

# The Evolution of Pandemic Influenza Virus Threats in Swine

Martha Nelson<sup>1\*</sup>

<sup>1</sup>. National Institutes of Health

## Background/Objective

Swine are important zoonotic hosts for the evolution of pandemic influenza A viruses. However, there are major gaps in surveillance of influenza in pigs globally. As a result, the origins of the 2009 H1N1 pandemic influenza virus in swine, prior to emergence in humans, remain unknown. To further understand the diversity and evolution of influenza viruses in swine globally we sequenced the entire genome of 247 influenza viruses collected in swine in Canada, Mexico, and the United States.

## Method

We employed Bayesian methods of phylogeography, including the newly developed GLM model, to determine how influenza viruses migrate spatially in swine, using genetic sequence data collected from swine globally and empirical data on live swine trade between nations. We also included background sequence data from influenza viruses collected from humans to better understand the frequency of viral transmission between humans and swine.

## Result

Our analysis demonstrated that the live swine trade is a strong predictor of how influenza viruses disseminate globally in swine. As a result of the large numbers of swine imported from Europe and North America to Asia, extensive viral diversity circulates in Asian swine. However, China is not a major exporter of live swine and consequently is not an important source of influenza virus diversity in swine in other Asian countries.

## Conclusion

Our study provides a model for predicting influenza virus diversity in swine globally, including in the many countries where little viral genetic data is available from swine due to gaps in surveillance. However, our study also raises critical questions about the origins of the 2009 H1N1 pandemic virus, and how a virus that is most likely to have emerged in the Eastern hemisphere sparked the first outbreak in humans in Mexico.