Human Coronavirus (HCoV)

Subjects: Virology | Immunology
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Coronaviruses (CoVs) were identified in the 1930s as zoonotic spherical pathogens causing mostly respiratory or enteric diseases. Coronaviruses vary in size and are enveloped with club-shaped spikes on their surface. A helically symmetrical nucleocapsid comprising positive-sense single-stranded RNA is one of the largest virus genomes, ranging from 26 to 32 kilobases in length. Although CoVs are distributed mainly among mammals and birds, since 1960 seven species of human coronaviruses (HCoVs) have been described and some HCoVs infections (SARS-CoV, MERS-CoV and SARS-CoV-2) have resulted in lethal epidemics. The global range and high fatality rate of the newest HCoV pandemic has made SARS-CoV-2 the focus of the scientific world.

Keywords: COVID-19 ; human coronavirus ; HCoV ; immune response ; immune system ; MERS ; SARS ; SARS-CoV-2

1. Introduction

Next-generation sequencing of the viral genome and a phylogenetic analysis have shown the high homology of SARS-CoV-2 to other HCoVs that have led to local epidemics in the past. The experience acquired in SARS and MERS epidemics may prove useful in understanding the SARS-CoV-2 pathomechanism and lead to effective treatment and potential vaccine development.

2. Different types of HCoV

Since 1960, when the first human coronavirus (HCoV) was identified, seven HCoVs species have been described [1]. Four of them, HCoV-229E, HCoV-OC43, HCoV-NL63 and HCoV-HKU1, lead to mild diseases such as the common cold, while the SARS-CoV, MERS-CoV, and SARS-CoV-2 caused severe disorders, manifesting acute respiratory system failures and fatalities[2]. The first identified HCoV, SARS-CoV, originated from southern China in 2003 and induced an epidemic of Severe Acute Respiratory Syndrome (SARS) with a mortality rate of 10–15%[3][4][5]. The first case of MERS-CoV, inducing Middle East Respiratory Syndrome (MERS), was reported in Saudi Arabia in 2012. The fatality rate of MERS was estimated at 34.4%[6][7][8]. The most recent HCoV causing severe pneumonia, first detected in Wuhan City, Hubei Province, China, was reported to the World Health Organization (WHO) in December 2019[9]. Next-generation sequencing of the viral genome showed high homology to the SARS-CoV and MERS-CoV (79% and 50%, respectively)[5][10][11][12]. According to its phylogenetic tree and taxonomy analysis, the virus was identified as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and SARS-CoV-2-associated severe respiratory disease was called Coronavirus Disease-19 (COVID-19)[13]. Although pathogenic HCoVs, including the bat-derived CoV-like coronaviruses (the source of SARS-CoV-2) originated from different animal hosts, all of them are classified as being part of the β-CoV genera[1][5].

Although there are similarities between the genome sequences of SARS-CoV, MERS-CoV, and SARS-CoV-2, the transmission force and spectrum of diseases caused by the above HCoVs seem to be different. The fatality rate of COVID-19 in June 2020 oscillated around 5.3%; however, the changing scale of the pandemic may influence this ratio. Transmission of SARS-CoV-2 is more effective than in SARS-CoV or MERS-CoV because of human-to-human SARS-CoV-2 transfer[14][15], but the transmission ways are the same[16][17]. Moreover, virus transfer occurs independently of the onset of symptoms[18][19]. The presence of an intermediate host of SARS-CoV-2 facilitating the emergence of the virus in humans also cannot be excluded, such as civet cats being intermediate hosts for SARS-CoV and dromedary camels for MERS-CoV[20][21][22][23].

The similarities between SARS-CoV and SARS-CoV-2, manifested in high genome homology, mechanism of cell admission, and connection to specific human receptors, allow an easier understanding the pathomechanism of SARS-CoV-2 action and its influence on the immunological system of COVID-19 patients. Furthermore, the experience acquired within previous epidemics of SARS and MERS, having similar clinical symptoms and course of the disease to COVID-19, may provide a useful tool in determining the treatment and support vaccine development.

3. Immune Response

The presence of the pathogens generates an immune response in the host organism, directed against the structural components of the extraneous unit. Among the principal structural proteins, common for all HCoVs, the most involved in effective infection and related to immune response are envelope (E) and the nucleocapsid (N) proteins, which participate in viral assembly and budding, and the spike (S) protein, binding to the specific receptors present in the host cells[24][25][26][27]. It has also been documented that the structure of SARS-CoV-2 receptor-binding domain is similar to that of SARS-CoV[28][29][30][31]. Although both cell-mediated and humoral immune responses generated against the structural proteins of SARS-CoV and MERS-CoV have been reported, the immunological information about SARS-CoV-2 remains poorly described and incomplete.

The first studies related to COVID-19 suggested a protective role of both cell-dependent and humoral immune responses in humans. Similar to SARS-CoV and MERS-CoV, the SARS-CoV-2 infection primarily affected T lymphocytes, particularly CD4+ and CD8+ T cells, resulting in a reduction in their numbers and changes in cytokines secretion, including enhanced IFN-γ production by CD4+ T cells. Several studies have also shown the diagnostic utility of serology in SARS, MERS, and COVID-19 investigation. Moreover, the correlation between the severity of the disease and potential immunological markers was documented, which may be a useful prognostic tool of the disease progression, and thereby, in the further course of the pandemic. Based on previous experience, immune-informatic tools were used to define the structure of cytotoxic T lymphocyte and B cell epitopes. However, since SARS-CoV-2 antibody persistence and re-exposure occurrence are still unknown, further studies and a better understanding of the molecular mechanisms of immune responses to SARS-CoV-2 are essential in the new therapeutics development and evaluation of the efficiency of potential vaccines against SARS-CoV-2.

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