

How lethal bird flu viruses evolved

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Deadly H7N9 avian flu viruses infected people for the first time earlier this year in China, but little is known about how they evolved to become harmful to humans. In a study published by Cell Press on September 19 in *Cell Host & Microbe*, an in-depth evolutionary analysis of whole-genome sequences of different types of avian flu viruses has revealed that new H7N9 viruses emerged from distinct H9N2 viruses in a two-step process, first occurring in wild birds and then continuing in domestic birds.

"A deep understanding of how the novel H7N9 viruses were generated is of critical importance for formulating proper measures for surveillance and control of these viruses and other potential emerging influenza viruses," says senior study author Taijiao Jiang of the Chinese Academy of Sciences.

First detected in people in late March, H7N9 viruses have resulted in more than 130 human infections and at least 44 deaths. Most of these infections occurred after exposure to infected poultry or contaminated environments rather than person-to-person contact, but these viruses could evolve to become more readily transmissible among humans. This possible threat highlights the importance of understanding the evolutionary history of H7N9 viruses for developing appropriate strategies to monitor and control outbreaks.

To address this problem, Jiang teamed up with Daxin Peng of Yangzhou University and their collaborators to analyze whole-genome sequences of avian [flu viruses](#) from humans, poultry, and wild birds from China. They discovered that H7N9 viruses are genetically diverse, suggesting that complex genetic events were involved in their evolution.

Their analysis revealed that the new H7N9 viruses emerged through a two-step process involving the exchange of genetic material between distinct viruses. In the first step, which took place in wild birds, genetic material from H9N2 viruses and unspecified H7 and N9 viruses was mixed to

create precursor H7N9 viruses. The second step, which occurred in domestic birds in eastern China early last year, involved the exchange of genetic material between the precursor H7N9 viruses and other H9N2 viruses to create new, genetically diverse H7N9 viruses.

"Our work not only re-enforces the important role of wild birds in the emergence of novel influenza [viruses](#) but also highlights the necessity of integrating data from infections in humans, poultry, and [wild birds](#) for effective influenza surveillance," Jiang says.

More information: Wu et al.: "Sequential Reassortments Underlie Diverse Influenza H7N9 Genotypes in China" *Cell Host & Microbe*, 2013.

Provided by Cell Press

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