Journal of
Antivirals & Antiretrovirals
ISSN: 1948-5964

Tripp, J Antivir Antiretrovir 2013, 5:3
DOI: 10.4172/jaa.1000e108

Editorial Open Access

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 antivirals. 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

Citation: Tripp RA (2013) Risk Assessment and Anti-Viral Approaches for Novel H7N9 Influenza Virus. J Antivir Antiretrovir 5: xix-xx. doi:10.4172/jaa.1000e108

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

1. Lu SH, Xi XH, Zheng YF, Cao Y, Liu XN, et al. (2013) Analysis of the clinical characteristics and treatment of two patients with avian influenza virus (H7N9). Biosci Trends 7: 109-112.
2. Li Q, Zhou L, Zhou M, Chen Z, Li F, et al. (2013) Preliminary Report: Epidemiology of the Avian Influenza A (H7N9) Outbreak in China. N Engl J Med.
3. Hvistendahl M, Normile D, Cohen J (2013) Influenza. Despite large research effort, H7N9 continues to baffle. Science 340: 414-415.
4. Samson M, Pizzorno A, Abed Y, Boivin G (2013) Influenza virus resistance to neuraminidase inhibitors. Antiviral Res 98: 174-185.
5. McKimm-Breschkin JL (2013) Influenza neuraminidase inhibitors: antiviral action and mechanisms of resistance. Influenza Other Respi Viruses 7 Suppl 1: 25-36.
6. Ison MG (2011) Antivirals and resistance: influenza virus. Curr Opin Virol 1: 563-573.
7. Osterholm MT, Kelley NS (2012) Mammalian-transmissible H5N1 influenza: facts and perspective. MBio 3: e00045-00012.
8. Fukuyama S, Kawaoka Y (2011) The pathogenesis of influenza virus infections: the contributions of virus and host factors. Curr Opin Immunol 23: 481-486.
9. Tang JW, Shetty N, Lam TT, Hon KL (2010) Emerging, novel, and known influenza virus infections in humans. Infect Dis Clin North Am 24: 603-617.
10. Lee CW, Saif YM (2009) Avian influenza virus. Comp Immunol Microbiol Infect Dis 32: 301-310.
11. Liu Q, Lu L, Sun Z, Chen GW, Wen Y, et al. (2013) Genomic signature and protein sequence analysis of a novel influenza A (H7N9) virus that causes an outbreak in humans in China. Microbes Infect.
12. Brown IH (2010) Summary of avian influenza activity in Europe, Asia, and Africa, 2006-2009. Avian Dis 54: 187-193.
13. Belser JA, Blixt O, Chen LM, Pappas C, Maines TR, et al. (2008) Contemporary North American influenza H7 viruses possess human receptor specificity: Implications for virus transmissibility. Proc Natl Acad Sci U S A 105: 7558-7563.
14. Capua I, Alexander DJ (2002) Avian influenza and human health. Acta Trop 83: 1-6.
15. Chen Y, Liang W, Yang S, Wu N, Gao H, et al. (2013) Human infections with the emerging avian influenza A H7N9 virus from wet market poultry: clinical analysis and characterisation of viral genome. Lancet.