Risk Assessment and Anti-Viral Approaches for Novel H7N9 Influenza Virus

Ralph A Tripp*
Department of Infectious Diseases, University of Georgia, USA

Abstract

Human infection with avian influenza A/H7N9 virus emerged in eastern China in February 2013 and was associated with exposure to poultry. No evidence of ongoing human-to-human transmission for the current H7N9 outbreak has been found. The novel H7N9 virus has no vaccine so antivirals are the only option for control. The virus appears to be susceptible to neuraminidase inhibitors; however viral sequence data indicates the potential for antiviral resistance to the adamantanes. As influenza viruses constantly change it is possible that this virus could become able to spread between people triggering a pandemic. Thus, new antiviral options are needed and ongoing surveillance maintained or increased to assess the emergence and prevalence of H7N9 viruses resistant to available antivirals.

Keywords: Influenza; H7N9; Pandemic; Antivirals; Avian influenza; Flu; Avian flu

On March 31, Chinese Center for Disease Control and Prevention announced that scientists had isolated a novel influenza A virus from several patients in eastern China, three of whom had died [1]. Presently, multiple human cases have been confirmed with many resulting in hospitalization and death in mostly 60+ year old patients [2,3]. Although no vaccine for this strain is currently available, the virus appears to be susceptible to neuraminidase inhibitors. This feature, although is very tenuous as avian influenza viruses (AIV), members of the family Orthomyxoviridae, are known to undergo rapid mutations and acquire resistance to antiviral drugs [4-6].

Emerging viral diseases are a continuous threat to humans worldwide, and the majority of the emerging viruses originate from animal hosts. Of concern is zoonotic transmission of AIV viruses to humans with or without intermediate hosts, although historically such zoonotic transmission is usually self-limited, nevertheless these AIV pose a pandemic threat as they may adapt to humans. It is not uncommon for AIV to occasionally infect and cause disease in humans, as this has occurred for H5N1, H9N2, and H7N7 viruses [7-10]. Fortunately, no evidence of sustained human-to-human transmission for the current H7N9 outbreaks has yet been found. This suggests that the virus which normally circulates in a bird reservoir infects a person, but further human-to-human transmission does not occur because H7N9 has yet to acquire novel sequence variations that allow them to infect humans - but that may be a matter of time. It is not clear how people are becoming infected with the H7N9 virus; however, the majority of cases involve contact with animals or with environments where animals are housed. The virus has now been found in chickens, ducks, and captive-bred pigeons at live bird markets near locations where cases have been reported. The possibility of an animal source of the infection is being investigated, as is the possibility of person-to-person transmission.

As the human population has never seen the H7N9 AIV, there is little to no pre-existing immunity, thus this variant may rapidly replicate and perhaps be transmitted among humans and via zoonosis to other animals. The full genetic sequence for H7N9 suggests that some of H7N9 genes are adapted to mammals, having a propensity to infect mammals through alpha 2,6 sialic acid receptors [11]. The sequence information also suggests that H7N9 AIV may have passed through swine before moving back to birds and then infecting humans. Infection with H7 influenza viruses has occurred, but fortunately never swept through as a pandemic. For example, H7N2, H7N3, and H7N7 were reported in Canada, Italy, Mexico, the Netherlands, the United Kingdom, and the United States of America [12,13]. Most of these infections occurred in association with poultry outbreaks. The infections mainly resulted in conjunctivitis and mild upper respiratory symptoms, with the exception of one death, which occurred in the Netherlands [14].

As there is no vaccine for AIV H7N9, the frontline defense is antiviral. The H7N9 sequence indicates antiviral resistance to the adamantanes and susceptibility to neuraminidase inhibitors, except for a 292K mutation in the NA protein of the A/Shanghai/1/2012 virus [11,15]. The 292K mutation has been associated with in vitro resistance to neuraminidase inhibitors in another N9 NA subtype virus, thus it is critical to understand the significance of the mutation in H7N9. It is not clear if the 292K mutation was de novo, or associated with oseltamivir treatment that was generally given to all suspected H7N9 patients [1]. Enhanced surveillance is now needed to assess the emergence and prevalence of H7N9 viruses resistant to neuraminidase inhibitors. In addition, the usage of neuraminidase inhibitors and other anti-influenza virus drugs need to be carefully assessed for efficacy in the early stage of H7N9 infection, as is this period that proved to be effective for other sensitive AIV including H5N1. Additionally, drug repositioning studies need to be performed for H7N9, and this needs to be done diligently to add new antiviral tools to our toolbox.

In summary, AIV that develop the ability to infect humans theoretically can cause a pandemic. Whether H7N9 AIV will go this path remains unknown, but experience with proper use of antiviral drugs suggests these viruses can be controlled in the absence of a

*Corresponding author: Ralph A Tripp, Professor, Department of Infectious Diseases, University of Georgia, Athens, GA USA, Tel: 706-542-1557, E-mail: ratripp@uga.edu

Received May 21, 2013; Accepted May 23, 2013; Published May 25, 2013


Copyright: © 2013 Tripp RA. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.
vaccine. Surveillance and antiviral drug investigations are needed to be ramped up to provide critical information needed to make decisions and reduce the pandemic threat.

References


