We thank Dr. Viroj for his careful reading of our article and his description of some important considerations of the novel avian-origin influenza A (H7N9) virus in the human.

As Viroj mentioned, this virus (H7N9) has several human virus-like signatures, and possible pandemic would most likely be due to the wide spreading of the pathogenic virus from infected avian. In our overview of the emergence of a new form of avian-origin influenza A virus-H7N9 — causing first time human infection, we noted that there has been speculation as to whether this virus will be the agent of the next influenza pandemic. Liu et al. reported that this novel avian influenza A H7N9 virus originated from multiple reassortment events. They hypothesized that human infection with H7N9 viruses resulted from a reassortment of avian influenza viruses of at least four origins—duck origin for HA, duck (probably also wild bird) origin for NA, and at least two H9N2 chicken viruses for the internal genes. Mutations in H7N9 strains that could favor high-affinity interaction with human receptors in the upper respiratory tract are a prerequisite for virus transmission by the aerosol route. As the H7N9 virus does not cause disease in poultry, a decline in the number of new human cases was noted when there was closure of poultry markets and culling of birds in China. But the timing and probability that this H7N9 will acquire the capacity for human-to-human transmission is impossible to estimate. Chen et al. reported that, so far, out of the four confirmed clusters of two or more cases that were in close contact, the patients did not appear to have known exposure to each other. Hu Y et al. also reported the emergence of the oseltamivir-resistant virus with the Arg292Lys mutation in two patients among 14 adults infected with H7N9 viruses. Due to the fact that the process of resistance emergence is associated with variant virus fitness, the fitness and stability of the Arg292Lys mutation in avian influenza A (H7N9) needs to be investigated. The appearance of antiviral resistance emerging in avian influenza A (H7N9) viruses is concerning, and should be closely monitored and considered for future pandemic response plans.

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