Centenario de la Gripe Española de 1918. La peor pandemia en la historia contemporánea mundial: lecciones para el futuro

Centenary of the 1918 Spanish Influenza, the Worst Pandemic in the Recent History of the World: Lessons for the future

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ABSTRACT

Influenza virus and annual influenza seasons

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During years, our work focused on influenza surveillance impulses for research in the field of molecular simultaneous detection of influenza and other respiratory viruses allowing a better knowledge of the circulation of these viruses and the pathogenesis of their infections.

Virological data are important for the quantification of influenza-associated epidemics because the circulating strains of the virus subtypes vary from year to year, which can affect annual spread and intensity of epidemics.

Influenza A and B viruses express two surface glycoproteins which have essential functions in the viral life cycle. The more abundant glycoprotein is the hemagglutinin, a type I transmembrane protein. The hemagglutinin is a trimer and mediates binding of the virus to host cells via interactions between its receptor binding site and the terminal sialic acids on host cell glycans. Many antibodies that target the hemagglutinin are neutralizing because they block the ability of the receptor binding site of hemagglutinin to interact with sialic acids on the host cell surface, thus preventing attachment and entry. Because protection was classically recognized to be related to anti- hemagglutinin antibodies, currently licensed vaccines are designed to induce antibodies against hemagglutinin.

Technical improvements applied to the surveillance of influenza virus, have resulted in a better knowledge of the circulation of these virus each epidemic season. At the beginning of last Century, the isolation of influenza virus in embryonated eggs and cell cultures. Next, the implementation of generic and specific molecular detection methods that permitted the developing of the molecular epidemiology data which are validated for the surveillance systems and improve the studying of specific genes of influenza A and B directly in clinical samples. Now, deep sequencing techniques which permit the simultaneous analysis of every genome segment of the influenza virus, directly in the clinical samples from patients and the results are becoming rapidly available supplementing traditional infection control procedures in the investigation and management of epidemics.

In this talk the virological data of influenza epidemic seasons produced by the Spanish Influenza Surveillance System are presented. How our data contribute to the European Influenza Surveillance System, patterns of circulation of virus and the particularities of our Country at the South of Europe.