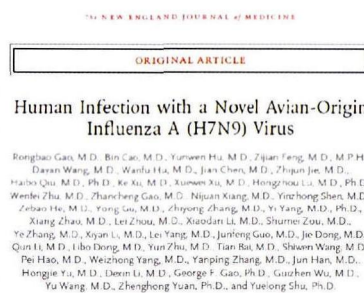
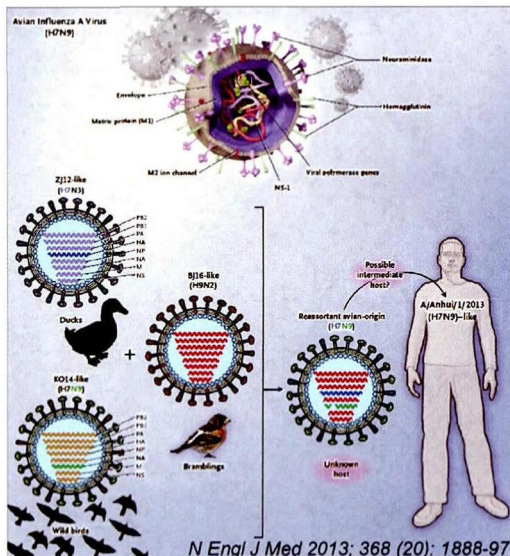


A novel avian H7N9 influenza virus: The discovery, infectivity, transmissibility and pathogenicity

A research team led by Prof. Shu Yuelong in the National Institute for Viral Disease Control and Prevention, China CDC, collaborated with Shanghai Public Health Clinical Center and other partners, firstly discovered that a novel avian H7N9 influenza virus caused severe human infection in China that has not been detected in humans and animals previously, with great global public health concern. The novel H7N9 virus was an avian-origin reassortant containing hemagglutinin derived from avian H7N3-like, neuraminidase from avian H7N9-like and six internal gene segments from avian H9N2 virus (*N Engl J Med*, **2013**, 368 (20): 1888—1897). His team further identified the special “dual-receptor” binding profile of avian H7N9 virus, which indicated that the H7N9 virus could infect human more easily than H5N1; and that the “cytokine storm” contributed to the clinical severity of human infection with H7N9 virus (*Nature*, **2013**, 499(7459): 500—503). With collaboration of Hong Kong University, they demonstrated that H7N9 virus was efficiently transmitted via direct contact, but less efficiently by airborne exposure in ferret model, which highlight the pandemic potential of the novel H7N9 influenza virus (*Science*, **2013**, 341(6142): 183—6). The findings provided scientific insights for the infectivity, transmissibility and pathogenesis of the novel H7N9 virus, and were essential for global risk assessment and response strategies development.

These scientific studies were supported by the National Natural Science Foundation of China, the National Basic Research Program (973) of China and Emergency Research Project on human infection with avian influenza H7N9 virus from the National Ministry of Science and Technology.



LETTER

Biological features of novel avian influenza A (H7N9) virus

Hanfeng Zhou¹, Dayan Wang^{1*}, Rongbao Gao^{1*}, Baihui Zhao^{1*}, Jingfeng Song¹, Xian Qi¹, Yanjun Zhang¹, Yanglin Shi¹, Lei Yang¹, Wendei Zhu¹, Tian Bai¹, Kun Qin¹, Yu Lan¹, Shumei Zou¹, Junfeng Gao¹, Jie Dong¹, Libo Dong¹, Ye Zhang¹, Hejiang Wei¹, Xiaotian Li¹, Jian Liu¹, Liqi Liu¹, Xiang Zhao¹, Xiyun Li¹, Weijuan Huang¹, Leying Wen¹, Hong Bo¹, Li Xin¹, Yongkun Chen¹, Cailin Xu¹, Yuquan Pei¹, Yue Yang¹, Xiaodong Zhang², Shiwen Wang², Zijian Feng², Jun Han², Weizhong Yang², George F. Gao¹, Guizhen Wu¹, Dexin Li¹, Yu Wang¹ & Yuelong Shu¹

Human infection associated with a novel reassortant avian influenza H7N9 virus has recently been identified in China¹. A total of 52,6 binding of H7N9 may attribute to single or multiple substitutions in haemagglutinin including Ala188ser in SH1 or Gly186Val and

Figure The research team led by Prof. Shu Yuelong published the initial studies on novel influenza A (H7N9) virus.