



Phylogenetic analysis of HA and NA genes of influenza H1N1 viruses from 1918 to 2017 worldwide

Huixin Yan and Guoying Dong

Beijing Normal University, College of Global Change and Earth System Science, China (yanhuixin148@outlook.com)

The 1918 “Spanish” Pandemic was the earliest known about influenza H1N1 virus. Then H1N1 viruses circulated between humans and animals continuously. With the increased samples of H1N1 viruses and technology development, researchers have been working on how the viruses evolved during the long period. In which evolutionary studies of HA and NA genes are the most basic and necessary research. Here, we analyzed HA and NA genes of H1N1 viruses from three aspects: host distribution, geographical distribution and phylogenetic analysis. The data showed hosts were predominantly human, swine and poultry, and other hosts were mainly cat, ferret, wild bear, canine, cheetah and seal. In terms of geographical distribution, the North America and Eurasia were the mainly H1N1 influenza pandemic area. Of them, the United States, China, Japan, Canada, the United Kingdom, India and Singapore were the most. On phylogenetic analysis of HA and NA genes of influenza H1N1 viruses from 1918 to 2017 worldwide, the distribution of all avian influenza viruses showed a clear geographical difference, mainly concentrated on Eurasia and America. American and Eurasian swine viruses might be the ancestors of 2009 Pandemic viruses HA and NA genes, respectively. Swine influenza viruses played an important role in the spread of influenza virus across species. To our knowledge, it was the first large-scale phylogenetic analysis of HA and NA genes of influenza H1N1 viruses worldwide until now. Our findings further emphasized the importance of surveillance on the genetic diversity of influenza H1N1 viruses in different hosts and raised more concerns about the long time monitoring.