

下一個流感大流行會是誰？該如何預防？

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The question to ask about the next pandemic influenza is not “if”, but “when”. Several candidate viruses have been speculated to be the next pandemic strain so far, including the influenza A(H5N1), A(H7N9), A(H3N2v), A(H7N7), A(H9N2), and A(H2N2). However, many uncertainties remain unanswered on the formation of a pandemic influenza, including the puzzling emergence, the factors that affect the severity, the recurrent patterns, and the replacement among different strains. At the genetic level, pandemic influenza viruses may arise through genetic reassortments and/or genetic mutations.

As for the emergence of the 1918 pandemic influenza, the theory of direct transmission from bird to human proposed by Taubenberger et al. is now being questioned. Phylogenetic relationships suggest that the A/Brevig Mission/1/1918 virus (BM/1918) was generated by reassortment between mammalian viruses and a previously circulating human strain, either in swine or, possibly, in humans. The relatively low incidence rate among the elders in the 1918 pandemic could also be partly explained by the hypothesis that preexisting immunities acquired from the 1850 pandemic might render certain protections.

To transform into a human pandemic influenza, an avian flu virus has to go through several molecular adaptations, including lowering the viral genome GC content, changing the hemagglutinin receptor binding specificity for α -2,6-SAs, modifying viral RNP complex to adapt the mammalian body temperature, and some other alterations to the remaining viral genes. It is hard for a virus to complete all the changes without joining a common host, such as pigs, to serve as the ‘mixing vessel’ in which reassortment of human and avian viruses can occur.

In conclusion, although it is not possible to answer the question of which and when to the next pandemic influenza, the best way to do is to keep vigilant surveillance of human/avian/swine influenza viruses globally.