



UNIVERSITY OF MINNESOTA

Swine Disease Eradication Center

SDEC Partners Research Update

April 2017
Volume 7, Issue 4

[www.vetmed.umn.edu/
Centers-programs/swine-
program/research](http://www.vetmed.umn.edu/Centers-programs/swine-program/research)

Project Update: Influenza herd-level prevalence and seasonality in sow farms

Investigators: Fabian Chamba, Anna Alba, Pere Puig, Joel Nerem, Bob Morrison, Montse Torremorell

Funded by: Rapid Agricultural Respond Fund (RARF)

Background

- Influenza A virus is a major cause of respiratory disease in pigs. Influenza can increase mortality and feed conversion ratio, and decrease average daily weight gain in finishing pigs. Business continuity can be affected when strains are linked to human health.
- Piglets prior to wean can unnoticeably maintain, diversify and transmit influenza at weaning.
- Sow farms play a critical role on influenza transmission, epidemiology and control.

Objective

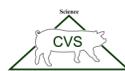
To assess influenza herd-level prevalence and seasonality in piglets in sow farms, investigate the association between influenza herd-level prevalence and air temperature and humidity, and characterize the genetic diversity of influenza viruses over time.

Material and methods

- Oral fluid samples for influenza testing were obtained from piglets prior to weaning in breeding herds.
- Samples were obtained monthly for 5 years approximately.
- Seasonality was evaluated using time series analysis including ARIMA models in which influenza herd-level prevalence was the outcome and sine and cosine functions at different time periods in months were the predictors of seasonality. Within-farm sensitivity was assessed to guarantee a high confidence of the results obtained. Meteorological data was gathered from 14 local stations. Outside air temperature, relative humidity and absolute humidity were aggregated monthly and then lag correlated with influenza herd-level prevalence.
- Hemagglutinin gene sequencing was attempted from viral isolates recovered throughout the study.
- Influenza hemagglutinin gene sequences were annotated and clade classified using H1 and H3 swine influenza reference strains within phylogenetic trees.

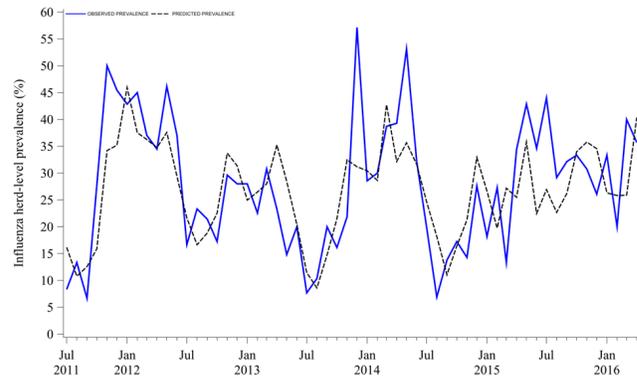
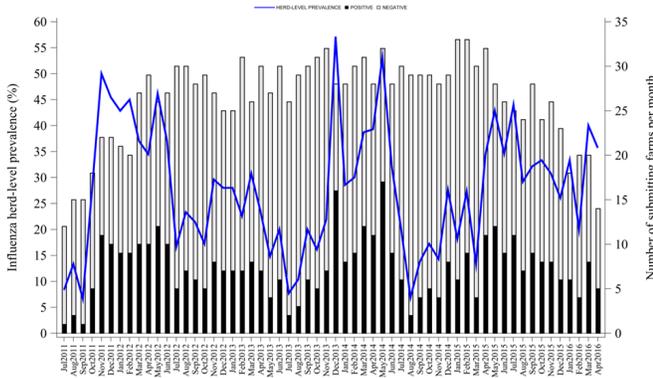


SCHWARTZ
FARMS, INC.

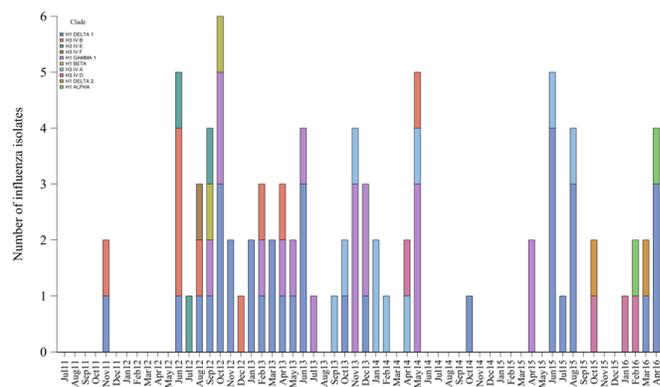
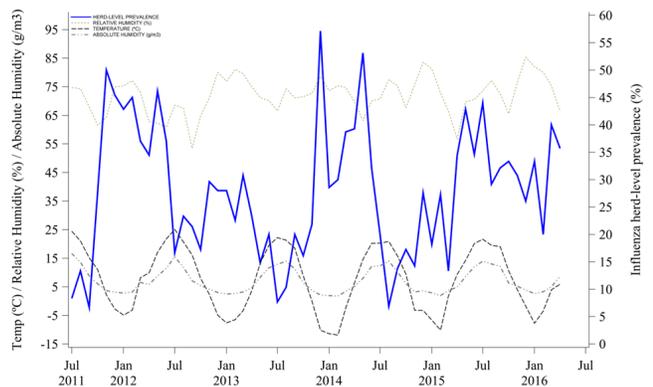


Results:

- There were 6,585 oral fluid samples (1,523 submissions) from 34 sow farms sampled from July 2011 to April 2016.
- Median influenza herd-level prevalence was 28% and influenza herd-level prevalence had a seasonal pattern as shown below.



- Mean outdoor air absolute humidity and temperature observed at 0, 1 or 2 months before a given month were correlated with influenza herd-level prevalence ($p = 0.01$ to 0.001). Relative humidity was not correlated with influenza herd-level prevalence.
- There were 85 influenza isolates that grouped in 10 genetically distinct H1 and H3 clades and clusters of contemporary US swine influenza viruses as shown below. Most common isolates were H1 delta 1 (40%), H1 gamma 1 (21%), H3 IV A (12%) and H3 IV B (11%). Also, 21% of farms had 3 genetically distinct viruses circulating over time; 18% had 2 and 41% had 1.



Conclusions and Implications:

- Influenza herd-level prevalence in sow farms had a seasonal pattern with higher levels in winter (Dec) and spring (May), and lower levels in summer. This is important to better allocate influenza control strategies in sow farms.
- Influenza seasonality was partially explained by air absolute humidity and temperature although other factors may play a role in the observed seasonality.
- Co-circulation of genetically distinct viruses between and within farms was common.