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New emerging H5N8 influenza: A new risk for human?

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ABSTRACT

The new emerging influenza is usually important problem in medicine. There are many new emerging influenza infections that exist at present. One of the new influenza is the H5N8 influenza. This new disease has just been emerged in 2014. This disease becomes a new consideration in global public health. The remained query is whether this disease is a new risk for human beings.

1. Introduction

Influenza is an important pathogenic respiratory virus. The virus can affect a large numbers of both human beings and animals causing diseases around the world. As a genetic labile virus, the mutation within the influenza virus can be expected and some sense mutations can result in new emerging pathogenic influenza virus. The new emerging influenza is usually important problem in medicine. There are many new emerging influenza infections that exist at present[1,2]. One of the new influenza is the H5N8 influenza. This new disease has just been emerged in 2014. This disease becomes a new

consideration in global public health. The remained query is whether this disease is a new risk for human beings.

2. New emerging of H5N8 influenza in 2014

The H5N8 influenza is a new emerging infection. It is classified into the group of avian influenza or bird flu similar to H5N1 influenza. As noted the new emerging H5N8 influenza has just been reported in 2014. This new disease existed in many parts of the world and caused infection in thousands of avian population.

2.1. Eastern global hemisphere

The first reported of new mutant H5N8 influenza virus was firstly reported from China[3]. Wu *et al.* successfully "isolated 2 novel influenza A(H5N8) viruses from domestic

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ducks in Eastern China, sequenced their genomes, and tested their pathogenicity in chickens and mice[3]. Wu *et al.* proposed that “circulation of these viruses may pose health risks for humans[3].” The similar observation on new genetic reassortment new H5N8 influenza virus was also reported from South Korea[4-6]. Jeong *et al.* analyzed the genetic sequences of the new virus and reported that “all of the isolates belonged to clade 2.3.4.6 of the hemagglutinin (HA) gene[6].” Jeong *et al.* concluded that “migratory birds played a key role in the introduction and spread of viruses during the initial stage of the 2014 outbreak[6].” Song *et al.* proposed that “the novel H5N8 viruses had different transmissibility to previous H5N1 HPAI viruses, possibly due to genetic changes[7].” Considering China, there is a similar report to that of Jeong *et al.*[8]. Fan *et al.* found that “the HA, NA, PB1, PA, NP, and M segments of SH-9 were most closely related to the corresponding segments of A/duck/Jiangsu/k1203/2010 (H5N8)[8]. Fan *et al.* concluded that “wild birds could acquire the H5N8 virus from breeding ducks and spread the virus via migratory bird flyways[8].”

2.2. Western global hemisphere

After the emerging outbreak of the novel H5N8 influenza in East Asia, there were also the emerging problem in Europe as well[9,10]. How the new disease reach Europe is still a myth[11]. However, EU presently strictly perform the surveillance to control of this new bird flu[9,10].

3. Human infection risk

As a new emerging influenza, the remained question in public health is the chance of human beings to get infection. In fact, the H5N8 influenza virus has been isolated from the avian for a long time[11,12]. However, the past H5N8 influenza is considered not serious and considered low pathogenic. The recent outbreak in 2014 is the new facet of this virus. The nature of highly pathogenic virus can be seen and the infections in thousands of avian populations bring attention from medical scientists [9,10]. As already mentioned, the new mutation in the novel H5N8 influenza virus could be seen and this is believed to be the reason that the disease outbreak in 2014 occurs[5,6]. However, there is no evidence that the new mutation support the cross species transmission to human beings.

4. Conclusion

The new emerging H5N8 influenza is a new emerging avian

flu. This new avian flu is considered highly pathogenic and causes several infections in avian population. However, at present, there is still no cross species infection to human beings. Further surveillance on the possible new cross species infection by this new virus is suggested.

Conflict of interest statement

We declare that we have no conflict of interest.

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