

Novel Avian Flu A (H₇N₉) Epidemic: A China's Lesson Learned

Attapon Cheepsattayakorn^{1,2*}

¹10th Zonal Tuberculosis and Chest Disease Center, Chiang Mai, Thailand

²10th Office of Disease Prevention and Control, Chiang Mai, Department of Disease Control, Ministry of Public Health, Thailand

Keywords: H₇N₉; Epidemic; China

Avian influenza A (H₇N₉) virus, the latest avian influenza virus strain was once considered a relatively rare cause of infection and low pathogenic [1,2]. This virus is similar to its closer cousins, H₇N₂, H₇N₃ and H₇N₇ and its more distant cousin H₅N₁ viruses which are all influenza A viruses and usually infect birds [1]. The virus has 8 single stranded ribonucleic acid (RNA) segments with 11 proteins (cap recognition RNA polymerase (basic) (PB2), endonuclease, elongation RNA polymerase subunit (basic) (PB1: Pol & PB1-F2), RNA polymerase subunit (acidic) (PA), hemagglutinin (HA), Nucleoprotein RNA binding RNA synthesis (NP), neuraminidase (NA), matrix protein 1 (M1), ion channel (M2), NS1 and NEP encoding [1]. It currently remains unknown zoonotic outbreak if the H₇N₉ virus is being transmitted from wild bird reservoir to poultry with sporadically transmission to humans in multiple unknown locations, most probable the live-bird markets (72% of cases reported some recent contacts with live-poultry and live-bird markets [3]), probably facilitated by the fact that people in China still buy poultry for domestic consumption underwent through both intra-provincial and inter-provincial trading [4] and supported by a reduction in the number of new human cases that associated with the closure of live-poultry markets in Shanghai [3] or if the virus has spread to the affected provinces through poultry-to-poultry transmission like scenario in eastern China whereas the novel virus causes mild or no disease in birds and poultry [3,4] and lower pathogenic compared with avian influenza A (H₅N₁) viruses [4]. This evidence was supported by no detection of bird influenza virus in dead pig specimens from a river in Shanghai [5] and genetically supported by demonstration of a single Arg at the HA cleavage site [3]. While live-birds is the most probable reservoir, reservoir of H₅N₁ viruses presently is still unknown, but H₅N₁ viruses are detected in both domestic poultry in some countries and wild birds on occasion [4]. Only domestic birds in some live-bird markets in eastern China were demonstrated H₇N₉ infections and yet unknown distribution in wild birds whereas H₅N₁ virus distribution among domestic animals is entrenched and occasionally identified in a limited number of species, including identification in Europe [4]. This novel virus is transmissible among birds and has possibly distributed itself among the poultry populations [4], but currently, demonstrates no evidence of person-to-person transmission [2,5] same as H₅N₁ viruses [4]. The H₇N₉ viruses seem more common than H₅N₁ viruses which are very rare in transmission

from animals to humans [4]. Influenza A (H₅N₁) virus spreading has persisted and evolved over nearly two decades whereas durability as an animal infection of H₇N₉ viruses is yet unknown [4]. Most laboratory-confirmed cases were reported with underlying chronic medical conditions [2,4] and progressed to respiratory distress syndrome [2] or severe pneumonia [3] liked most cases of H₅N₁ virus infections. Most cases had older age range than cases of H₅N₁ virus infections [2,3,4] and male cases were twice as common as female cases [2,4] whereas there were equal numbers of male and female cases with of H₅N₁ virus infections and were most common in children and younger adults [4]. This is an unusual and unexplained age and gender distribution in cases with H₇N₉ virus infections in China [4]. Nevertheless, identification of the virus in any particular species of bird does not necessarily mean that the species is the reservoir for transmission to humans [4]. Whether is being circulating in other animal reservoirs is to be identified yet [4]. Some cases with asymptomatic H₇N₉ virus infections had been notified whereas asymptomatic H₅N₁ virus infections were hardly ever [4]. Case-fatality was high (20% [2,4]) among H₇N₉ virus infected cases, but was very high among H₅N₁ virus infected cases (60% [4]). Genetically, either E627K [3,5] from some human isolates or D701N demonstrated in PB2 gene in different strains are both markers of mammalian adaptation of H₇N₉ viruses, such as PB2 Asp701Asn substitution [4]. Identification of association between Gln226Leu and Gly186Val substitutions in human virus H₇ and increased affinity for α-2,6-linked sialic acid receptors that found in upper respiratory tract of both humans and other mammals is able to cause severe respiratory infections [3]. The presumed incubation period ranged 3 to 8 days [1], thus close contacts must be under medical observation at least 10 full days [4,5].

References

1. Mackay IM (2013) Avian influenza A (H₇N₉) virus-2013's bird flu.
2. World Health Organization (2013) Overview of the emergence and characteristics of the avian influenza A (H₇N₉) virus.
3. China-WHO Joint Mission on Human Infection with Avian Influenza A (H7N9) Virus 18-24 April 2013 Mission Report.
4. Updated rapid risk assessment: Human infection with a novel avian influenza virus, A(H₇N₉)-China (2013) European Centre for Disease Prevention and Control, Stockholm.
5. China-Three confirmed cases of human infection with H₇N₉ avian influenza-Two fatalities (2013).

*Corresponding author: Attapon Cheepsattayakorn, 10th Zonal Tuberculosis and Chest Disease Center, 143 Sridornchai Road, Changklan Muang, Chiang Mai-50100, Thailand, Tel: 66-53-140767; E-mail: attaponche@yahoo.com

Received November 14, 2013; Accepted November 15, 2013; Published November 18, 2013

Citation: Cheepsattayakorn A (2013) Novel Avian Flu a (H₇N₉) Epidemic: A China's Lesson Learned. Poult Fish Wildl Sci 1: e105. doi:10.4172/2375-446X.1000e105

Copyright: © 2013 Cheepsattayakorn A. 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.