

Novel 2013 Influenza A (H7N9) Virus: Potential Pandemic Threat

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Received: April 20, 2013; Revised: April 30, 2013; Accepted: May 2, 2013

Keywords: Influenza A (H7N9) Virus; Disease Outbreaks

1. Introduction

Avian influenza A viruses have a large genetic diversity. They are capable of producing new strains through re-assortment and mixing their genomic segments in proper hosts. Observations have shown that such avian novel viruses can sporadically infect humans, and in some cases these infections may be so serious. The emergence of avian influenza A virus with pandemic potential in humans has become a matter of concern for the public health (1).

2. Influenza A (H7N9) Virus in 2013

In March 2013, three cases of severe respiratory diseases with high grade fever were reported in eastern China. Immediately afterwards, in a study using Real-Time Reverse Transcription PCR, isolation of virus in embryonated eggs and the complete genomic sequencing of the isolates, it was demonstrated that the respective etiologic agent was a novel avian- origin influenza A (H7N9) virus (2).

Also, there have been reports between 1996-2012, indicating human infections caused by influenza A H7 lineage including H7N2, H7N3 and H7N7 in different parts of the world. The above mentioned report from China was the first documented cases of H7N9 infection in humans. Obviously, all cases of novel influenza A (H7N9) virus infections have been among the individuals who were in direct or indirect contact with poultry and respective products. No transmission from human to human has been reported yet. As findings indicate, the virus can cause serious respiratory complications with high grade fever, which are fatal in many cases. According to most recent WHO report 87 individuals have been laboratory-confirmed with human infection with avian influenza A (H7N9) virus in China; including 17 deaths (3). All aspects of the novel avian 2013 influenza A (H7N9) virus are not

clearly known to us, but we may be able to categorize it under highly pathogenic avian influenza group.

Evolutionary genomics study on avian 2013 influenza A (H7N9) virus has demonstrated that the virus has emerged through re-assortment between three influenza A viruses. In this study the genome of six avian influenza A (H7N9) viruses were entirely sequenced and compared with the existing related data. The haemagglutinin gene comes from H7 family virus (H7N3), the neuraminidase gene (NA) comes from N9 family virus (H7N9) and six internal genes (PA, NS, PB2, PB1, NP and M) come from H9N2. The six viruses included 4 human and 2 bird isolates. In addition, it was revealed that within the short period following the emergence of the novel virus the point mutations have changed 8 amino acids in HA of one isolate (4).

3. Conclusions

No respective vaccine has been developed yet. However influenza H7N9 A/ Anhui/1/2013 strain could be an appropriate for vaccine production because it can proliferate with high titer in embryonated eggs. Evidence shows that avian influenza A (H7N9) virus has a high capacity to cause sequence diversity, which can be a warning of mutation accumulation which can in turn change the virulence and epidemiological characteristics such as host tropism and transmissibility. Although currently the virus has been detected in the eastern China, WHO daily report indicate new cases regularly found in other parts of China as well. Potentially, the infection can spread to the neighboring countries and even other parts of the world.

Given the above mentioned findings, it is suggested that Iranian health authorities closely monitor domestic and wild poultry populations, keep them under surveillance because the emergence of this viral infection is primarily through infecting the poultry and then trans-

Implication for health policy/practice/research/medical education:

Our aims are to answer the elementary questions about: origin, diseases, transmissibility and surveillance of newly emerged avian- origin influenza A (H7N9) virus.

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mission to humans. Also monitoring and screening for novel and seasonal influenza viruses in susceptible and high risk human groups, can help control the infections and make reasonable decisions (5, 6). In conclusion such measures on the part of health authorities are highly recommended.

Financial Support

There is no Financial Support.

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