

Unique epidemiological patterns of human infections with H7N9 avian influenza virus discovered by combined risk factor surveillance and epidemiology

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Abstract

Background: An outbreak of a novel human avian influenza (H7N9) [h-H7N9 AI] took place in China from February 2013 to April 2015, with 628 reported cases. However, there were no exact answers on epidemiological patterns and its origin. **Purpose:** To examine the epidemiological patterns and its origin compared with other influenza outbreaks by combined analysis of risk factor surveillance and epidemiological characteristics, and to explore new surveillance methods for tracking infectious disease outbreaks.

Study/Intervention Design: An analysis of combined epidemiological and risk factor surveillance data.

Methods: Subjects were the 628 confirmed H7N9 cases from February 2013 to April 2015. Data were collected from the World Health Organization (WHO), the Chinese Center for Disease Control (CDC), and other sources. Descriptive epidemiological methods were used in the analysis. The incidence distribution and exposure rates of risk factors were examined. Differences across age groups were tested by Fisher's exact and/or chi-square tests. Correlation was estimated by Spearman rank correlation. **Results:** The distribution and exposure rates of risk factors in time, space and population showed vast differences between human H7N9 and H5N1 infections. First, compared with 18 H5N1 cases reported within 7 months in Hong Kong in 1997, there were 628 H7N9 cases reported over more than 2 years in China. Second, while H5N1 cases were localized in Hong Kong, H7N9 cases in China covered many provinces. Moreover, while human H7N9 cases were reported in China, there were no cases of human H7N9 cases reported in countries with extensive H7N9 outbreaks in birds, such as Korea and Mongolia. Our study found that the infectious source of H7N9 was live poultry in the markets, not wild birds. The mean age of H7N9 cases was 60 years which is much older than those of other pathogenic influenza cases. It appears that the seniors in China have no specific immunity to the virus, which indicates that human avian influenza (H7N9) virus is a

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new virus in both birds and humans in China. **Conclusion:** Unique patterns in infection pathways and distributions of risk factors suggest that human H7N9 avian influenza might have complex infectious sources. This finding is very important for identifying the origin. We suggest that combined analysis of epidemiological and risk factor surveillance data can be a new surveillance tool to identify the origin of infectious outbreaks.