

Case Report

Review on Covid-19 (Corona Virus Disease - 19)

Yashwant Sompura, Tansukh Barupal, Deepa Hada, Mukesh Meena*

Department of Botany, Mohanlal Sukhadia University, Udaipur, Rajasthan

ABSTRACT

The coronavirus disease 19 (COVID-19) is a highly transmittable and pathogenic viral infection caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which emerged in Wuhan, China and spread around the world. Genomic analysis revealed that SARSCoV-2 is phylogenetically related to severe acute respiratory syndrome-like (SARS-like) bat viruses, therefore, bats could be the possible primary reservoir. The intermediate source of origin and transfer to humans is not known, however, the rapid human to human transfer has been confirmed widely. There is no clinically approved antiviral drug or vaccine available to be used against COVID-19. However, few broad-spectrum antiviral drugs have been evaluated against COVID-19 in clinical trials, resulted in clinical recovery. In the current review, we summarize and comparatively analyse the emergence and pathogenicity of COVID-19 infection and previous human coronaviruses severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV). We also discuss the approaches for developing effective vaccines and therapeutic combinations to cope with this viral outbreak.

Keywords: COVID19, Infection, Symptoms, Prevention.

INTRODUCTON

The disease COVID19 is caused by Corona virus and the virus name corona is given because of its structure just like crown (Corona is Latin word it mean crown like). This disease is pandemic and Zoonotic disease. The Contain a single stranded RNA as a nucleic material. The virus is also called severe acute respiratory syndrome corona virus 2 (SARS COV-2). The subgroups of corona virus's family are alpha, beta, gamma and delta. These viruses were thought to infect only animals until the world witnessed. A SARSCOV-1 outbreak caused by SARs-COV, 2003 in Guangdong, China [1]. Only a decade later, another pathogenic corona virus, known as middle east respiratory syndrome (MERscov) caused an endemic in middle eastern countries [2]. Recently at the end of 2019 Wuhan an emerging business hub of china expressed. An outbreak of a novel corona virus that killed more than 177000and infected over sixteen lac. This virus was reported to be a member of the beta group of corona viruses. The novel virus was named as Wuhan corona virus or 2019 novel corona virus (2019-NCOV) by the Chinese researcher's. The international committee on taxonomy of viruses (ICTV) Named the virus as SARS-COv-2 and the disease as covid-19 [3-5]. In the history as SARSCOV (2003) infected 8098 individual with mortality rate of 9% across 26 countries in the world, on the other hand, novel corona virus 2019 infected 4098018 individual with (283271 deaths) mortality rate of 2.9%, across 215 countries, till date.

NOMENCLATURE

1. Covid-19 named by ICTV (International committee for taxonomy of virus)

2. According to WHO (world health organisation)

CO-corona

VI-virus

D-disease

19-2019

3. SARS COv-2= severe acute respiratory syndrome corona virus-2.

CLASIFICATION

Phylum - Incertaesedis

Order - Nidoverales

Family - Coronaviraceae

TRANSMISSION

It can be transmitted from animals to humans and then spread person to person.

Like

Correspondence to: Mukesh Meena, Department of Botany, Mohanlal Sukhadia University, Udaipur, Rajasthan, India ; E-Mail: mukeshmeenamlsu@gmail.com

Received: February 05, 2020; Accepted: February 20, 2020; Published: April 27, 2020

Citation: Yashwant S, Tansukh B, Deepa H, Mukesh M (2021) REVIEW ON COVID-19 (CORONA VIRUS DISEASE - 19). Virol Mycol. 10:207

Copyright: © 2021 Mukesh M. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Mukesh Meena, et al.

- a. Coughing and sneezing
- b. Close personal contact
- c. Use of infected thing
- d. Respiratory droplets and aerosol
- (Figure 1)

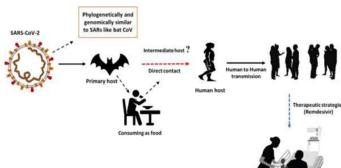


Figure 1: Origin and transmission of corona virus

SYMPTOMS

- 1. Cough
- 2. Fever
- 3. Tiredness
- 4. Difficulty breathing

5. People may be sick with the virus for 1-14 days before developing symptoms.

6. The disease can be serious and even fatal older people and people with other medical Condition (such as asthma, diabetes, etc.)

(Figure 2)

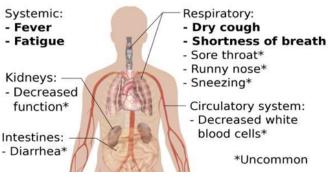


Figure 2: Symptoms of COVID-19

TREATMENT

No specific treatment to treat this disease only self-care.

PREVENTION

DO

HAND WASHING AVOID CLOSE CONTACT STAY HOME SELF ISOLATION

QURANTINE

DON'T



TOUCH YOUR EYES NOSE

DO NOT USE OLA

Structure of SARs COv-2 or Corona (COVID-19)

- 1. Positive stranded RNA virus (26-32 kb).
- 2. Comprises four genera (alpha, beta, lemda and delta)
- 3. Six human COVs have been confirmed

HCOV-NL63 and HCOV29E - alpha cov genus

HCOV-OC43, HCOVNKU1, SARsCOv - beta cov genus.

MERS-COV - beta cov genus

(Figure 3)

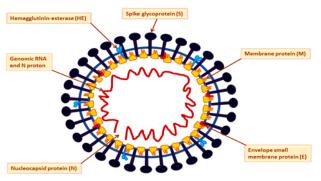


Figure 3: Corona virus structure

• An enveloped, single positive strand RNA genome encodes four major virul structure protein-

Spike (S) - play a vital role in viral entery

Envelope - play important role in viral assembly

Membrane (M) - play important role in viral asembly

Nucleocapsid protien (N) - for RNA synthasis

Human coronaviruses

1. The first human corona virus (HCoV), B814, was described in 1965.

2. In the following years, over 30 additional strains were characterized.

3. Ten of those strains could only be isolated from primary embryonic tracheal organ culture.

4. Others were readily isolated from monolayer cultures and were antigenically related to the prototype strain HCoV-229E.

5. HCoV-OC43 for organ culture 43 was isolated and found to be distinct from the 229E protypestrain [6, 7].

6. In the subsequent decades, research on HCoVs would center on these twodistinct viruses.

7. However, in 2002, an unknown respiratory illness,termed Severe Acute Respiratory Syndrome (SARS), surfaced in Asia.

8. Research determined it to be caused by anovel coronavirus [8, 9]. At the end of the epidemic, this virus had infected over 8000 people, most in China and caused 774 deaths [10].

9. Following the discovery of this virus, two additional CoVs causing human disease were identified. HCoV-NL63 was isolated in

Mukesh Meena, et al.

the Netherlands in 2004 from an infant with bronchiolitis [11].

10. HCoV-HKU1 in 2005 from a patient with pneumonia in Hong Kong [12]. In 2012, another respiratory HCoV, Middle East Respiratory (MERS)-CoV, was isolated from a patient with pneumonia in Saudi-Arabia [13].

11. Unlike SARS-CoV, this virus is still intermittently present in the human population and most recently caused a large outbreak in South-Korea [14]. (Table 1)

Features	SARs COV-1	SARs COV-2
Emergence date	Nov. 2002	Dec. 2019
Area of emergence	Guangdong (china)	Wuhan (china)
Date of fully con- trol	July 2003	Not controlled yet
Key host	Bat, Palmcivet	Bat
No. of countries in- fected	26	215
Entry receptor in human	ACE-2	ACE-2
Sign and symptoms	Fever, malaise, my- algia, headache, diarroea, shivering, cough, and short- ness of breath	Cough, and short- ness of breath
Disease caused	SARS, ARDS	SARS, COVID-19
Infected patient	8098	4098018

Table 1: Comparative analysis of biological features of SARsCOv-1 and SARs COv-2

Host of corona virus

1. In the case of SARs-cov, raccoon dog and palm civets as a key reservoir of infection.

2. However, only the samples isolated from the civets at the food market showed positive results for viral RNA detection, suggesting that the civet palm might be secondary hosts.

3. Later on, rinolophus bats were also found to have anti SARS-CoV antibodies suggesting the bats as a source of viral replication.

4. The Middle-East respiratory syndrome (MERS) coronavirus also pertains to beta coronavirus and having camels as a zoonotic source or primary host.

5. Further analysis of homologus recombination revealed that spike binding glycoprotein of novel corona virus is developed from SARS CoV (covzxc21 or covzc45) and a yet unknown beta CoV [15]

Key features and entry mechanism of human coronaviruses

1. All corona viruses contain specific genes in ORF1 downstream regions that encode proteins for viral replication, nucleocapsid and spike protein formation.

2. The spike protein helps for the attachment and entry of the virus to host cells.

3. The receptor binding domain (RBD) is loosely attached among virus, the virus may infect multiple hosts.

4. The entry mechanism of a coronavirus depends upon cellular proteases which include human airway trypsin lie protease (HAT), cathepsin and trans-membrane protease serine 2 (TM-PRSS2) that split the spike protein and establish further penetration changes.

5. MERS Coronavirus employs dipeptidyl peptidase 4(dpp4) while HCoV- NL63 and SARS Coronavirus require angiotensin converting enzyme 2(ACE2) as a key receptor.

6. SARS-CoV-2 possesses the typical corona virus structure with spike protein and also expressed other polyproteins, nucleoproteins, and membrane proteins, such as RNA polymerase, 3- chymotrypsin-like protease, papain-like protease, helicase, glycoprotein and accessory proteins.

7. The spike protein of SARS-CoV-2 contains a 3-D structure in the RBD to region to maintain the vanderwal forces.

8. The 394 glutamine residue in the RBD region of SARS-CoV-2 is recognized by the critical lysine 31 residue on the human ACE2 receptor [15].

9. The entire mechanism of pathogenicity of SARS-CoV-2, from attachment to replication is well mentioned in (Figure 4)

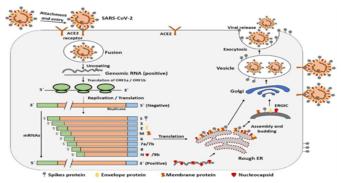


Figure 4: Entry mechanism of coronavirus

Vaccine's for SARs-COV-2

There is no available vaccine against COVID-19, while previous vaccines or strategies used to develop a vaccine against SARS-CoV-2 can be effective.

CONCLUSION

The novel coronavirus originated from the Hunan seafood market at Wuhan, China where bats, snakes, raccoon dogs, palm civets, and other animals are sold, and rapidly spread up to 109 countries. The zoonotic source of SARS-CoV-2 is not confirmed, however, sequence-based analysis suggested bats as the key reservoir. DNA recombination was found to be involved at spike glycoprotein which assorted SARS-CoV (CoVZXC21 or CoVZC45) with the RBD of another Beta CoV, thus could be the reason for cross-species transmission and rapid infection.

Conflict of interest statement

None declared

Funding sources

None

REFERENCES

1. Zhong N, Zheng B, Li Y, Poon L, Xie Z, et al. Epidemiology and cause of severe acute respiratory syndrome (SARS)

OPEN OACCESS Freely available online

Mukesh Meena, et al.

in Guangdong, People's Republic of China. Lancet. 2003; 362(9393):1353-8.

- 2. Wang N, Shi X, Jiang L, Zhang S, Wang D, et al. Structure of MERS-CoV spike receptor-binding domain complexed with human receptor DPP4. Cell Res. 2013; 23(8):986.
- 3. Cui J, Li F, Shi ZL. Origin and evolution of pathogenic coronaviruses. Nat Rev Microbiol. 2019; 17(3):181–92.
- 4. Lai CC, Shih TP, Ko WC, Tang HJ, Hsueh PR. Severe acute respiratorysyndrome coronavirus 2 (SARS-CoV-2) and corona virus disease-2019 (COVID-19): the epidemic and the challenges. Int J Anti Microb Agents. 2020; 105924.
- 5. Organization WH. Laboratory testing for coronavirus disease 2019 (COVID-19) in suspected human cases: interim guidance, 2 March 2020. World Health Organization, 2020.
- 6. Hamre D, Procknow JJ. A new virus isolated from the human respiratory tract. Proc Soc Exp Biol Med. 1966; 121:190–193.
- McIntosh K, Dees JH, Becker WB, Kapikian AZ, Chanock RM. Recovery in tracheal organ cultures of novel viruses from patients with respiratory disease. Proc Natl Acad Sci U S A. 1967;57:933–940.
- Drosten C, Gunther S, Preiser W, van der Werf S, Brodt HR, et al. Identification of a novel coronavirus in patients with severe acute respiratory syndrome. N Engl J Med. 2003; 348:1967–1976.

- 9. Rota PA, Oberste MS, Monroe SS, Nix WA, Campagnoli R, et al. Characterization of a novel coronavirus associated with severe acute respiratory syndrome. Science. 2003; 300:1394–1399.
- 10. Summary of probable SARS cases with onset of illness from 1 November 2002 to 31 July 2003.
- 11. Van der Hoek L, Pyrc K, Jebbink MF, Vermeulen-Oost W, Berkhout RJ, et al. Identification of a new human coronavirus. Nat Med. 2004; 10:368–373.
- Woo PC, Lau SK, Chu CM, Chan KH, Tsoi HW, et al. Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. J Virol. 2005; 79:884–895.
- Zaki AM, van Boheemen S, Bestebroer TM, Osterhaus AD, Fouchier RA. Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. N Engl J Med. 2012; 367:1814–1820.
- Korea Centers for Disease, Control, Prevention. Middle East Respiratory Syndrome Coronavirus Outbreak in the Republic of Korea, 2015. Osong Public Health Res Perspec. 2015; 6:269–278.
- 15. Muhammad A S, Suliman K, Abeer K, Nadia B, Rabeea S. COVID-19 infection: Origin, transmission, and characteristics of human coronaviruses. J Adv Res. 2020; 24: 91-98.