The influenza pandemic of 1918 or “Spanish flu” killed 20–50 million people. It is considered the “most deadly pandemic in recorded human history. The virus antigen were extremely different to those encountered previously so people carried no immunity to this virus strain and were highly susceptible to illness and even death. It was caused by the H1N1 type of flu virus. It has been found to be very similar to the bird flu of today mainly H5N1 and H7N2.

The emergence of another human influenza pandemic virus is considered inevitable and may be imminent according to influenza experts, hence the characterization of the 1918 virus may enable us to recognize the potential threats posed by new influenza virus strains, and it will shed light on the prophylactic and therapeutic countermeasures that will be needed to control pandemic viruses.

Resurrecting the 1918 influenza virus

Genomic RNA of the 1918 virus was recreated from preserved virus samples and from the frozen cadaver of a victim buried in the Alaska potmation. Influenza virus contains eight pieces of RNA, ranging in size from 0.9 to 2.4 kb, and each RNA segment encodes one or more proteins. With the final sequences in hand, Peter Palese’s team at Mount Sinai School of Medicine found that the eight 1918 genes are very similar to the virus genome contained within bacteria DNA. They inserted these eight plasmids into T7 polyoma, a virus that inserted into the human cell and made working cells. In experiments in 2007, the virus containing the eight genes killed mice in 5 to 7 days, also the mice long produced 39,000-fold more 1918 viruses than contemporary H1N1 human viruses.

Resurrecting the 1918 influenza virus

File virus from the Alaska Potmation since 1919

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Neuraminidase

The neuraminidase (NA) protein of the influenza virus is a glycoprotein expressed on the virus surface. Its principal biological role is the cleavage of the terminal sialic acid residues that are receptors for the viral hemagglutinin (HA) protein. Removal of these residues from the surface of infected cells results in a new form of virus which prevents the virus from spreading. Hemagglutinins from each of the eight strains of the influenza virus.

Neuraminidase

The 1918 flu virus was caused by a H1N1 virus. We did alignment of the 1918 H1N1 from 1918 and the similar found recently and drew the phylogenetic tree shown in Fig. 6. The results show that the H1N1 strain seen in Thailand in 2004 are very close to each other. This may mean that the H1N1 strain may cause a pandemic like the H1N1 of 1918.

Investigation into changes or mutations in the gene for influenza N antigen.

We can run multiple sequence alignment using H3N2 viral sub-strains using Clustal alignment tool. The alignment was translated into the corresponding amino acids. Here we show the first 80 amino acids.

Fig. 7 Multiple Sequence alignment of H3N2 sequences

References

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