



Title	Genetic characterisation of H5N1 viruses isolated from different regions of southern China.
Author(s)	Guan, Y
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Genetic characterisation of H5N1 viruses isolated from different regions of southern China

Key Messages

1. H5N1 viruses in different types of poultry in southern China and Southeast Asia have spread throughout South East Asia, Europe and Africa.
2. Multiple sublineages of H5N1 viruses were established in different regions. These sublineages were genetically and antigenically distinct, for which reason and based on our study, the World Health Organization selected different pandemic vaccine candidates.
3. Based on the recognition of multiple regional sublineages, a prediction of H5N1 spread to Europe was proposed.
4. Phylogenetic analysis revealed that Gs/Gd-like H5N1 was most likely derived from a low pathogenic H5 virus strain from migratory birds.
5. Some H5N1 novel reassortants contain internal genes that are only closely related to viruses isolated during 1970s, which suggests an unnatural evolutionary pathway.

Introduction

Preparing for a possible pandemic caused by highly pathogenic avian influenza A subtype H5N1 has been a global priority. The spread of the virus throughout Eurasia and Africa highlights the need for continued surveillance of influenza A virus in wild bird populations and poultry markets.

From July 2004 to June 2006, surveillance of poultry was carried out in live poultry markets in six provinces of southern China. From July 2005 to June 2006, of 53 220 poultry specimens, 2.4% were H5N1 positive (chickens, 0.5%; ducks, 3.3%; geese, 3.5%). This prevalence was higher than that determined from July 2004 to June 2005 (overall, 0.9%; chickens, 0.2%; ducks, 1.3%; geese, 2.0%). A winter-seasonal peak was observed throughout the surveillance period.¹

Phylogenetic analysis of H5N1 viruses isolated from migratory birds showed that this virus is vectored by migratory birds. Identification of the first outbreak of H5N1 virus in migratory waterfowl from Qinghai lake and identification of regionally distinct sublineages showed that this virus had spread from its established source in southern China to other regions through poultry transport and bird migration (data not shown).^{2,3}

Through the characterisation of low-pathogenic avian influenza H5 subtype viruses isolated from poultry and migratory birds in southern China and Europe from 1970s to 2000s, the dynamic nature of the influenza gene pool was revealed. Phylogenetic analysis revealed that Gs/Gd-like virus was probably derived from a low-pathogenic H5 virus in migratory birds. Phylogenetic analysis revealed frequent transmission between the eastern and western ends of the Eurasian continent that contributed to the spread of highly pathogenic H5N1 influenza A viruses (data not shown).⁴

Discussion

Long-term influenza surveillance in southern China enabled understanding of the genesis and transmission of this highly pathogenic H5N1 virus, and provided information for the World Health Organization to improve global pandemic preparedness plan. This may help avert avian-to-human transmission, and thereby reduce the chance of viral establishment in humans and human-to-human transmission. The importance of animal and human influenza surveillance operations in affected regions deserves highlighting.

Acknowledgment

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State Key Laboratory of Emerging Infectious Diseases, Department of Microbiology, The University of Hong Kong

Y Guan

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Principal applicant and corresponding author:
Prof Yi Guan

State Key Laboratory of Emerging Infectious Diseases, Department of Microbiology, The University of Hong Kong, Faculty of Medicine Building, 21 Sassoon Road, Pokfulam, Hong Kong SAR, China

Tel: (852) 2819 9829

Fax: (852) 2817 1958

Email: yguan@hkucc.hku.hk

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