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Research Progress on the Differences Between Influenza A and B Viruses and Their Epidemiological Characteristics

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Abstract: Influenza is a prevalent acute respiratory disease caused primarily by influenza A (IAV) and B (IBV) viruses, both of which significantly impact global public health. Understanding the distinctions between IAV and IBV, especially regarding their structure, immune responses, and epidemiological patterns, is essential for developing effective preventive and treatment strategies. This study comprehensively compares IAV and IBV, examining differences in virus structure, including their segmented RNA genomes, and the unique mutations that characterize each. It explores how these differences affect immune response, pathogenicity, and clinical manifestations, highlighting IAV's diverse subtypes and IBV's distinct lineages. Epidemiological comparisons underscore differences in transmission modes, seasonal patterns, and infection rates, which are critical for tailoring public health responses. The study also discusses current vaccine developments and their respective impacts on managing IAV and IBV. Findings emphasize the necessity for continued research, particularly for a universal vaccine, improved early detection, and understanding the long-term health impacts of influenza, to advance public health protection.

Keywords: Influenza A virus, influenza b virus, virus structure, immune response, epidemiology.

1. Introduction

Influenza (Flu) is a common acute respiratory disease caused by influenza virus, It is mainly caused by influenza A virus (IAV) and influenza B virus (IBV), Their existence and spread deeply affect global public health security. A thorough understanding of the research progress on the differences between influenza A and B viruses and their epidemiological characteristics plays an important role and is of great significance for the prevention of influenza, the control of influenza transmission, and the protection of human life and health. Flu is a kind of acute respiratory infection caused by influenza virus (IVs). IAV, IBV, and ICV are three members of the Orthomyxoviridae family, which belongs to the RNA virus [1]. Among them, the most prevalent viruses in humans are mainly IAV and IBV. The above two viruses belong to the Orthomyxoviridae family and are eight-segmented, single-stranded negative-sense RNA viruses [2]. According to the glycoproteins, neuraminidase and hemagglutinin on the surface of influenza A virus, IAV can be further classified into types such as H1N1 and H5N1. Influenza B can be divided into two major lineages, Yamagata and Victoria, according to the nucleotide sequence of the hemagglutinin gene and certain antigenic properties.

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Influenza viruses can spread rapidly in a short period of time and have extremely strong transmissibility, which will bring serious impacts and burdens to society. The research on influenza A and influenza B plays a very important role in public health. However, relatively few studies have been conducted on comparing the two. In-depth research on the differences between the two can improve the understanding of public health and be of help.

This paper will elaborate in detail the differences in virus structure between IAV and IBV, including differences in genotypes and characteristics of gene structure mutations. This paper will discuss the differences in immune response and pathological mechanism between influenza A and B viruses, and the impact of their differences on clinical manifestations. The epidemiological characteristics of influenza A and B will be compared, including the comparison of transmission routes and the analysis of differences in morbidity. The research and development of influenza A and B vaccines and their impact on public health will be discussed.

2. Comparison of the Structure and Genome of IAV and IBV

IAV and IBV are both influenza viruses and belong to the Orthomyxoviridae family. The influenza virus is generally spherical in shape with a diameter of 80-120 nanometers. The structure of the virion includes the viral genome, nucleocapsid and envelope.

2.1. Genotypic differences

2.1.1. Genotypic characteristics of IAV

IAV, a common influenza virus, is most prone to mutation. Influenza A virus is a negative-strand RNA virus. The IAV genome is composed of eight single-stranded viral RNA segments. Each RNA segment is composed of a central coding region and noncoding regions (NCRs) at both ends. These eight segments are named PB2, PB1, PA, HA, NP, NA, M, and NS respectively, representing different genes. These segments exist in separate viral ribonucleoprotein (vRNP) complexes, and these complexes make up the virus particle.

2.1.2. Genotypic characteristics of IBV

IBVs, often break in large numbers in local areas. The genome of IBV has eight segments of single negative strand. Among them, the hemagglutinin (HA) gene is located in segment 4, and the neuraminidase (NA) gene is located in segment 6 [3]. HA exists in the form of a trimer on the viral envelope, recognizes and binds to the receptor binding sites (RBS) on the surface of host cells, and is specific [3]; at the same time, it stimulates the host to produce protective neutralizing antibodies and is a common target for designing influenza vaccines [3]. NA is composed of four glycoprotein chains. The monomer head is the NA active center and has type specificity; in addition, NA has neuraminidase activity (involving the release of mature viruses in infected cells) and antigenicity (antigen specificity). Among the eight segments of influenza B, the biological functions of HA and NA genes are the most important [4].

2.1.3. Comparative analysis of genotypic differences between the two

Since only influenza viruses are included in Orthomyxoviridae. Influenza viruses are divided into human influenza viruses and animal IAV and IBVs both belong to human IVs, and the two have similar morphological structures. The influenza virus genome is segmented single-stranded negative-sense RNA with a full length of 13.6 kb. The 12 to 13 nucleotides at the end are highly conserved and are related to virus replication. Virus replication occurs in the nucleus [5].

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2.2. Classification and variation

According to the different antigenicity of NP and MP, influenza viruses are divided into three types: A, B, and C.

NP is the viral ribonucleoprotein of the virus. It is the main structural protein and covers the surface of the core of the virus body. The antigenic structure of NP is stable and rarely mutates. It is a part of the viral nucleocapsid.

MP is a part of the viral envelope. It is the matrix protein on the inner layer and has the function of maintaining the shape and integrity of the virus

2.2.1. Variation of influenza A virus and influenza B virus

Influenza A virus is further divided into several subtypes according to the different antigenicity of surface HA and NA. As of now, influenza A virus mainly be divided into 16 HA subtypes and 9 NA subtypes.

Influenza B virus only has differences in the degree of variation and has not been classified into subtypes.

2.2.2. Mutation and influence of influenza virus

Variations of influenza virus include antigenic variation, temperature sensitivity variation, host range variation and sensitivity variation to non-specific inhibitors and so on [5]. The main form of influenza virus variation is antigenic variation. The main variant components are the surface antigens HA and NA of the virus. Among the two types of influenza viruses that infect humans, influenza A virus has strong variability while IBV has weak variability. IAV and IBV often appear in the form of seasonal epidemics. Influenza A virus can even cause a worldwide influenza pandemic due to its extremely strong variability.

3. Immune response and pathological mechanism

3.1. Immune response

3.1.1. The Immune Response to Influenza A Virus

IAV can directly infect almost all types of human innate immune cells through corresponding pathological modifications [6]. Including dendritic cells, mast cells, neutrophils, monocytes, and macrophages. IAVs can directly infect primary human T cells, especially CD8+ Effector Memory T Cells with protective memory function, and induce apoptosis of infected cells [6].

3.1.2. The immune response to IBV

Similar to the way IAV binds to target cells, the HA of IBV recognizes and binds to sialic acid receptors on the surface of respiratory epithelial cell membranes, inducing cells to endocytose it. After cells endocytose virus particles, the low pH environment triggers a conformational change in IBV HA, causing the virus particle membrane to fuse with the host cell membrane [7].

3.1.3. The correlation between the immune responses of IAVs and IBVs

After being infected with the IV, the body can form a specific immune response. The sIgA antibody secreted locally in the respiratory mucosa can block virus infection and play a protective role, but the retention time is relatively short. There are neutralizing antibodies in the serum, which are anti-HA specific antibodies. They have the effect of anti-viral infection and reducing the severity of the disease

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and can exist for a long time. Anti-NP specific antibodies have type specificity and can be used for virus typing.

3.2. Pathological mechanism and clinical manifestations

3.2.1. The pathogenicity of IAV

IAVs affect and damage the respiratory tract in two ways: direct viral infection and damage caused by immune system responses. IAVs can infect not only humans but also animals such as poultry, pigs and horses.

3.2.2. The pathogenicity of IBV

IBVs can infect humans and pigs. After IBVs is inhaled through the respiratory tract, it invades the epithelial cells of the respiratory tract and replicates. With the action of neuraminidase, it is released, causing degeneration and necrosis of other epithelial cells and an inflammatory reaction.

3.2.3. Pathological changes and clinical symptoms

Influenza virus binds to sialic acid receptors on the surface of respiratory epithelial cells through HA. The viral genome infects respiratory epithelial cells and undergoes transcription and replication in the nucleus. It quickly produces progeny viruses and spreads and infects adjacent cells, causing extensive degeneration of cell vacuoles. After influenza virus infects the human body, patients often experience chills, headache, fever, stuffy nose, cough, and runny nose. In severe cases, it can induce cytokine storm and lead to infectious toxemia. Within 1 to 2 days after the symptoms appear, the virus is massively excreted with secretions and rapidly decreases in the body. Influenza virus has a high incidence rate but a low mortality rate. The main pathological changes are as follows: shedding and metaplasia of respiratory ciliated epithelial cells, accompanied by pathological changes such as mucosal cell edema in the lamina propria and mononuclear cell infiltration. Severe cases may cause pneumonia, and critically ill patients may have diffused alveolar damage.

4. Comparison of epidemiological characteristics

4.1. Mode of transmission

4.1.1. Transmission of IAV

IAV is prone to variation and has high infectivity. Many influenza virus pandemics around the world are related to it. The main sources of infection of influenza A are humans and poultry. Among humans, it is mainly transmitted through droplets. Among poultry, it is mainly transmitted through contact.

4.1.2. Transmission of IBV

Since IBV lacks a definite animal host, it is generally considered that it will not cause a worldwide epidemic [8]. IBVs is a respiratory virus with humans as the main source of infection. It is mainly transmitted through droplets such as coughing and sneezing. The virus can survive in the air for about 30 minutes.

4.1.3. Modes of transmission and comparison

Influenza viruses are widely prevalent seasonally and are mainly transmitted from person to person through respiratory droplets and aerosols. In temperate regions on Earth, the incidence of influenza

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virus is significantly increased in spring and winter. In tropical or subtropical regions, the epidemic time is more diverse.

4.2. Pathogenicity rate

According to influenza virological patterns and influenza surveillance data from 11 countries in Southeast Asia by the WHO [9]. Except for the co-circulation of influenza A and B in 2012 and 2016, IAV was the main epidemic type in other years. Influenza A (H1N1) pdm09 virus was dominant in 2009, 2010, 2015, and 2017, accounting for 77%, 76%, 72%, and 54% respectively; Influenza A (H3N2) virus accounted for about half of the positive specimens in 2011, 2013, and 2014, accounting for 46%, 51%, and 47% respectively.

4.3. Influenza epidemic and prevention and control

IAV has strong transmission ability. The infectivity and transmission ability of IBV are weaker than those of IAV, and it only infects humans. In recent years, influenza epidemics dominated by IAV or IBV have occurred all over the world [10]. The main source of influenza virus is patients. Animals may also exist as intermediate hosts or main reservoir hosts.

5. Vaccines and public health impacts

Vaccines have had a profound impact on public health. They play a crucial role in preventing the spread of infectious diseases and are one of the great achievements of modern medicine, saving countless lives.

5.1. Research and application of vaccines

As of now, human vaccines for preventing influenza mainly include vaccines for four influenza virus subtypes (influenza A virus H1N1, influenza A virus H3N2, influenza B virus Victoria lineage, and influenza B virus Yamagata lineage).

5.1.1. M2 channel inhibitor of IAV

The M2 protein is a tetrameric integral membrane protein present on the surface of influenza viruses. This protein is the main target of adamantane antiviral drugs. The main effects of adamantane drugs include blocking the ion channel activity of M2. Adamantane drugs, including amantadine and rimantadine, have antiviral properties against all IAV, but are ineffective against influenza C viruses (ICV) or influenza D viruses (IDV) [11].

5.1.2. NA nhibitor of IBV

NA is a homotetrameric glycoprotein that is fixed by the fibrous stalk on the influenza virus membrane. It is one of the important targets of antiviral drugs. Some researchers inoculated guinea pigs intramuscularly or intranasally with recombinant influenza B virus NA. The results showed that the guinea pigs inoculated with NA showed a reduced virus titer. The data shows that supplementing vaccine formulations with NA and vaccinating through the intranasal route can widely prevent the spread of influenza B virus [12,13].

5.2. Impact on public health

Strengthening the understanding and differentiation of influenza A and B viruses, improving the speed of distinguishing between influenza A and B viruses, and strengthening the analysis and

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research on influenza A and B conditions can reduce the infection rate and contribute to human life and health.

At present, one of the best choices for preventing influenza is to get vaccinated against influenza. Vaccination can prevent 50% or more of influenza infections in a timely manner. The types of prevalent viruses often change, so influenza vaccines also need to be replaced annually. Before immune cells become ineffective, replacing and injecting an immunogenic and effective vaccine can greatly reduce the prevalence of influenza viruses. If a universal influenza virus vaccine can be popularized and promoted on a global scale, it will greatly and widely prevent the spread of influenza viruses.

6. Conclusion

This study comprehensively analyzed the differences between influenza A and B viruses in various aspects. In terms of virus structure and genome, the genotypic characteristics, including the composition of RNA segments and the location of key genes like HA and NA, were compared. The classification and variation showed that influenza A has more subtypes based on HA and NA antigenicity compared to influenza B. In immune response and pathological mechanism, differences in how they interact with immune cells and the resulting pathogenicity and clinical manifestations were explored. Regarding epidemiological characteristics, the transmission modes, pathogenicity rates, and epidemic patterns were contrasted. Vaccines for influenza A and B were also discussed, with the M2 channel inhibitor for IAV and NA inhibitor for IBV being highlighted.

The significance of this research lies in enhancing the understanding of the two viruses, which is crucial for influenza prevention and control. It provides valuable insights for differentiating and treating them, and contributes to public health by reducing the infection rate. However, this study has limitations. It may not have covered all possible aspects of the viruses, and further research could explore more detailed molecular mechanisms and potential interactions with other factors. Future studies should focus on developing more effective vaccines, especially a universal influenza vaccine, and improving the early detection and diagnosis methods. Additionally, more in-depth research on the long-term impact of influenza viruses on human health and the environment is needed. Overall, continued research is essential to better combat influenza and protect public health.

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