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Virological and pathological characterization of an avian H1N1 influenza A virus

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Gene segments from avian H1N1 influenza A viruses have reassorted with other influenza viruses to generate pandemic strains over the past century. Nevertheless, little effort has been invested in understanding the characteristics of avian H1N1 influenza viruses. Here, we present the genome sequence, a molecular and virological characterization of a novel avian influenza A, A/wild bird/Korea/SK14/2014 (A/SK14, H1N1), isolated from migratory birds in South Korea during the winter season of 2014-2015. Full-genome sequencing and phylogenetic analyses revealed that the virus belongs to the Eurasian avian lineage. Although it retained avian-receptor binding preference, A/SK14 virus also exhibited detectable human-like receptor binding and was able to replicate in differentiated primary normal human bronchial epithelial cells. In animal models, A/SK14 virus was moderately pathogenic in mice and viral titers were detected in nasal washes from inoculated guinea pigs, but not direct-contact guinea pigs. Although A/SK14 showed moderate pathogenicity and no evidence of transmission in a mammalian model, our results suggest the dual receptor specificity of A/SK14-like may allow for a more rapid adaptation to mammals emphasizing the importance of further continuous surveillance and risk assessment activities.

Biography

Sun-Woo Yoon has completed his PhD in Department of Microbiology in Chungnam National University in South Korea on August 2008. His Post-doctoral training was at the St. Jude Children's Research Hospital (Memphis, TN, USA) in the laboratory of Dr. Richard J Webby where he studied the pathogenesis of influenza viruses including swine H1N1, HPAI H5N1, and H7N9 viruses. After his Post-doctoral fellowship, he joined the faculty in the Korea Research Institute of Bioscience and Biotechnology where he began his own lab in December 2013. His lab focuses on establishment of active surveillance program of the influenza viruses and assessment of pathogenesis about emerging infectious disease viruses including novel influenza viruses, MERS-CoV as well as other animal viruses.

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