwH1-clade γ

H1N2 (1999)

or

rH1N1 (2007)

Date, host, place ?

Eurasian avian-like swine H1N1 (1979)

Swine-Origin A/H1N1 H1N1pdm09

Prevalence in European pigs ?

Classical swine H1N1

Human H3N2 (1998)

Avian H9N2 (1998)

Avian H1N1 (1979)

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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Regional variation in the epidemiology of SI in Europe (ESNIP3)

H1avN1 (53%)

H3N2 (9%)

H1huN2 (16%)

Enzootic lineages

Epizootic lineages (occasional detections)

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
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

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

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Red = pandemic
Purple = Human H1/H3 N1/N2
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Grey = Eurasian avian
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

• Interest from commercial companies to sponsor an annual meeting

No immediate prospect for continued funding of the network 😞
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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