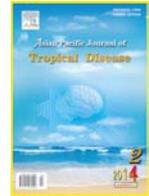




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Cross species influenza: emerging zoonosis

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ABSTRACT

Emerging infection is usually an important public health concern. Within the past decade, there are many new emerging infectious diseases. An important concern is on the pandemic of those new emerging infections. The cross species infection from animal to human, zoonosis, is usually problematic and hard to manage. The well-known situations are on new emerging atypical influenza infections. In this brief article, the author discuss on three important cross species emerging influenza, H5N1 bird flu, H1N1 swine flu and H7N9 bird flu. The basic details of those new influenza's genetic aberration and the concept for surveillance and prediction of new mutation that result in the new cross species emerging zoonosis are also mentioned in this article.

1. Introduction

Emerging infection means the occurrence of an infection in a new setting. If that disease is newly discovered, it will be classified as a new emerging infection. Due to the fact that the new emerging infection is a new disease in medicine, the knowledge for diagnosis and management is usually limited. Emerging infection is usually an important public health concern. Within the past decade, there are many new emerging infectious diseases.

An important concern is on the pandemic of those new emerging infections. Of several new infections, the cross species infection from animal to human, zoonosis, is usually problematic and hard to manage^[1,2]. The well-known situations are on new emerging atypical influenza infections^[1,2]. In this brief article, the author discusses on the three important cross species emerging influenza, H5N1 bird flu, H1N1 swine flu and H7N9 bird flu. The basic details of those new influenza's genetic aberration and the concept for surveillance and prediction of new mutation that result in the new cross species emerging zoonosis are also mentioned in this article.

2. New emerging influenza infections

Influenza virus infection is a kind of respiratory viral

disease. This disease is common and causes morbidity and mortality around the world. Microbiologically, there are many groups of influenza viruses, classified by its *H* and *N* gene components^[1,2]. The specificity of pathogenicity can be seen. This means a kind of influenza virus specifically infects a kind of animal. However, in some situations, the cross species infection occurs and this becomes the great concern for pandemicity.

As already mentioned, there are many new emerging influenza virus infections within the few years. This attracts the interest of the medical scientists around the world. The three important well-known new influenza infections include H5N1 bird flu, H1N1 swine flu and H7N9 bird flu. The underlying genetic aberration of those infections will be further discussed.

2.1. H5N1 bird flu

This is a kind of zoonosis that results from the primary influenza virus of avian. The pathogenic virus is the H5N1 avian influenza virus^[3,4]. It was firstly reported in Asia and caused a wide scale outbreak. Li *et al.* firstly published in Nature about the domestic ducks in Southern China had a central role in the generation and maintenance of this virus, and that wild birds may have contributed to the increasingly wide spread of the virus in Asia^[5]. This infection is considered the first cross species zoonosis that brings attention to the medical society on the harmful of emerging cross species

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influenza zoonosis.

2.2. H1N1 swine flu

This is a very big worldwide pandemic situation. The emerging of the new H1N1 swine flu results in outbreaks around the world affecting million of world population[6]. The genetic reassortment of this new virus, which emerged in 2009, is well defined. This new virus is proved to be the result of a reassortant between viruses of the American triple-reassortant and Eurasian avian-like swine influenza[7].

2.3. H7N9 bird flu

This is the newest emerging cross species infection. It occurs in the first trimester in 2013, China. The pathogenic virus is successfully discovered to be a new human virus. The primary pathogenic virus is a kind of avian influenza virus as already mentioned[8,9], which existence as a human pathogen is a true problematic condition[10]. The new H7N9 influenza virus is a kind of genetic mutated classical avian H7N9 influenza virus[8]. The sequence of this new pathogen consists of the sequence with the origins from at least four primary sequences[11]. Virologically, the *HA* gene comes from duck and the *NA* gene comes from migratory birds[11].

3. Surveillance of new mutation

Surveillance is a needful action corresponding to any problematic infection. It is routinely performed for newly emerging infections including the cross species influenza, especially at present, the surveillance of the new emerging influenza zoonoses. The simplest meaning is the use of recording the new cases of influenza infections with special focus on the identified atypical infections[12]. Serological monitoring is usually done for supporting the surveillance program[13,14]. Nevertheless, with the good molecular biology technology, the present trend is to monitor the genetic components of the circulating influenza virus in both humans and animals[15]. This new technique is proposed to be the best tool for the surveillance of new emerging influenza zoonosis at present[16].

4. Prediction of new mutation

Although the surveillance system has been implemented for a long time it seems not to be the best method for forecasting the emerging of infection. In fact, surveillance is monitoring the existence but it is not the tool for prediction. There are many attempts to set a predictive system for emerging influenza zoonosis. Basically, the mathematical model based on the accumulated data on epidemiological and geographical parameters is developed for this purpose[17].

Nevertheless, with the advent in bioinformatics, the manipulation for genetic prediction can be done. This is better than simple mathematical model which is based on epidemiology data[18]. With use of standard bioinformatic tools, the mutation prone point within the sequence of the existed influenza viruses can be predicted and the possibilities for causing of sense mutation can be further predicted.

Conflict of interest statement

I declare that I have no conflict of interest.

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