

Abstract

Influenza virus infection is a major public health problem worldwide. Comparison to the other respiratory viruses, influenza virus can cause severe morbidity and mortality (1). In 21st century, influenza virus causing three global pandemics, it was H1N1 in 1918, H2N2 in 1957 and H3N2 in 1968 respectively. According to warning from specialists in World Health Organization (WHO), every 30 years worldwide influenza spreading may break out recently (2). In addition to antigen drift and antigen shift, gene assortment between either human, avian birds or pigs could make it become a super virulent virus and could cause more severe epidemic situation than 1997 H5N1 in Hong Kong.

This project refers to others references and compiles the methods of diagnosis of flu virus sequence mutation and screen out the virus type, carrying out the general real-time PCR in the instrument of Roche Lightcycler, switch the wavelength channel to 705 nm can performance the fluorescence signal sending out from hybrid probe LC, relying it we can detect the influenza A virus particle in the specimen. In the other hand, making use of another analytic method (melting curve) to collect the continuous fluorescence signal, can find out the subtype of influenza A virus within a short time. The melting peak temperature of H3 and H1 are respectively at 58 °C and 64 °C. Relying the melting peak temperature shift, we could monitor virus sequence mutation synchronously. Combination with real-time PCR and high resolution analysis, we also established a method to distinguish H1, H3 and possible new isolated strain virus.

Establishing the fast and efficient diagnostic methods of influenza virus subtype and gene polymorphism in this project, is not only being helpful for understand the influenza virus gene sequence variation and popular type in the Taiwanese region, but also provide the epidemic situation monitor. And it may contribute to reducing the damage of global influenza virus explosion in the future.

Key word: influenza virus, subtype differentiation, virus gene polymorphism