

# Influenza in animals

Carlton L. Gyles

*Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada*

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Records of human disease attributed to influenza viruses date back to 412 BC and include several pandemics in the 1700s. However, the pandemic caused by the ‘Spanish flu’ of 1918, with an estimated death toll ranging from 20 to 100 million, was the most devastating. The characterization of the reconstructed H1N1 1918 pandemic virus has allowed for comparisons with contemporary human H1N1 viruses and for the identification of features of the 1918 virus that made it so virulent (Tumpey *et al.*, 2005). The contribution of genetics to our understanding of the factors that determine virulence is enormous. However, as noted in the papers in this collection, there is still much that is not understood about several aspects of influenza viruses, their evolution, interactions with their hosts and their transmissibility.

The series of seven papers on influenza in this issue of Animal Health Research Reviews is timely, given the recent concerns about the pandemic H1N1 influenza and the critical role of animals in disease in both animals and humans. Three colleagues, Paul Gibbs from the College of Veterinary Medicine, University of Florida and Mo Saif and Chang-Won Lee from the Ohio Agricultural Research and Development Center, The Ohio State University, organized this virtual symposium on influenza in animals. They determined the topics that were appropriate, identified authors and obtained their commitment, did some writing themselves and reviewed the manuscripts. They invested considerable time and thought in this project and their leadership is the reason readers have this series of in-depth and comprehensive articles on influenza in animals. We are deeply indebted to them.

The authors are international experts in their fields and we are extremely grateful to them for taking the time required to write thorough, thoughtful and critical reviews on influenza in animals. Forrest and Webster start off with an exceptional paper that focuses on the evolution of the high pathogenicity (HP) H5N1 and pandemic H1N1 influenza viruses. They discuss important gaps in knowledge and research in areas such as molecular determinants of pathogenicity and transmissibility, host

susceptibility and vaccination. They highlight the significance of surveillance in wild and domesticated animal populations. They point to recent developments in genomics and hold out hope that the gaps they identify are amenable to resolution.

David Suarez presents an authoritative account of several aspects of avian influenza (AI). He presents a clear discussion of the adaptation of AI viruses to various avian hosts and methods of measuring the extent of adaptation. He identifies the changes that suggest adaptation to gallinaceous birds and shows how control becomes more difficult following adaptation and endemicity in poultry populations. Dr Suarez devotes much attention to the Asian lineage H5N1 HPAI virus that first appeared in China in 1996 and comments on the spread of this virus and the extensive variation that has since occurred in this lineage. Samantha Gibbs continues the avian theme, emphasizing the significance of avian physiology, behavior and migration on interactions with AI viruses. She provides examples of the impact of human behavior on the transmission of AI viruses and discusses surveillance for AI in wild birds.

Paul Gibbs and Tara Anderson then review equine and canine influenza. These authors note the promiscuity and plasticity of influenza viruses and warn that interspecies transmission may occur more frequently than previously recognized. They discuss the susceptibility of humans, dogs and pigs to the equine H3N8 influenza virus which has been circulating in horses for almost 50 years. Nonetheless, they differentiate a group of canine H3N8 influenza viruses which has diverged from its equine ancestors. The authors also discuss the occurrence of avian H3N2 and HP H5N1 and pandemic H1N1 viruses in dogs.

Yassine and co-workers extend the theme of inter- and intra-species transmission of influenza viruses. These researchers highlight the role of the transmission of viruses between wild and domestic birds and the significance of the high susceptibility of turkeys to avian and swine influenza viruses. The authors also discuss the transmission of recent influenza viruses (notably HPAI H5N1 and pandemic H1N1) in human populations. The role of other mammals including swine in the creation of

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E-mail: [cgyles@ovc.uoguelph.ca](mailto:cgyles@ovc.uoguelph.ca)

reassortants of influenza viruses is also discussed. Finally, the authors discuss data on viral and host factors that affect the transmission of influenza viruses.

Daniel Janies and colleagues write about the excitement of a new era in data sharing and in integration of genomic, geographic and phenotypic data on influenza so as to facilitate public health policy and decision-making. They describe the analytical tools they have developed, which involve the mapping of pathogen lineages and markers into geographic information systems, enabling scientists to track viral mutations that are important in virulence and drug resistance, for example. They make it clear that bioinformatics has a critical role to play in the rapid and effective conversion of sequence and other data into information that can be used by public health scientists.

The series of papers ends, appropriately, with a presentation on swine influenza vaccines. Following an introduction to swine influenza viruses and immunity to infection of swine with influenza virus, Ma and Richt launch a detailed analysis of swine influenza vaccines. It is a rich discussion of currently available vaccines and a wide range of vaccines that are currently under

investigation. The chapter provides a good description of the present and a glimpse into the fascinating possibilities for the future.

Although each paper addresses specific aspects of influenza in animals, certain themes recur with great frequency. These themes include the enormous contribution of the analysis of sequence data for understanding influenza viruses, the need for continued and enhanced surveillance in animal populations, gaps in our understanding of interactions between influenza viruses and their hosts and the critical need for vaccines that are predictably effective against the target influenza virus(es). There has been considerable investment in influenza research and the expectation is that breakthrough discoveries will continue to be made.

## Reference

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