

## What does H7N9 mean and how can we be prepared for the next flu pandemic?

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Received June 12, 2013; accepted July 2, 2013; published online July 19, 2013

**Citation:** Xu J, Yu X Z, Walline J. What does H7N9 mean and how can we be prepared for the next flu pandemic? *Sci China Life Sci*, 2013, 56: 1057–1058, doi: 10.1007/s11427-013-4528-7

In early 2013, the novel H7N9 influenza virus was identified as a human-infecting virus in China. The virus causes pneumonia, respiratory failure, acute respiratory distress syndrome, multi-organ failure and death [1]. As of 27 May 2013, 130 known cases of H7N9 infection were confirmed for mainland China. Of these cases, 36 resulted in death, while 57 patients have recovered according to the Chinese National Health and Family Planning Commission. At the commencement of the H7N9 outbreak, health care providers worldwide, especially those in front-line clinical areas such as emergency rooms and outpatient clinics, began to prepare to cope with a potential flu pandemic. All cases of infection to date have been sporadic, without evidence of human-to-human transmission. Chinese provincial governments terminated their emergency response to H7N9 on 30 May 2013 after no new human infection was reported for 21 consecutive days. However, the H7N9 bird flu is still of global concern from a public health standpoint, as the resulting mortality of H7N9 infection [2] is very high.

The H7N9 virus is a serotype of influenza virus A, also known as an avian influenza serotype or, more colloquially as a “bird flu” virus. Hemagglutinin (HA) and neuraminidase (NA) are two large glycoproteins on the outside of the viral particles which aid in classifying influenza A into subtypes based on antibody responses to HA and NA. HA is a lectin that mediates binding of the virus to target cells, and serves as an entry point for the viral genome into the target

cell. NA is involved in the release of progeny virus from infected cells by cleaving sugars that bind to the mature viral particles. Different types of HA and NA help in differentiating between serotypes such as H5N1 and H7N9. There are 16 HA and 9 NA subtypes that are known to exist; however, H1–H3 and N1–2 are commonly found in humans. Because of the high mutation rate of the virus, H5, N7, and N9 have also been observed in humans.

What will be the next novel serotype to infect humans? This is hard to predict because of the high mutation rates and variations in influenza viruses. Because of these factors, it is also very difficult to prevent novel influenza subserotypes from spreading. Human beings are susceptible to influenza viruses, and there are no known effective methods to predict which strain of virus will be the next serotype to cause a pandemic. It is known that some serotypes of influenza virus, such as H7N9, H5N1 and H1N1 are fatal. There is no single vaccine that covers all known and unknown strains. It usually takes about six months to produce and distribute a vaccine against a new strain of influenza. All of these contributing factors make humans particularly susceptible to infection by novel influenza viruses.

Although the H7N9 emergency response system was terminated at the end of May 2013, H7N9 could cause more problems in the future. Because of the high mutation rate of the virus, we should not only focus on researching variations of the virus to investigate what is the most likely emerging serotype, but also assess the pathogenicity of serotypes. As the current flu vaccine is reformulated each

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season for a few, but not all influenza strains, it is impossible to offer protection against emerging pandemic strains that may happen to break out. Therefore, multivalent vaccines should be further explored as these will assist with protecting against multiple influenza strains. Developing and improving the monitoring network of influenza infections, and pneumonia with unknown causes, along with

strengthening the current early warning system is a key strategy in preventing an influenza pandemic.

- 1 Gao R B, Cao B, Hu Y W. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med*, 2013, 368: 1888–1897
- 2 Uyeki T M, Cox N J. Global concerns regarding novel influenza A (H7N9) virus infections. *N Engl J Med*, 2013, 368: 1862–1864

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