



Epidemiological and Molecular Analysis of Avian Influenza A (H7N9) Virus in Shanghai, China, 2013-2017

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Editorial

Shanghai located in the East Asia/Australian migratory flyway has several coastal wetlands and the significant congregation sites of migratory birds, increasing the risk of the emergence of novel influenza viruses because the migratory shorebird is a natural reservoir for avian influenza virus. Since the human infections with a novel avian influenza virus (H7N9) were first reported in Shanghai province in March 2013, there have been six seasonal epidemics observed in China [1-10]. A novel highly pathogenic avian influenza (HPAI) H7N9 virus emerged in late February 2017 with existing low pathogenic avian influenza (LPAI) H7N9 virus have been the pandemic potential to human beings [11,12].

The aims of this study were to elucidate the epidemiological characteristics of H7N9 infected cases in Shanghai and to investigate the mutations of signature amino acids in the Hem Agglutinin (HA), neuraminidase (NA) and other internal proteins of the virus. In the epidemiological study, the 59 laboratory confirmed human cases and 26 birds and environmental contaminated cases were collected as of December 31, 2017, from World Health Organization (WHO) website and Food and Agriculture Organization emergency prevention system for animal health (FAO EMPRES) [13-25]. We generated epidemic curve and analyzed the occurrence pattern of H7N9 infected cases in Shanghai. In the molecular evolutionary study, full sequences of H7N9 viruses emerged in Shanghai as well as WHO recommended four H7N9 vaccine candidates were collected from Global Initiative on Sharing Avian Influenza Data (GISAID) and constructed phylogenetic trees with MEGA 7.0 software. The amino acid homology of HA and NA was calculated using the pairwise distance method. And the mutations of amino acids sequences were analyzed with Bioedit software [26-30].

We found that genetically new H7N9 strains had been emerged every epidemic in Shanghai and most of the H7N9 strains circulated have the affinity to human type receptors. The Shanghai strains had the characteristics of high virulence and low pathogenic influenza viruses, given that its NA deletion (position 69-73) and single basic amino acid insertion in the HA cleavage site. Furthermore, our finding suggests that NA inhibitor antiviral drugs could be still effective for the treatment of H7N9 infected patients in Shanghai based on the fact that only 3 Shanghai strains in the first epidemic contained the R292K mutations and no environmental or birds samples were reported [31,32]. This study also indicates that the first HPAI H7N9 virus (A/Guangdong/17SF003/2016) emerged in the fifth epidemic is avian origin because it is phylogenetically closely related to Shanghai chicken strains. It is reported that the human case-patients were most likely infected from poultry in live poultry markets (LPMs). But it seems that the closure of LPMs might not be the deciding factor for preventing the human infection with H7N9 in Shanghai because few of H7N9 human cases remain occurred at the market closure period of 2015 to 2017 [33-35]. The gradual decrease of human cases with H7N9 in Shanghai was probably due to the control measures by Shanghai government and the improved public awareness of a reduced risk of H7N9 virus infection. But LPAI H7N9 viruses with poultry and environmental samples were continually detected in Shanghai across the epidemics, increasing the risk of new emerging H7N9 outbreaks [36,37]. Also LPAI or HPAI H7N9 viruses in contaminated area could spread through the poultry transportation and the bird migration. Therefore it is important to take sufficient surveillance and prevention measures against H7N9 viruses in Shanghai province, consistently. Prevention and control program included the closure of the LPMs, slaughtering the poultry and investigation of environmental samples as well as implementing the emergency monitoring plan [38-40].

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Because China has large land size and each province has different, wide range of population and climate and environment, province based quarantine measures could be more efficient to control the outbreaks. As World Health Organization and Chinese experts assessed quarantine measures conducted by Shanghai government as appropriate and effective, it could be a good example for H7N9 control and prevention in other regions.

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