



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

Seong Jin Wang, Xue Wei Liu, Xiaojuan Shen, Xiu Guo Hua and Li Cui*

School of Agriculture and Biology, Shanghai Jiaotong University, China

Keywords

Epidemiology; H7N9 virus; Phylogenetic tree; Molecular evolutionary study

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].

OPEN ACCESS

*Correspondence:

Li Cui, School of Agriculture and Biology, Shanghai Jiaotong University, Shanghai 200240, China, Tel: +86-21-34206367;

E-mail: lcui@sjtu.edu.cn

Received Date: 04 Jul 2018

Accepted Date: 01 Aug 2018

Published Date: 08 Aug 2018

Citation:

Wang SJ, Liu XW, Shen X, Hua XG, Cui L. Epidemiological and Molecular Analysis of Avian Influenza A (H7N9) Virus in Shanghai, China, 2013-2017. *Ann Infect Dis Epidemiol.* 2018; 3(2): 1031.

ISSN: 2475-5664

Copyright © 2018 Li Cui. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

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.

References

- H7N9 situation update, Food and Agricultural Organization. 2018.
- Yang L, Zhu W, Li X, Chen M, Wu J, Yu P, et al. Genesis and Spread of Newly Emerged Highly Pathogenic H7N9 Avian Viruses in Mainland China. *J virol*. 2017.
- Wang X, Jiang H, Wu P, Uyeki TM, Feng L, Lai S, et al. Epidemiology of avian influenza A H7N9 virus in human beings across five epidemics in mainland China, 2013-17: an epidemiological study of laboratory-confirmed case series. *Lancet Infect Dis*. 2017;17(8):822-32.
- Peiris JS, Cowling BJ, Wu JT, Feng L, Guan YI, Yu H, et al. Interventions to reduce zoonotic and pandemic risks from avian influenza in Asia. *Lancet Infectious Diseases*. 2016;16(2):252-8.
- Zhang F, Bi Y, Wang J, Wong G, Shi W, Hu F, et al. Human infections with recently-emerging highly pathogenic H7N9 avian influenza virus in China. *J Infect*. 2017;75(1):71-4.
- Quan C, Shi W, Yang Y, Yang Y, Liu X, Xu W, et al. New Threats from H7N9 Influenza Virus: Spread and Evolution of High- and Low-Pathogenicity Variants with High Genomic Diversity in Wave Five. *J Virol*. 2018;92(11):JVI.00301-18.
- Qin Y, Horby PW, Tsang TK, Chen E, Gao L, Ou J, et al. Differences in the Epidemiology of Human Cases of Avian Influenza A(H7N9) and A(H5N1) Viruses Infection. *Clin Infect Dis*. 2015;61(4):563-71.
- Iuliano AD, Jang Y, Jones J, Davis T, Wentworth DE, Uyeki TM, et al. Increase in Human Infections with Avian Influenza A (H7N9) Virus During the Fifth Epidemic - China, October 2016-February 2017. *Mmwr Morbidity & Mortality Weekly Report*. 2017;66(9):254.
- Zhu Y, Qi X, Cui L, Zhou M, Wang H. Human co-infection with novel avian influenza A H7N9 and influenza A H3N2 viruses in Jiangsu province, China. *Lancet*. 2013;381(9883):2134.
- Kile JC, Ren R, Liu L, Greene CM, Roguski K, Iuliano DA, et al. Update: Increase in Human Infections with Novel Asian Lineage Avian Influenza A(H7N9) Viruses During the Fifth Epidemic - China, October 1, 2016-August 7, 2017. *Mmwr-Morbidity and Mortality Weekly Report*. 2017;66(35):928-32.
- Gao R, Cao B, Hu Y, Feng Z, Wang D, Hu W, et al. Human infection with a novel avian-origin influenza A (H7N9) virus. *N Engl J Med*. 2013;368(20):1888-97.
- Capua I, Alexander DJ. Avian influenza: recent developments. *Avian Pathol*. 2004;33(4):393-404.
- Alvarez P, Mattiello R, Rivailler P, Pereda A, Davis CT, Boado L, et al. First isolation of an H1N1 avian influenza virus from wild terrestrial non-migratory birds in Argentina. *Virology*. 2010;396(1):76-84.
- Bai Q, Chen J, Chen Z, Dong G, Dong J, Dong W, et al. Identification of coastal wetlands of international importance for waterbirds: a review of China Coastal Waterbird Surveys 2005-2013. *Avian Research*. 2015;6(1):12.
- Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, et al. Clustal W and Clustal X version 2.0. *Bioinformatics*. 2007;23(21):2947-8.
- Kumar S, Stecher G, Tamura K. MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Mol Biol Evol*. 2016;33(7):1870.
- Xiong X, Martin SR, Haire LF, Wharton SA, Daniels RS, Bennett MS, et al. Receptor binding by an H7N9 influenza virus from humans. *Nature*. 2013;499(7459):496-9.
- Munier S, Larcher T, Cormier-Aline F, Soubieux D, Su B, Guigand L, et al. A Genetically Engineered Waterfowl Influenza Virus with a Deletion in the Stalk of the Neuraminidase Has Increased Virulence for Chickens. *J Virol*. 2010;84(2):940-52.
- Riel DV, Munster VJ, de Wit E, Rimmelzwaan GF, Fouchier RA, Osterhaus AD, et al. H5N1 Virus Attachment to Lower Respiratory Tract. *Science*. 2006;312(5772):399.
- Li Z, Chen H, Jiao P, Deng G, Tian G, Li Y, et al. Molecular basis of replication of duck H5N1 influenza viruses in a mammalian mouse model. *J Virol*. 2005;79(18):12058-64.
- Ren L, Yu X, Zhao B, Wu F, Jin Q, Zhang X, et al. Infection with possible precursor of avian influenza A (H7N9) virus in a child, China, 2013. *Emerging Infectious Diseases*. 2014;20(8):1362-5.
- Rogers GN, Paulson JC, Daniels RS, Skehel JJ, Wilson IA, Wiley DC. Single amino-acid substitutions in influenza hemagglutinin change receptor-binding specificity. *Nature*. 1983;304(5921):76-8.
- Imai M, Watanabe T, Hatta M, Das SC, Ozawa M, Shinya K, et al. Experimental adaptation of an influenza H5 haemagglutinin (HA) confers respiratory droplet transmission to a reassortant H5 HA/H1N1 virus in ferrets. *Nature*. 2012;486(7403):420.
- Wang D, Yang L, Gao R, Zhang X, Tan Y, Wu A, et al. Genetic tuning of the novel avian influenza A (H7N9) virus during interspecies transmission, China, 2013. *Euro Surveill*. 2014;19(25).
- Webster RG, Bean WJ, Gorman OT, Chambers TM, Kawaoka Y. Evolution and ecology of influenza A viruses. *Microbiol Rev*. 1992;56(1):152-79.
- Schrauwen EJ, Herfst S, Leijten LM, van Run P, Bestebroer TM, Linster M, et al. The multibasic cleavage site in H5N1 virus is critical for systemic spread along the olfactory and hematogenous routes in ferrets. *J Virol*. 2012;86(7):3975-84.
- Shinya K, Makino A, Hatta M, Watanabe S, Kim JH, Hatta Y, et al. Subclinical brain injury caused by H5N1 influenza virus infection. *J Virol*. 2011;85(10):5202-7.
- Shinya K, Makino A, Tanaka H, Hatta M, Watanabe T, Le MQ, et al. Systemic Dissemination of H5N1 Influenza A Viruses in Ferrets and Hamsters after Direct Intragastric Inoculation. *J Virol*. 2011;85(10):4673-8.
- Horimoto T, Kawaoka Y. Reverse genetics provides direct evidence for a correlation of hemagglutinin cleavability and virulence of an avian influenza A virus. *J Virol*. 1994;68(5):3120.
- Mckimm-Breschkin J, Trivedi T, Hampson A, Hay A, Klimov A, Tashiro M, et al. Neuraminidase sequence analysis and susceptibilities of influenza virus clinical isolates to zanamivir and oseltamivir. *Antimicrob Agents Chemother*. 2003;47(7):2264-72.
- Sha J, Chen X, Ren Y, Chen H, Wu Z, Ying D et al. Differences in the epidemiology and virology of mild, severe and fatal human infections with avian influenza A (H7N9) virus. *Arch Virol*. 2016;161(5):1239-59.
- Zhou L, Ren R, Yang L, Bao C, Wu J, Wang D, et al. Sudden increase in human infection with avian influenza A(H7N9) virus in China, September-December 2016. *Western Pacific Surveillance & Response Journal Wpsar*. 2017;8(1):6-14.
- Fouchier RA. Epidemiology of Human Infections with Avian Influenza A (H7N9) Virus in China - NEJM. *N Engl J Med*. 2014;370(6):520-32.
- Su S, Gu M, Liu D, Cui J, Gao GF, Zhou J, et al. Epidemiology, Evolution, and Pathogenesis of H7N9 Influenza Viruses in Five Epidemic Waves since 2013 in China. *Trends Microbiol*. 2017;25(9):713-28.

35. Shen Y, Lu H, Qi T, Gu Y, Xiang M, Lu S, et al. Fatal cases of human infection with avian influenza A(H7N9) virus in Shanghai, China. *Biosci Trends*. 2015;9(1):73.
36. Shanghai municipal commission of Health and Family Planning, Press release. 2018.
37. Kim SM, Kim YI, Pascua PN, Choi YK. Avian Influenza A Viruses: Evolution and Zoonotic Infection. *Semin Respir Crit Care Med*. 2016;37(04):501-11.
38. He Y, Liu P, Tang S, Chen Y, Pei E, Zhao B, et al. Live Poultry Market Closure and Control of Avian Influenza A(H7N9), Shanghai, China. *Emerg Infect Dis*. 2014;20(9):1565-6.
39. Shanghai municipal agricultural commission. Information abstract (internal data). *Shanghai agricultural network*. 2013;303(7):1-8.
40. PR of China. Experts: Positive for the shanghai's preventive measures to H7N9 outbreaks. 2013: 2018.