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Influenza A virus: Origin and its subtypes

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ABSTRACT
INTRODUCTION: It is known that flu epidemics arise quite frequently, but there are no regular intervals between these events. Epidemics may differ in their consequences, but they often cause an increase in mortality in elderly people. The great flu epidemic of the last century claimed millions of human lives. Scientist Richard E. Shope, who investigated swine flu in 1920, suspected that the cause of the illness was a virus. As early as 1933, scientists at the National Institute for Medical Research in London isolated the virus for the first time. Thus, the present study seeks to understand how the influenza A virus emerged and was identified. METHOD: Approach used this is a literature review, where research was conducted through scientific articles, published in the MEDLINE and SciELO database, where 4 were selected because they fit the inclusion method. RESULTS and DISCUSSION: The viral etiology of influenza was proven in 1933, and the three serotypes that infect humans were only identified in 1950. In that same year, it became clear that the strain responsible for the 1918-1919 episode belonged to the variety particular antigen of subtype A. In 1957, with the emergence of subtype A, influenza reached China and, in 1968, in Hong Kong, subtype A appeared, causing a moderately severe pandemic. Even after almost a century after the recognition of this strain, the flu virus remains one of the greatest health control challenges due to its easy antigenic variability and contagiousness. FINAL CONSIDERATIONS: For the formation of new subtypes, there is recombination, which corresponds to a mixture of, for example, genes from a virus that infects human beings with genes from viruses that infect other animals, such as birds, thus explaining how the retrovirus Influenza type A can become more aggressive due to mutations derived from the mixture of genes from animal viruses, especially birds and swine.

Keywords: Virus, Influenza, The flu.

1 INTRODUCTION

The first description of influenza, also known as Influenza, the Italian word for "influence", in the context of medicine and epidemiology, before the microbial theory, was made by Hippocrates, in the fifth century, year 412 BC who described the disease among the inhabitants of the island of Crete, in Greece; and, attributed the disease to environmental causes and climatic variations, Within the miasmatic theory, influence of the stars and the air.

However, the first medical description with interesting observations is attributed to the physician Molineux in Ireland and England between 1688 and 1693. References to seventeenth-century influenza epidemics are found in North America and Europe. From the beginning of the eighteenth century, data on the disease increased in quantity and quality, as chroniclers and doctors

recorded information and comments on the number of people infected, whether epidemic or pandemic, the countries involved and the possible origins of viral strains.

From the genus Mixovirus influenzae, it belongs to the family Orthomixoviridae, which contains a segmented RNA genome and single strand. It is classified into 03 types: A, B, and C and its isolations occurred in the years 1933, 1940 and 1947, respectively. The type A virus, the most important, can infect both humans and animals and is implicated in episodes epidemic and pandemic; the type B virus, which infects only humans, is linked to moderate outbreaks; and the C virus, more stable, affects humans and pigs, causes subclinical disease, without epidemic potential. According to FORLEO NETO et al (2003), pandemics occur irregularly, usually 30 to 40 years apart. Since the century. At least 30 pandemic episodes have been described.

Due to its ability to penetrate the body through the mucous membranes of the respiratory tract and eyes performing its dissemination through the bloodstream and reach the cells, subtype A presents mutations and rearrangements with higher frequencies in relation to subtypes B and C. That subtype has two surface glycoproteins: hemagglutinin (HA) and neuraminidase (NA) that enable the transport of the virus in the host cells. The function of HA is the fixation and fusion of the virus in the host cell, and is divided into 18 different subtypes, of which 16 circulate in waterfowl and two were isolated from bats. NA subtypes play an important role in the release of viral particles after virus replication, as well as the spread of the virus from one host to another. These proteins are responsible for the viral classification and its morbidity, mortality, lethality and pathogenicity.

The present work aims to carry out a historical approach to the origin and knowledge of the influenza A virus as well as its subtypes, in order to highlight its main occurrences in the world.

2 METHOD

The study is characterized as a bibliographic study of systematic review of the specialized literature, carried out through scientific research available in the database of MEDLINE (Medical Literature Analysis and Retrieval System Online) and SciELO (Scientific Electronic Library Online) using the keywords: Virus, influenza and influenza. Articles or theses published between 2000 and 2016 were used as inclusion methods, since these were the most recent containing relevant information for the study, with texts available in full in the aforementioned databases.

3 RESULTS AND DISCUSSION

In 2009, the world faced its first influenza pandemic of the twenty-first century, caused by the influenza A/H1N1/California/2009 strain that contains swine, poultry and human genes. Popularly known as "swine flu", swine influenza A had its first cases in Mexico in March 2009 and due to its high contagiousness and virulence spread rapidly to Europe, Canada, Southeast Asia, Africa and Latin

America. In June 2009, the World Health Organization officially declared a flu pandemic. In the post-pandemic period that lasted until August 2010, it had reached 214 infected countries, causing death of 18,500 people and infection of 575,400. (The Lancet Infectious Diseases, 2012).

In March 2013, a new strain of the influenza A virus was described in Asian countries. This strain has the proteins hemagglutinin serotype 7 and neuraminidase serotype 9, and is therefore called influenza A (H7N9). This new variant is a recombination of strains circulating among birds that has been shown to infect humans and, as cases outside the Asian continent have not yet been described, classifying the epidemic as geographically restricted.

Among the communities, influenza epidemics and pandemics begin abruptly and peak in two or three weeks, with a total duration of 5 to 8 weeks. The impact of influenza epidemics is a reflection of the interaction between viral antigenic variation, the level of protection of the population for circulating strains, and the degree of virulence of viruses. Minor antigenic variations occur every two or three years for subtypes of virus A and every 5 or 6 years for viruses of type B. Such variations are due to point mutations in segments of the viral genome that result in changes in the amino acids that make up surface glycoproteins, particularly in hemagglutinin. The largest antigenic variations are those associated with the complete replacement of one or both segments of the viral genome, which control the production of surface glycoproteins.

> The challenge is, for WHO screening, to correctly predict or detect emerging strains at an early stage, because due to the 6 or more months required to prepare a vaccine, there is a possibility that to date a vaccine is manufactured to support a global campaign, it is no longer compatible with circulating viruses. Any vaccination approach that targets the classic neutralizing responses to HA and/or NA must deal with antigenic drift effectively. (KIM et al., 2018)

The worst epidemic of the influenza virus occurred in the early twentieth century, between the years 1918 and 1920, still with dubious origin, began in Asia or in the military camps in the interior of the United States of America, due to the intense movement of troop transport of allied nations and, had as a biological agent causing the disease was identified as the virus of type A (H1-N1). The Spanish designation is given by the fact that Spain, neutral in World War 1, made official notification to the World Health Organization about the disease that devastated lives in the country with great power of contagion, morbidity and lethality. In Brazil, for example, although the number of infected and dead are variable, it is estimated that 35,240 people were fatal victims of the virus, among them the 5th president of Brazil, the lawyer and Counselor of the Empire, Mr. Francisco de Paula Rodrigues Alves. This disease was introduced into the country by crew members of the English ship "Demerara" that left Liverpool, England, docked and disembarked passengers in the ports of Recife, Salvador and Rio de Janeiro.

> This pandemic was marked by extreme scope, aggressiveness and contagiousness, believed to have killed 38 million people in Europe and America. Although in many parts of the world there is no data, it is estimated that it has infected 50% of the world's population, 25% have suffered a clinical infection and the total mortality has been between 40 and 50 million. The number of 20 million deaths, often cited, is noticeably very low (Costa, L et al., Influenza Pandemics).

Again on the Asian continent, this time originating in China during the 50s, the Influenza A/Singapore/1/57 (H2N2) virus, with the glycoproteins HA and NA different from all the previous types, led to the death of 4 million people affecting about 25% to 50% of the world's population. The virus was first isolated in Japan in 1957, followed by the United States and England in the same year. Years later, during 1968 and 1969, a genetic variation of H2N2, H3N2 gave rise to the Hong Kong Flu, whose virus was identified and isolated in this Chinese city in 1968, with a higher incidence of 40% in the population aged 10 to 14 years, and hospitalization and mortality among the elderly, young people and individuals at defined risk for chronic and cardiopulmonary diseases.

In 1930, researchers began the development of the flu vaccine in order to find a solution containing the damage caused by the influenza virus. After 10 years, in 1940, the first influenza vaccine was approved in the northern hemisphere, while in Brazil, the applications began 40 years later, in 1980, being composed of different strains of the Myxovirus influenza virus and inactivated, fragmented and purified and, usually containing elements of the surface of the virus, such as hemagglutinin and neuraminidase, being an inactivated vaccine, that does not cause the disease and provides protection based on the induction of the production of neutralizing antibodies of the virus, mainly against the viral hemagglutinin contained in the vaccine. The immunity conferred by the vaccine develops after 15 days of vaccination and its duration is about 6 months to 1 year. As the maximum titers of antibodies, obtained within 1 to 2 months after vaccination. Currently, there are four brands of the tetravalent influenza vaccine available: Fluarix Tetra (GSK), Fluquadri (Sanofi-Pasteur), Influvac Tetra (Abbott) and Vaxitetra (Sanofi-Pasteur).

4 CONCLUSIONS

The retrovirus Influenza type A may acquire greater aggressiveness due to mutations derived from the mixture of genes of viruses of animals, especially poultry and pigs. In order for new subtypes to form, recombination occurs, which corresponds to the mixing of, for example, genes from a virus that infects humans with genes from viruses that infect other animals, such as birds. The severity of the infection is attenuating as the population is immunized, either by vaccines or by the flu clinic itself.

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