

Sponsors

We thank the following sponsors:

Platinum

Bayer Animal Health
National Pork Board
Pfizer Animal Health

Silver

Boehringer Ingelheim Vetmedica, Inc.

Bronze

Cargill
Merck Animal Health
Novartis Animal Health

Copper

AgStar Financial Services
Elanco Animal Health
IDEXX
Newport Laboratories
PIC USA
PRRS CAP

University of Minnesota Institutional Partners

College of Veterinary Medicine
University of Minnesota Extension
College of Food, Agriculture and Natural Resources Sciences

Formatting

Tina Smith Graphics
www.tinasmithgraphics.com

CD-ROM

David Brown
www.davidbrown.us

Logo Design

Ruth Cronje, and Jan Swanson;
based on the original design by Dr. Robert Dunlop

The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, or sexual orientation.

Spatial dynamics of human-origin H1 Influenza A virus in North American swine

Martha I. Nelson^{1*}; Philippe Lemey²; Yi Tan¹; Amy Vincent³; Tommy Tsan-Yuk Lam⁴; Susan Detmer⁵; Cécile Viboud¹; Marc A. Suchard⁶; Andrew Rambaut^{1,7}; Edward C. Holmes^{1,4}; Marie Gramer⁵

¹Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, Bethesda, Maryland; ²Department of Microbiology and Immunology, Katholieke Universiteit Leuven, Leuven, Belgium; ³Virus and Prion Diseases of Livestock Research Unit, National Animal Disease Center, USDA-ARS, Ames, Iowa; ⁴Department of Biology, The Pennsylvania State University, University Park, Pennsylvania; ⁵The University of Minnesota Veterinary Diagnostic Laboratory, St. Paul, Minnesota; ⁶Departments of Biomathematics and Human Genetics, David Geffen School of Medicine at UCLA, and Department of Biostatistics, UCLA School of Public Health, Los Angeles, California; ⁷Institute of Evolutionary Biology, University of Edinburgh, Ashworth Laboratories, Edinburgh, United Kingdom

Abstract

The emergence and rapid global spread of the swine-origin H1N1/09 pandemic influenza A virus in humans underscores the importance of swine populations as reservoirs for genetically diverse influenza viruses with the potential to infect humans. However, despite their significance for animal and human health, relatively little is known about the phylogeography of swine influenza viruses in the United States. This study utilizes an expansive data set of hemagglutinin (HA1) sequences (n = 1516) from swine influenza viruses collected in North America during the period 2003-2010. With these data we investigate the spatial dissemination of a novel influenza virus of the H1 subtype that was introduced into the North American swine population via two separate human-to-swine transmission events around 2003. Bayesian phylogeographic analysis reveals that the spatial dissemination of this influenza virus in the US swine population follows long-distance swine movements from the Southern US to the Midwest, a corn-rich commercial center that imports millions of swine annually. Hence, multiple genetically

diverse influenza viruses are introduced and co-circulate in the Midwest, providing the opportunity for genomic reassortment. Overall, the Midwest serves primarily as an ecological sink for swine influenza in the US, with sources of virus genetic diversity instead located in the Southeast (mainly North Carolina) and South-central (mainly Oklahoma) regions. Understanding the importance of long-distance pig transportation in the evolution and spatial dissemination of the influenza virus in swine may inform future strategies for the surveillance and control of influenza, and perhaps other swine pathogens.

***Corresponding author:** Division of International Epidemiology and Population Studies, Fogarty International Center, National Institutes of Health, 16 Center Drive, Building 16, Room 202, Bethesda, Maryland 20892 USA. Tel: 1-301-402 5203; Fax: 1-301-496-8496; E-mail: nelsonma@mail.nih.gov.



Martha I. Nelson; Philippe Lemey; Yi Tan; et al.