Passing through: the role of transmission bottlenecks in influenza virus host adaptation

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Abstract: Novel influenza viruses emerge unpredictably from avian reservoirs, causing occasional human pandemics. A handful of recent studies in ferrets have shown that surprisingly few molecular changes may be required for airborne transmission of avian influenza viruses between mammalian hosts. We used deep sequencing to trace the evolutionary pathways of 2 such avian viruses as they replicated and were transmitted in ferrets. Airborne transmission involved genetic bottlenecks that were most often driven by strong selection on the gene encoding the viral attachment protein, hemagglutinin (HA). Bottleneck stringency varied among transmission events, and no single viral genotype was consistently transmitted in each event we observed. The strength and nature of transmission bottlenecks could play an important role in determining the ability of a given avian virus to successfully emerge in humans. *All work with infected ferrets was performed prior to the current pause on "gain-of-function" research.*





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