

Evidence of host adaptation of avian-origin influenza A virus

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The connection between human avian-origin influenza A (H7N9) virus infection and environmental sources of the virus were determined based on clinical data, epidemiology, and virological characteristics of the three early H7N9-infected cases in Hangzhou, Zhejiang Province, China. These H7N9 influenza virus sequences show genomic sequence diversity and key amino acid substitutions, including the novel mammalian-signature substitution Q226I, which is related to human adaptation. This study will be published on *Science China Life Sciences* 2013, No.6.

A novel avian-origin reassortant influenza A (H7N9) virus emerged in China in February 2013, and is associated with severe [lower respiratory tract](#) diseases. To date, more than 100 human cases of infection, including at least 20 deaths, have been reported in China. Three early cases of infection were described in Hangzhou, Zhejiang Province, China. The general clinical features of the three patients were similar to the previously reported cases in China. Two of the three patients had a history of direct contact with live poultry markets. Interestingly, poultry cage swabs and feces from the free market visited by Patient 2 one week prior to the onset of symptoms were positive for the novel avian influenza A (H7N9) virus. This indicates a direct connection between human infection with the novel H7N9 virus and an environmental source.

Researchers analyzed the [DNA sequences](#) from the Hangzhou viruses and other human H7N9 [viral sequences](#) available from the databases, together with those from other H7 [influenza viruses](#). This showed that the virus sequenced from Patient 2 was most closely related to the virus derived from the environmental source associated with Patient 2, while Hangzhou/1 and Hangzhou/3 were more divergent. These data suggest that several H7N9 viruses are circulating in Hangzhou. It is uncertain whether the diversity of H7N9 in Hangzhou is the

result of host adaptation, or predates the transmission to humans from an avian source.

The pathogenesis of the novel avian-origin H7N9 virus in humans remains unknown, although a series of substitutions that have been confirmed as pathogenicity factors in animal models were found in viruses from Hangzhou. A glutamine to isoleucine substitution was observed at position 226 of the hemagglutinin amino acid sequence in the newly sequenced virus. Isoleucine has similar characteristics to leucine, which was previously shown to be a pivotal amino acid in the binding of avian- or human-type receptor, and might be essential for pathogenicity in cases of airborne viral transmission. This substitution was observed for the first time at this site in H7N9, which may indicate a novel host adaptation feature of the H7 virus.

Findings from the current study implied a rapid evolution of the novel H7N9 virus. This may assist in determining the source and mode of transmission of these infections, and provide a reference for selecting candidate vaccine strains. The receptor binding properties of Q226I and the significance of the substitutions in H7N9 need further exploration, including both in vitro and in vivo experiments, and extensive field surveillance.

More information: Li J, Yu X F, Pu X Y, et al. Environmental connections of novel avian-origin H7N9 influenza virus infection and virus adaptation to the human. *Sci China Life Sci*, 2013, 56(6), 485-492. [doi: 10.1007/s11427-013-4491-3](https://doi.org/10.1007/s11427-013-4491-3)

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