Modeling the evolution of virulence and host-range switching in influenza A virus

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Earl G. Brown is a Professor, in the Department of Biochemistry, Microbiology and Immunology, Faculty of Medicine, University of Ottawa as well as the executive director of the Emerging Pathogens Research Centre of the University of Ottawa. He obtained a Bachelor's degree in Microbiology for the University of Guelph in 1974 and has since specialized in virology obtaining a Ph.D., studying vesicular stomatitis virus, from McMaster University in 1981 and subsequent postdoctoral training in reovirus genetics in Dr. B.N. Fields laboratory, Harvard Medical School. Dr Brown then took a Research Scientist, position in the Influenza Section, Laboratory Centre for Disease Control, Health Canada fro 6 yr, before moving to the University of Ottawa in 1989 where he pursues genetic studies of RNA viruses with a focus on evolution of virulence in influenza virus, reovirus replication and oncolysis, and hepatitis C immune evasion. The work focuses on understand viral replication so that virus infection can both be prevented and alternatively be applied as therapy to treat diseases. As a recognized influenza researcher in Canada he sits on various committees and institutions (CIHR workshop on influenza research priorities 2005; CIHR Pandemic Preparedness Strategic Research Initiative Task group; Organizing and program committee Chair of the 2008 of Canadian Pandemic Preparedness Meeting ; Pandemic Vaccine Working Group of the Public Health Agency of Canada) dealing with influenza pandemic preparedness. Dr Brown is also an active spokesman on virology and infectious diseases with national and international broadcasting and print media.

Abstract
Given the current concerns that the pathogenic avian H5N1 virus in Eurasia will become a human pathogen and the recent transmission of swine H1N1 to humans, there is a need to expand our understanding of the genetic basis and control of host range and virulence in influenza viruses. Although mammalian influenza A virus are of avian origin the genetic changes that are required to switch from being an avian to a mammalian pathogen are only beginning to be identified and are largely incomplete. Using the mouse model I will present data on the nature of genomic evolution of human prototype influenza on becoming a mouse pathogen with high virulence. The data will largely focus on the evolution of the properties of the hemagglutinin receptor and the interferon antagonist NS1. Many mutations selected in mouse virulent variants are also independently selected on natural adaptation of avian influenza including highly pathogenic H5N1 Z genotype in animals demonstrating the utility of models of experimental evolution in predicting and understanding events in nature.