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Recent trends in rapid detection of influenza infections by bio and nanobiosensor

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ABSTRACT

A literature update has been made about the progress and improvements in the use of biosensors for sensitive, rapid and specific detection of influenza virus. Background information about influenza virus and its structure together with a general discussion about the characteristics and significant aspects of different types of biosensors were used as a frame to put inside the main recent developments on the use of nanobiosensors for the detection of influenza virus. Working criteria of biosensors and their applications in different species of influenza virus diagnosis have been the primary concern of this review, which critically discusses the main advantages and limitations of studies in this field during the last two decades and their applications.

1. Introduction

1.1. Influenza

Since the 16th century an acute, serious and infectious respiratory illness, known as influenza, has been frequently occurred in community outbursts [1]. Influenza epidemics approximately in 30,000,000–5,000,000 people caused acute respiratory illness and led to 2,50,000–5,00,000 people's death globally every year because of different kinds of influenza [2]. Influenza viruses, as enveloped viruses with negative sense RNA segmented genomes, are members of the orthomyxoviridae family, and their differentiation was based on expression of hemagglutinin and neuraminidase surface glycoproteins. Influenza virus categorized into three species, A, B and C (Fig. 1) that cause two types of influenza in which influenza A and B viruses lead to epidemic influenza (interpandemic or seasonal), and influenza A viruses lonely caused sporadic pandemics, while mild diseases usually generated by influenza C viruses. Among these three types of illnesses the most virulent type is related to influenza A viruses which are epidemic and lead to acute and fatal severe respiratory diseases which is sometimes globally pandemic [3]. In addition, influenza A and B viruses cause vast number of diseases in humans, whereas influenza C virus leads to diseases mainly in animals [4].

Linkage between influenza virus and host respiratory tissue depends on surface glycoproteins. In the surface glycoproteins of influenza virus different mechanisms of antigenic variety create epidemiological types of influenza which are called antigenic shift and antigenic drift (Fig. 2). A continuous action termed as antigenic drift takes place in both, influenza A and B viruses which is stem from collection of point mutations in the neuraminidase genes and viral hemagglutinin. Due to the lack of proofreading potential in viral RNA-dependent RNA polymerase, viral mutations occur in a high rate and leads to antigenic drift [1]. The virus can escape from the induced immunity through the permission that antigenic drift gives, therefore, it can result in seasonal epidemics [1]. Influenza epidemics expand very fast with average reproductive number (R) of 1.28 and 10–20% attack rate; the R explaining an average number of infected persons. If value of reproduction number is larger than 1,

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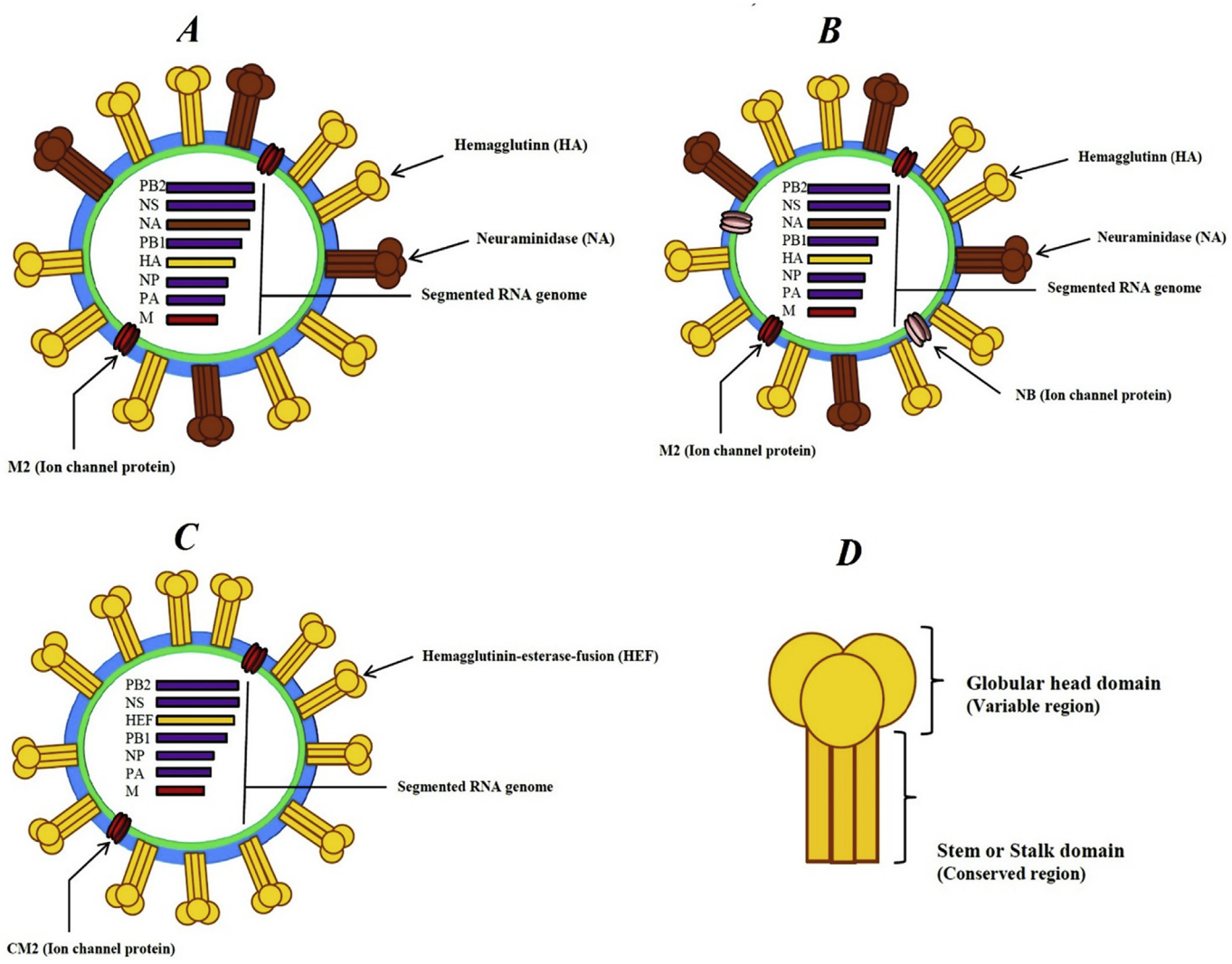

Fig. 1. Demonstrated structure of influenza viruses. A) influenza A virus, B) influenza B virus, C) influenza C virus, and D) two domains of hemagglutinin-esterase-fusion (HEF).

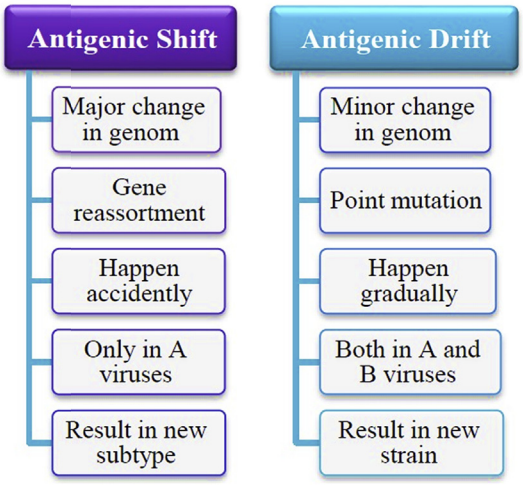

Fig. 2. Differences between antigenic shift and antigenic drift.

it will demonstrate that the infection might grow and last in the population. The attack rate, thus, is a significant parameter describing transmission of a disease [5–7]. Predominance of H3N2 strains in influenza epidemics give rise to the highest total morbidity and mortality of them. On the other hand, influenza A virus and introduction of novel virus strain to human in which an enormous ratio of population has immunity shortage related to a sporadic event named antigenic shift [1].

When a new influenza virus sustainably and effectively expands from one person to another, it can lead to universal pandemia. Within the past 100 years four types of influenza pandemia happened in the world: in 1918 H1N1 Spanish, in 1957 H2N2 Asian, in 1968 H3N2 Hong Kong, and in 2009 H1N1 swine influenza pandemia. The 1918 pandemia was the most acute, severe and which caused the death of 50 million people [7].

Table 1 provides a resume of factors related to the increase of morbidity and mortality of influenza pandemia concerning the main factors of age, pregnancy and immuno-deficiency stage and genetic susceptibility, taken from Ref. [5].

Due to severe range of influenza symptoms and through overlapping with those created from different respiratory viruses, influenza diagnosis is a difficult task. So, diagnostic tests of influenza should be done in the early stages of illness [8]. Generally, the conventional laboratory methods for viral diagnosis are hard and laborious, time consuming, expensive and top of that they require high standards of biosafety in the laboratories and equipment. The