Transmission dynamics and impact of influenza A virus in pigs

Pia Ryt-Hansen, IVH 29-01-2020 piarh@sund.ku.dk

UNIVERSITY OF COPENHAGEN





Outline

Enzootic infections vs epizootic infections:

- Transmission dynamics
 - Age groups involved
 - Shedding patterns
 - Level of protection obtained by antibodies
 - MDAs
 - Impacts
 - Clinical signs

➤ Study 1 and Study 2

Enzootic infection over one year

- The role of the sows
- Genetic variability
- ➤ Study 3











Study 1 – study design



4 batches of:

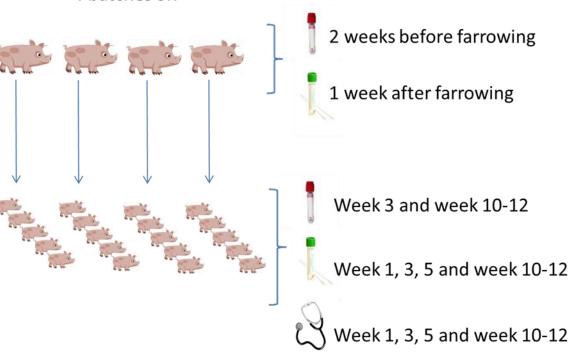
RESEARCH ARTICLE

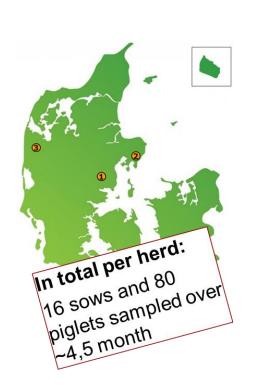
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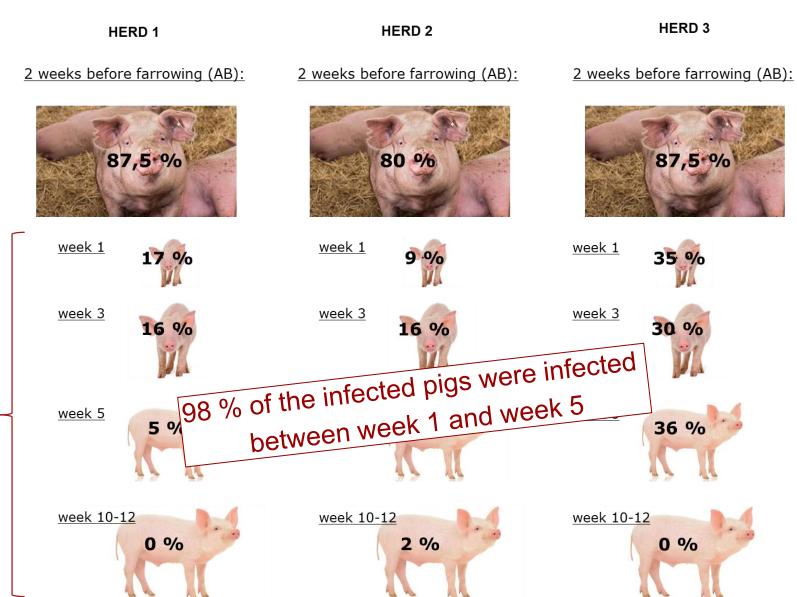
Longitudinal field studies reveal early infection and persistence of influenza A virus in piglets despite the presence of maternally derived antibodies

Pia Ryt-Hansen Open Access (2019) 50:36

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HERD 1

1 week after farrowing (virus)

HERD 2

1 week after farrowing (virus)

HERD 3

1 week after farrowing (virus)











Viral shedding

Consecutive shedding - "Prolonged shedders"

Herd 1: 2 pigs

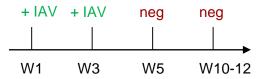
Herd 2: 1 pig

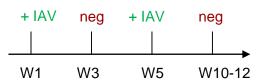
Herd 3: 11 pigs

Non-consecutive shedding – "re-infections"

Herd 1: 1 pig

Herd 3: 13 pigs





Coughing index (CI)

$$CI = \frac{no. of coughs and sneezes}{no. of pigs in the pen x 3 min}$$

• Correlation in Herd 1



Nasal discharge

- Correlation in Herd 2
- · Overall correlation in all tree herds



Study 2 – study design

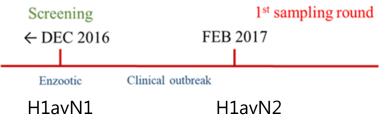
@ PLOS ONE

Acute Influenza A virus outbreak in an enzootic infected sow herd: Impact on viral dynamics, genetic and antigenic variability and effect of maternally derived antibodies and vaccination

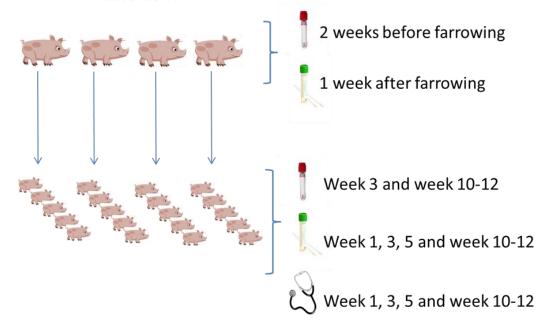


1 National Veterinary Institute, Technical University of Denmark, Kongens Lyngby, Denmark, 2 Department of Health Technology, Section for Bioinformatics, Technical University of Denmark, Kongens Lyngby, Denmark, 3 University of Copenhagen, Dpt. of Veterinary and Animal Sciences, Frederiksberg C, Denmark



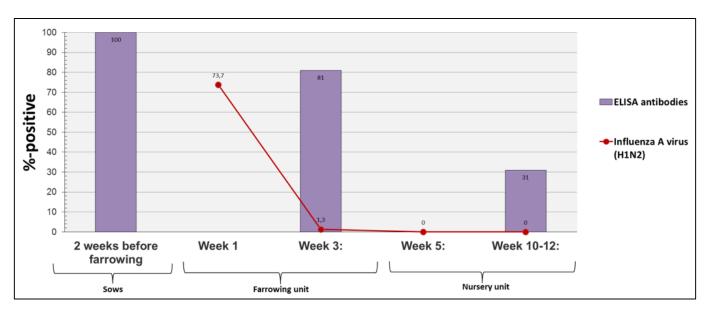


4 batches of:



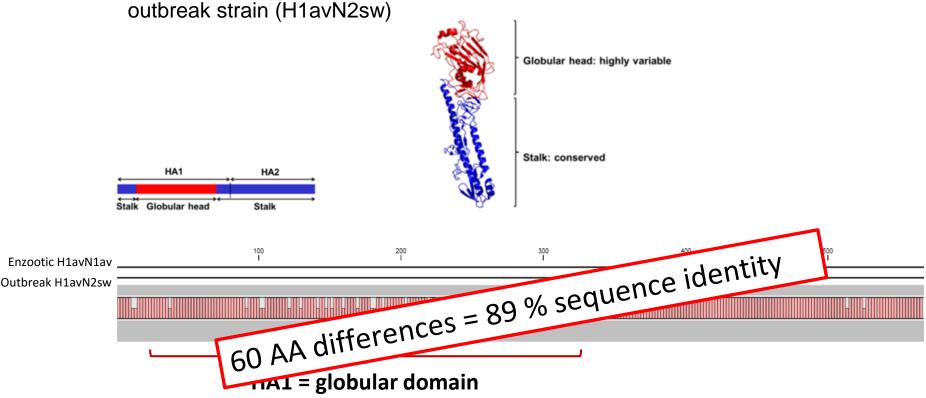
Study 2 – results

1st sampling round - outbreak with H1avN2sw



- HI-test:
 - 100 % of the sows had antibodies towards the old H1avN1
 - 40 % of the sows had antibodies towards the outbreak H1avN2sw
- ➤ Impaired level of cross-reactive antibodies within the same lineage

HA sequence identity between the enzootic strain (H1avN1av) and the



11

Study 3 – study design

Herd 3

- 480 sows
- Weekly batches
- No IAV vaccination
- IAV circulating in the farrowing unit and in the nursery

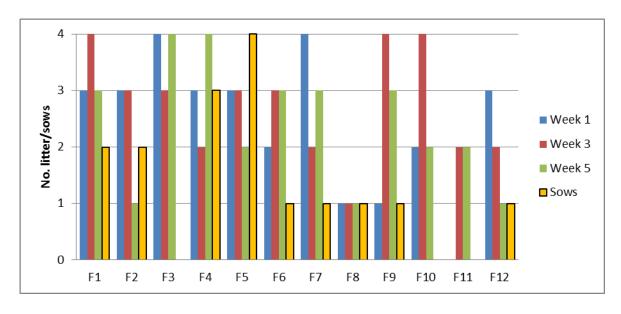
Sampling

- Monthly nasal swabs (cross-sectional)
 - 20 from four one-week-old litters
 - 20 from four three-week-old litters
 - 20 from four pens with five-weeks-old pigs
 - Four from the sows of the one-week-old litters
- Coughing index from all sampled litters and pens





November 2017 - October 2018



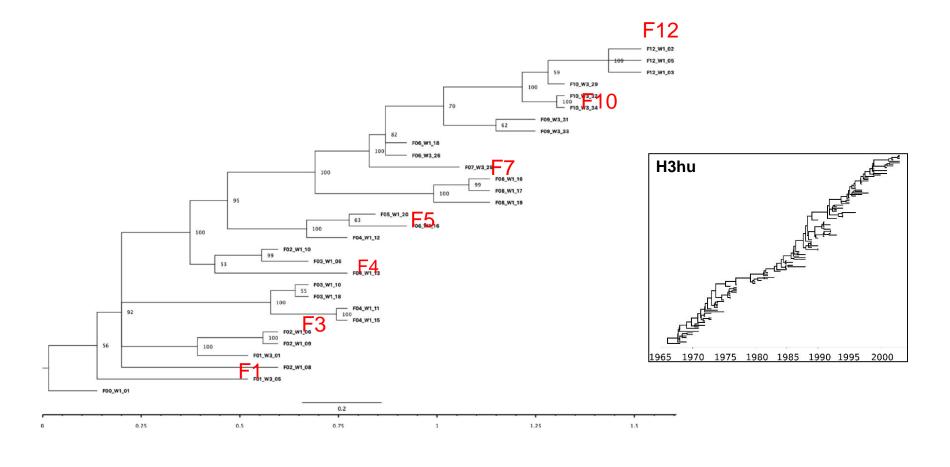
- 60-70 % of all litters/pens positive
- 33 % of sows (88 % also had a positive litter)
 - 1st parity sows

Coughing index:

Significant correlation between positive litter and an increased coughing index



HA sequences (F0-F12):



Discussion and conclusions

Enzootic infected herds:

- IAV infections from day 3
 - MDAs do not protect against virus shedding
- Extended shedding time
- Re-infections
 - MDA wane
 - Genetic drift = antigenic drift (similar to humans)
- Sows/gilts are part of the transmission dynamics
 - Infection piglets ← sows/gilts

Epizootic infected herd:

- Cross protective antibodies cannot be expected within the same subtype
- Early infections

Clinical impact:

Correlated with upper respiratory infections

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Herds

Anonymous

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Thank you for your attention

• Questions?

