

Editorial Note: Ongoing Pandemic Covid-19

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The ongoing epidemic of viral pneumonia that started in December 2019 in the city of Wuhan, China, has now spread to different countries worldwide. A novel type of coronavirus that causes coronavirus disease 2019 (COVID-19), closely related to SARS-CoV, is the etiologic agent, extreme acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Our understanding of the novel virus is either based on or just beginning to emerge from the existing knowledge of SARS-CoV. Studies have shown that SARS-CoV-2 shares a SARS-CoV receptor, offering clues at the cellular level about its cell entry, route of viral infection, and pathogenic mechanisms.

By interacting with the virus to cause entrance infection, lung damage, and repair, stem cells in the respiratory tract/lung parenchyma appear to play a major role. To modulate the immune dysregulation underlying ALI/ARDS to restore lung function, exogenous mesenchymal stem cells (MSCs) represent a promising cell therapy. Exogenous stem cell transplantation may lead to lung repair and regeneration. It is important to develop vaccines and therapeutics to be ready for the worst-case scenario of coronavirus reemergence. Stem cell-derived natural killer cells (NK cells) and cytotoxic T lymphocytes (CTLs) specific to the off-the-shelf virus may be helpful in meeting this urgent medical need.

In Wuhan, Hubei Province, China, a series of pneumonia cases of unknown cause arose in December 2019. Chest computed tomography (CT) scans showed fever, dry cough, dyspnea, and bilateral ground-glass opacity in patients. Organ failure, such as shock, ARDS, acute heart injury, acute kidney injury, and even death have occurred in serious

cases. By deep sequencing of the bronchoalveolar lavage fluid from patients, a novel coronavirus subsequently called SARS-CoV-2 was identified and was assumed to be the etiologic agent of the new viral pneumonia. Phylogenic research showed that SARS-CoV-2 forms a distinct SARS-CoV clade but shares SARS-CoV homology with 79.5 percent. The World Health Organization (WHO) and the International Committee on Virus Taxonomy (ICTV) formally announced the disease as COVID-19 on February 11, 2020, and designated the virus itself as SARS-CoV-2. Some patients originally infected had a history of exposure, possibly involving animal interaction, to the Huanan Seafood Wholesale Wet Market. Therefore, the virus is believed to have a zoonotic nature, during which human-to-human transmission took place. Its genetic sequences have shown high similarity (96 percent) to bat coronaviruses, suggesting the ultimate cause is the possibility of bats. While an intermediate reservoir such as a pangolin has been suggested, it remains largely unknown the exact origins of the virus and how it crosses the species barrier and jumps to humans. From Wuhan, the infectious disease outbreak spread quickly to other regions in China and the world.

To date, the mode of SARS-CoV-2 interactions with host cells at the initiation of infection is very little understood. Fortunately, Chinese scientists' rapid release of genomic sequences showed that both SARS-CoV-2 and SARS-CoV belong to the β -genus of coronaviruses. A wide family of single-stranded enveloped RNA viruses are coronaviruses. For four structural proteins, including spike (S) glycoprotein, matrix (M) protein, small envelope (E) protein, and nucleocapsid (N) protein, the positive-sense RNA genome encodes.

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