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# Human genetic polymorphism and atypical influenza infection: a topic on human genetics in infectious medicine

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## ABSTRACT

The atypical influenza infection is an important concern in modern medicine. Due to the trend of pandemic outbreak of new emerging atypical influenza, the researching on it is very important. In clinical genetics, the study on the genetic factors underlying the susceptibility and resistance to atypical influenza infection is very interesting. In this short article, the author focused and discussed on human genetic polymorphism and atypical influenza infection.

## 1. Introduction

Influenza is a well-known respiratory infection. It causes million cases of infection around the world each year. The atypical influenza infection is an important concern in modern medicine. Emerging of new atypical influenza has been continuously reported since 2000. The well-known situation is atypical swine flu (H1N1) and atypical bird flu (H7N9)[1,2].

Due to the trend of pandemic outbreak of new emerging atypical influenza, the researching on it is very important. In clinical genetics, the study on the genetic factors

underlying the susceptibility and resistance to atypical influenza infection is very interesting[3]. More than 100 genes have been proposed for the interrelationship[3]. Horby *et al.* reported that the Mx genes encoding interferon inducible proteins are the best studied but their relevance to susceptibility in humans is unknown[3]. In this short article, the author focused and discussed on human genetic polymorphism and atypical influenza infection.

## 2. Genetic polymorphism and novel swine flu (H1N1 influenza)

There are many recent publications on the relationship between genetic polymorphism and clinical course of novel swine flu. Morales-García *et al.* studied *TNF*, *LTA*, *IL1B*, *IL6*, *IL8*, and *CCL* polymorphisms and found that

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the polymorphisms of genes involved in the inflammatory process contributed to the severity of the clinical behavior of infection by the pandemic influenza A/H1N1 virus[4]. In another report from China, Zhou *et al.* found that a functional variation in CD55 increases the severity of 2009 pandemic H1N1 influenza A virus infection[5]. Similarly, Zhang *et al.* found that interferon-induced transmembrane protein-3 genetic variant rs12252-C is associated with severe influenza in the Chinese with novel swine flu[6]. The finding of Zhang *et al.* confirmed the previous observation of Everitt *et al.* on the possible on effect of interferon-induced transmembrane protein-3 genetic variant on the morbidity and mortality in cases with novel swine flu[7]. Focusing on the recent study in Mexico, Zúñiga *et al.* reached a conclusion that gene polymorphisms located in chromosomes 1 and 17 contributed to susceptibility to development of severe pneumonia in novel swine flu[8]. In conclusion, many publications report on the effect of polymorphisms on severity of novel H1N1 influenza infection.

### 3. Genetic polymorphism and novel bird flu (H7N9 influenza)

H7N9 influenza is the newest emerging atypical influenza infection. The severity of this disease varied from cases to cases. Some cases are mild whereas the others are fatal[9,10]. A possible thing that might discriminate the cases with fatal and non-fatal outcome might be the genetic factor. Focusing on the present novel H7N9 bird flu, there is still no report on this aspect. However, since the effect of genetic polymorphism, similar to the case of novel H1N1 swine flu, is possible.

### 4. Conclusion

There are many evidences on the interrelationship between some specific genetic polymorphism in human beings and the clinical feature of atypical influenza infections. Many publications report on the effect of polymorphisms on severity of novel H1N 1 influenza infection. Focusing on the present novel H7N9 bird flu, there is still no report on this aspect. However, since the effect of genetic polymorphism, similar to the case of novel H1N1 swine flu, is possible,

future genetic study on this aspect is highly recommended.

### Conflict of interest statement

We declare that we have no conflict of interest.

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