A family cluster of three confirmed cases infected with avian influenza A (H7N9) virus in Zhejiang Province of China

Hua Ding, Yin Chen, Zhao Yu, Peter W Horby, Fenjuan Wang, Jingfeng Hu, Xuhui Yang, Haiyan Mao, Shuwen Qin, Shelan Liu, Enfu Chen, Hongjie Yu

Hangzhou Centre for Disease Control and Prevention, Hangzhou, Zhejiang Province, China
Zhejiang Provincial Centre for Disease Control and Prevention, Hangzhou, Zhejiang Province, China
Oxford University Clinical Research Unit - Wellcome Trust Major Overseas Programme, Chi Minh, Vietnam
Centre for Tropical Medicine, Nuffield Department of Clinical Medicine, Oxford University, Oxford, United Kingdom
Singapore Infectious Disease Initiative, Singapore, Singapore
XiaoShan District Centre for Disease Control and Prevention, Hangzhou, Zhejiang Province, China
ShangCheng District Centre for Disease Control and Prevention, Hangzhou, Zhejiang Province, China
Division of Infectious Disease, Key Laboratory of Surveillance and Early warning on Infectious Disease, Chinese Center for Disease Control and Prevention, No. 155 Changbai Road, Changping District, Beijing, China
Department of Infectious Diseases, Zhejiang Provincial Center for Disease Control and Prevention, 3399 Binsheng Road, Binjiang District, Hangzhou, Zhejiang 310051, China
Email: dh.dhua999@163.com

Abstract

A total of 453 laboratory-confirmed cases of human infected with avian influenza A (H7N9) virus (including 175 deaths) have been reported by WHO till October 2,2014, of which 30.68% (139/453) of the cases were identified from Zhejiang Province. We describe the largest reported cluster of virologically confirmed H7N9 cases, comprised by a fatal Index case and two mild secondary cases. A retrospective epidemiological investigation was conducted in January of 2014. Three confirmed cases, their close contacts, and relevant environments samples were tested by realtime reverse transcriptase-polymerase chain reaction (RT-PCR), viral culture, and sequencing. Serum samples from contacts and cases were tested by haemagglutination inhibition (HI) assay. The cluster was comprised of the Index case, a 49-year-old farmer with type II diabetes, who lived with his daughter (Case 2, aged 24) and wife (Case 3, aged 43) and his son-in-law (H7N9 negative). The Index case and Case 3 worked daily in a live bird market. Onset of illness in Index case occurred in January 13, 2014 and subsequently, he died of multi-organ failure on January 20. Case 2 presented with mild symptoms on January 20 following frequent unprotected bed-side care of the Index case between January 14 to 19, and exposed to live bird market on January 17. Case 3 became unwell on January 23 after providing bedside care to the Index case on January 17 to 18, and following the contact with Case 2 during January 21 to 22 at the funeral of the Index case. The two secondary cases were discharged on February 2 and 5 separately after early treatment with antiviral medication. Four virus strains were isolated and genome analyses showed 99.6 ~ 100% genetic homology, with two amino mutations (V192I in NS and V280A in NP). 42% (11/26) of environmental samples collected in January were H7N9 positive. Twenty-five close contacts remained well and were negative for H7N9 infection by RT-PCR and HI assay. In the present study, we reported that the Index case was infected from a live bird market while the two secondary cases were infected by the Index case during unprotected exposure. This family cluster is, therefore, compatible with non-sustained person-to-person transmission of avian influenza A/H7N9.

Keywords: H7N9 subtype, Family cluster, Live bird market, Death, Epidemiological investigation