



Establishment of Multiple Sub-lineages of H5N1 Influenza Virus in Asia - Implications for Pandemic Control

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Dr Guan has studied medicine at Jiangxi Medical College and Beijing Union Medical University. He obtained his medical bachelor and master degrees in 1983 and 1989 respectively. Then he changed his field to study virology at The University of Hong Kong and St Jude Children's Research Hospital in Memphis, Tennessee. He obtained his PhD in 1997, and joined the Department of Microbiology in 2000. His current position is Associate Professor.

He mainly focuses on studying influenza ecology, trying to understand the evolution of avian, swine, and also human-animal inter-phase influenza viruses from southern China region. Since early 2003, he started working on SARS-CoV. In addition, he has pursued an aggressive research programme that involves collaboration with both local and international partners including the Chinese Government and the WHO. For example, he initiated the application for the first state key laboratory outside the Mainland (State Key Laboratory for Emerging Infectious Diseases at HKU) and has been the director of State Key Laboratory since its establishment on October 4, 2005. He was appointed as a member of the WHO Animal Influenza Network in May 2000.

Preparedness for a looming influenza pandemic caused by highly pathogenic avian influenza (HPAI) A subtype H5N1 has become a global priority. H5N1 disease outbreaks in migratory waterfowl in western China, the continuing geographic spread of the virus in Eurasia, and the emergence of human infection in Indonesia have heightened pandemic concern. It remains unknown from where the pandemic strain may emerge; current attention is directed at Vietnam, Thailand, Cambodia, and more recently, Indonesia. Here we report that genetically and antigenically distinct sub-lineages of H5N1 virus have become established in poultry in different geographical regions of Southeast Asia, indicating the long-term endemicity of the virus. Our data show that H5N1 influenza virus has continued to spread from its established source in southern China to other regions through transport of poultry and bird migration. The identification of regionally distinct sub-lineages contributes to the understanding of the mechanism for the perpetuation and spread of H5N1 providing information that is directly relevant to control of the source of infection in poultry. It points to the necessity of surveillance that is geographically broader than previously supposed and that includes H5N1 viruses of greater genetic and antigenic diversity.