THE SCIENCE WORLD
A Monthly e Magazine
ISSN: 2583-2212
July 2022; 2(7), 878-882

Popular Article

A Review of the Novel Zoonotic Disease: COVID-19

Pyare Lal[*], Kalpana Josasia[**], Mayank Kumar Agarwal[***]
[*]Ph.D Scholar, Department of Veterinary Biochemistry, College of Veterinary & animal Science, RAJUVAS, Bikaner-334001, Rajasthan, India
[**]Assistant Professor, Apollo College of Veterinary Medicine, Jaipur, Rajasthan, India
***Assistant Professor, Arawali Veterinary college, Sikar, Rajasthan, India

Abstract

At the end of December 2019, a cluster of pneumonia cases with an unknown origin appeared in Wuhan, China. The market for seafood and animals was heavily linked to the cluster of pneumonia casess. The cause of the outbreak was swiftly determined to be a novel Betacoronavirus, which has genetic ties to SARS-CoV and other bat-borne SARS-related Betacoronaviruses. Cases multiplied quickly and spread to further Chinese provinces as well as to four additional nations. A "cordon sanitaire" was implemented in Wuhan on January 23, 2020, and it was later expanded to other cities in Hubei Province. On January 30, 2020, the World Health Organization's director general proclaimed the outbreak to be a Public Health Emergency of International Concern. The World Health Organization designated the disease “COVID-19” and the International Committee for the Taxonomy of Viruses gave the virus the name SARS-CoV-2. Some of precautions of COVID-19 are social distancing, isolation, contact tracing, intensive surveillance, quarantining of cases, intensive monitoring, and postponing large gatherings and community containment. After SARS-CoV and MERS-CoV, the COVID-19 virus is the third zoonotic coronavirus, although it seems to be the only one with pandemic potential. There is an urgent need to understand more about the new COVID-19 virus strains with their transmission dynamics, clinical severity, animal origins and genetic stability.

Key Words: COVID-19, WHO, Betacoronaviruses, Wuhan, Pneumonia

Introduction

On December 31, 2019, the Wuhan Municipal Health Commission reported that several pneumonia cases with unclear etiologies had been seen in the Chinese city of Wuhan. These cases were epidemiologically connected to the Hua Nan seafood and animal market. Utilizing a surveillance system created to gather information on instances of "pneumonia of undetermined cause" that had been established for influenza, local hospitals were able to identify the patients. On January 1, 2020, the market was subsequently shut down. A week later, on January 8, 2020, it was revealed that a previously unidentified Betacoronavirus had been isolated and reported. On January 12, 2020, the WHO received the entire genome sequence and it was put on GenBank. The Director General of WHO, Dr. Tedros Adhanom Ghebreyesus, rightly praised the Chinese government's quick response and transparency in releasing a warning about an unidentified agent causing pneumonia and then sharing information on the virus's identity and genetic makeup within two weeks.

The SARS-CoV-2 Novel Coronavirus

The new coronavirus was claimed to have been isolated and gnomically characterized by several researchers. It was discovered to be genetically related to SARS-CoV, with which it shared 79 percent nucleotide sequence homology, but it was genetically closest to a bat coronavirus, which had been isolated 7 years earlier from an intermediate horseshoe bat (Rhinolophus affinis), with which it shares 96 percent nucleotide homology. The virus was initially known as 2019-nCoV but later on the Study Group of International Committee for the Taxonomy of Viruses' renamed the Coronavirus, which was known as SARS-CoV-2. It belongs to a novel taxonomic group in the subgenus Sarbecovirus of the genus Betacoronavirus, which also includes the SARS-CoV and many bat SARS-like CoVs. The WHO officially designated the disease as coronavirus disease-19 (COVID-19).

Transmission of COVID-19

It is now widely accepted that SARS-CoV-2 spreads from person to person in contexts including hospitals, communities, and families. The primary routes of transmission from the respiratory tract are through droplets and indirectly through fomites, with aerosols playing a less significant role. According to some studies, transmission can happen throughout the incubation period. In one case, nasopharyngeal specimen from an asymptomatic 6-month-old newborn that were positive on admission day and remained positive through day 16 revealed the infant to have a high viral load. Thus, it is likely that a large number of cases go untreated and present a serious

risk for increased virus dissemination. The average incubation period appears to be between 4.75 and 7 days, with a range of 3 days to a maximum of approximately 11–14 days. The amount of viruses is a subject of growing knowledge. Higher viral loads were seen in one investigation of symptomatic patients shortly after the onset of symptoms, with the viral loads being higher in the nose than the throat. The viral load was the same in one asymptomatic patient as it was in the symptomatic patients. The viral loads reached their peak at 10^4–10^7 copies/mL around 5–6 days following the onset of symptoms. No indication of intrauterine transmission to the foetus was discovered in a study of nine pregnant women who were infected.

The Clinical Aspects of COVID-19

The most frequent clinical symptoms are fever and a respiratory illness; studies have shown that this combination causes a fever in 80% to 99% of cases, a dry cough in 48% to 76% of cases, fatigue or myalgia in 44% to 70% of cases, and dyspnea in 30% to 55% of cases. Anorexia and a productive cough are two more reasonably common symptoms. Headache, diarrhoea, nausea, dizziness, and vomiting are less common symptoms. Older people and possibly those with preexisting clinical illnesses such diabetes, hypertension, cardiovascular disease, and malignancies are more prone to experience severe sickness and mortality.

Diagnostic Tests for COVID-19

For the first 3 to 4 weeks of the outbreak, early diagnoses were largely based on clinical and nonspecific laboratory findings because there were no specific tests available. It wasn't until the virus was isolated and its genome was sequenced that it was possible to design specific nucleic acid-based assays. Clinical history, exposure history, test results, and chest x-ray abnormalities have all showed a significant role in clinical diagnosis. The severity of the disease will influence the laboratory results, however low lymphocyte counts are typical and persistent low counts are linked to worse outcomes. It is necessary to do testing for additional respiratory pathogens to rule out viral and bacterial coinfections.

Reverse transcriptase real-time PCR (rtPCR) is the most common method used for direct diagnostic testing to identify active SARS-CoV-2 infections Although other molecular technologies, such as CRISPR-mediated detection or loop-mediated isothermal amplification have also been used.

Currently, upper respiratory system samples obtained via swabs are commonly used in RT-PCR tests for COVID-19. RT-PCR is regarded as the gold standard for identifying the SARS-CoV-2 virus since it can amplify a small quantity of viral genetic material in a sample. RT-PCR has

traditionally been performed in one or two steps. One-step real-time RT-PCR runs the full RT-PCR reaction in a single tube that contains all essential primers. While two-step real-time RT-PCR requires more than one tube to execute the individual reverse transcription and amplification procedures, it is more flexible and sensitive than one-step RT-PCR. It enables for the storage of cDNA for the measurement of several targets and requires less starting material. The one-step protocol is typically the favoured method for detecting SARS-CoV-2 since it requires less sample handling and bench time, is simple to set up, and reduces the likelihood of pipetting mistakes and cross-contamination between the RT and real-time PCR phases.

In the beginning of RT-PCR, RNA-dependent DNA polymerase (reverse transcriptase) converts viral genomic RNA into DNA. A brief complementary DNA copy (cDNA) of the viral RNA is produced in this procedure using reverse transcriptase and small DNA sequence primers that are particularly engineered to identify complementary sequences on the RNA viral genome. The amplification of DNA is tracked in real time as the PCR reaction develops in real-time RT-PCR. This is accomplished by utilising a fluorescent dye or, as in the case of TaqMan assays, a sequence-specific DNA probe tagged with a fluorescent molecule and a quencher molecule. The amplification procedure is then repeated automatically for around 40 cycles until the viral cDNA can be seen, typically as a fluorescent or electrical signal.

Vaccines against COVID-19

Various COVID-19 vaccines have been approved for use by WHO.

- The Pfizer/BioNTech Comirnaty vaccine, 31 December 2020.
- The SII/COVISHIELD and AstraZeneca/AZD1222 vaccines, 16 February 2021.
- The Janssen/Ad26.COV 2.S vaccine, 12 March 2021.
- The Moderna COVID-19 vaccine (mRNA 1273), 30 April 2021.
- The Sinopharm COVID-19 vaccine, 7 May 2021.
- The Sinovac-CoronaVac vaccine, 1 June 2021.
- The Bharat Biotech BBV152 COVAXIN vaccine, 3 November 2021.
- The Covovax (NVX-CoV2373) vaccine, 17 December 2021.
- The Nuvaxovid (NVX-CoV2373) vaccine, 20 December 2021

References

Bai Y, Yao L, Wei T, et al. Presumed asymptomatic carrier transmission of COVID-19. *JAMA*. 2020;323:1406-1407.

Chen H, Guo J, Wang C, et al. Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records. *Lancet*. 2020;395:809-815

Chen Y, Guo Y, Pan Y, Zhao ZJ. Structure analysis of the receptor binding of 2019-nCoV [published online February 17, 2020]. *Biochem Biophys Res Commun*. doi:10.1016/j.bbrc.2020.02.071

Cui J, Li F, Shi ZL. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019;17:181-192

Kam KQ, Yung CF, Cui L, et al. A well infant with coronavirus disease 2019 (COVID-19) with high viral load [published online February 28, 2020]. *Clin Infect Dis*. doi:10.1093/cid/ciaa201

Lu R, Zhao X, Li J, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet. 2020;395:565-574

Pan Y, Zhang D, Yang P, Poon LLM, Wang Q. Viral load of SARS-CoV-2 in clinical samples. *Lancet Infect Dis*. 2020;20:411-412

To KK, Tsang OT, Yip CCY, et al. Consistent detection of 2019 novel coronavirus in saliva [published online February 12, 2020]. *Clin Infect Dis*. doi:10.1093/cid/ciaa149

van der Hoek L. Human coronaviruses: what do they cause? Antivir Ther. 2007;12(4 pt B):651-658.

Wong MC, Cregeen SJJ, Ajami NJ, Petrosino JF. Evidence of recombination in coronaviruses implicating pangolin origins of nCoV2019. Preprint. Posted online February 13, 2020. *bioRxiv*. doi:10.1101/2020.02.07.939207

World Health Organization. Pneumonia of unknown cause –China. Published January 5, 2020.https://www.who.int/csr/don/05-january-2020-pneumonia-of-unkown-cause china/en

Young BE, Ong SWX, Kalimuddin S, et al. Epidemiological features and clinical course of patients infected with SARSCoV- in Singapore. *JAMA*. 2020;323:1488-149