ISSN (Online): 2091-2609
DOI Prefix: 10.3126/ijasbt

International Journal of Applied Sciences and Biotechnology (IJASBT)

Review Article

Biological Property of Novel Coronavirus SARS-CoV-2 (2019-nCoV)

Emebet Mohammed Abdu[1]*, Abeba Haile Mariamenatu[2]

[1]Debre Berhan University, Collage of Natural and Computational sciences, Department of Biology, P.O. Box- 445, Debre Berhan, Ethiopia
[2]Debre Berhan University, Collage of Natural and Computational sciences, Department of Biotechnology, P.O. Box- 445, Debre Berhan, Ethiopia

Article Information

Received: 10 December 2020
Revised version received: 12 March 2021
Accepted: 15 March 2021
Published: 30 March 2021

Cite this article as:
E. Mohammed and A.H. Mariamenatu (2021) Int. J. Appl. Sci. Biotechnol. Vol 9(1): 16-22.
DOI: 10.3126/ijasbt.v9i1.33333

***Corresponding author**
Emebet Mohammed Abdu,
Debre Berhan University, Collage of Natural and Computational sciences, Department of Biology, P.O.Box 445, Debre Berhan, Ethiopia
Email: emuahmu2019@gmail.com

Peer reviewed under authority of IJASBT

Abstract

Novel coronavirus (2019-nCoV) is a positive-sense RNA virus that possesses four genes that encode the spike (S), membrane (M), nucleocapsid (N), and envelope (E) proteins. The virus was originated in seafood market selling live animals and responsible for coronavirus disease 2019 (COVID-19). The initial case was traced to the city of Wuhan in the province of Hubei, China, reported as an emerging respiratory virus, the outbreak was reported to WHO on December 31, 2019, and soon after identified the causative pathogen as a beta coronavirus named as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2); Furthermore, It is a highly contagious virus that spreads swiftly outside of China in March and the World Health Organization had to declare COVID-19 pandemic on March 11, 2020, and as of August 15, 2020, more than 21 million confirmed cases have been reported, with > 755 786 deaths worldwide. This day's novel coronavirus-2019 is the most infectious virus with high infectivity and low mortality rate where a high mortality rate was observed among people above the age of sixteen (60) years and with the pre-existing health condition. To date, there is no clinically approved antiviral drug or vaccine available to be used against COVID-19. However, Preventive measures such as masks, hand hygiene practices, avoidance of public contact, case detection, contact tracing, and quarantines have been discussed as ways to reduce transmission. Therefore, the purpose of this review is to summarize the basic biological properties of novel coronavirus 2019.

Keywords: Coronavirus; COVID-19; HCoVs; MERS-CoV; SARS-CoV-2

Introduction

Novel coronavirus-2019 is a member of a large family of viruses that are known to cause illness ranging from the common cold to more severe diseases like Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndromes SARS-CoV (Tok and Tar, 2017; Li *et al*., 2020). At the end of December 2019, a new infectious respiratory disease known as 2019-novel coronavirus (2019-nCoV) or the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, Hubei province, China (Ahn *et al.*, 2020). Later on, February 11, 2020, the World Health Organization named the disease as coronavirus disease 2019 (COVID-19) (Adhikari *et al*., 2020).

It is one of the emerging respiratory viruses which is originated in seafood market selling live animals and was transmitted to humans through yet unknown intermediary animals in Wuhan, Hubei province, China (Singhal, 2020). This novel virus is responsible for the current pandemic; its diverse biological and epidemiological characteristics make this virus more contagious than other Human coronaviruses (HCoVs); it has affected more people in a short period of time. Therefore, the purpose of this review is to highlighted the basic biological properties of 2019-nCoV or SARS-CoV-2.

Viral Composition and Structure

2019-nCoV is an enveloped, non-segmented, single-stranded, positive-sense RNA virus belong to order *Nidovirales, family Coronaviridae,* subfamily Coronavirinae, genus Coronavirus and subgenus sarbecovirus (Chen *et al.*, 2020). Similar, to SARS-CoV and MERS-CoV, SARS-CoV-2 belongs to the beta- genus Coronavirus and possesses the largest genome, 26.4–31.7 kilobases in size (Mousavizadeh and Ghaseimi, 2020; Schoeman and Fielding, 2019). The viral genome is packed inside a capsid with a helical symmetry, which is built by the nucleocapsid protein (N) and further surrounded by an envelope which is also associated with at least three structural proteins namely the membrane protein (M), envelope protein (E) and the spike protein (S) where the first two involved in virus assembly. Whereas, the S protein mediates virus entry into host cells and forms large protrusions from the virus surface, giving the appearance of having crowns (hence their name; *corona* in Latin means crown) (Li, 2016). In addition to mediating virus entry, the spike is a critical determinant of viral host range, tissue tropism and it is a major inducer of host immune responses; which implies that currently it is the most promising antigen formulation for SARS-CoV-2 vaccine research (Fig.1) (Zhang *et al*., 2020).

According to the findings of Lu et *al.* (2020), it was found that the genome sequence of SARS-CoV-2 is closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21, collected in 2018 in Zhoushan, eastern China, but were more distant from SARS-CoV (about 79%) and MERS-CoV (about 50%).

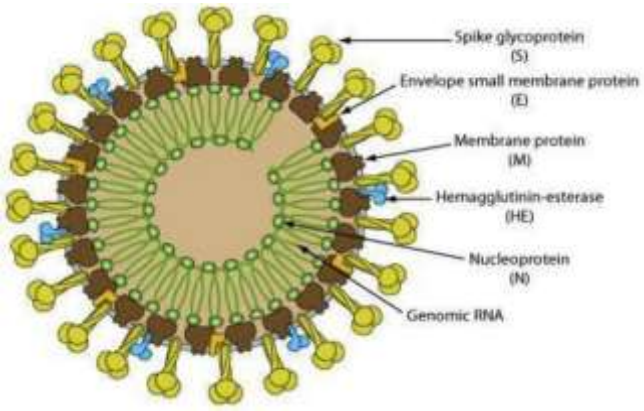

Fig. 1: The overall structure of SARS-CoV- 2 shown with structural proteins: - N: Nucleocapsid protein; S: Spike protein; M: Membrane protein and E: Envelop protein.

At the 5' terminal two-thirds of the genome contains two open reading frames (ORFs), ORF1 and ORF2 which encodes non-structural proteins (such as 3-chymotrypsin-like protease, papain-like protease (pp1a and pp1b), helicase, and RNA-dependent RNA polymerase) which are key enzymes in the viral life cycle and the last third of the genome encodes primarily structural proteins namely S, E, M and N located at the one-third 3' terminal of the genome (Fig.2) (Malik *et al.*, 2020).

The virus enters target cells via receptor-mediated endocytosis driven by the spike (S) glycoprotein, which protrudes from the surface of the virion; The S protein serves as the major viral attachment protein, critical to virus binding and fusion of the viral envelope (Schoeman and Fielding, 2019; Li, 2016). Angiotensin-converting enzyme 2 (ACE-2) and Cluster of Differentiation two hundred nine ligand (CD209L) were identified as functional receptors for SARS CoV-2 (Fig: 3). However, Angiotensin-Converting Enzyme 2 serves as a more efficient receptor (Zhang *et al.*, 2020).

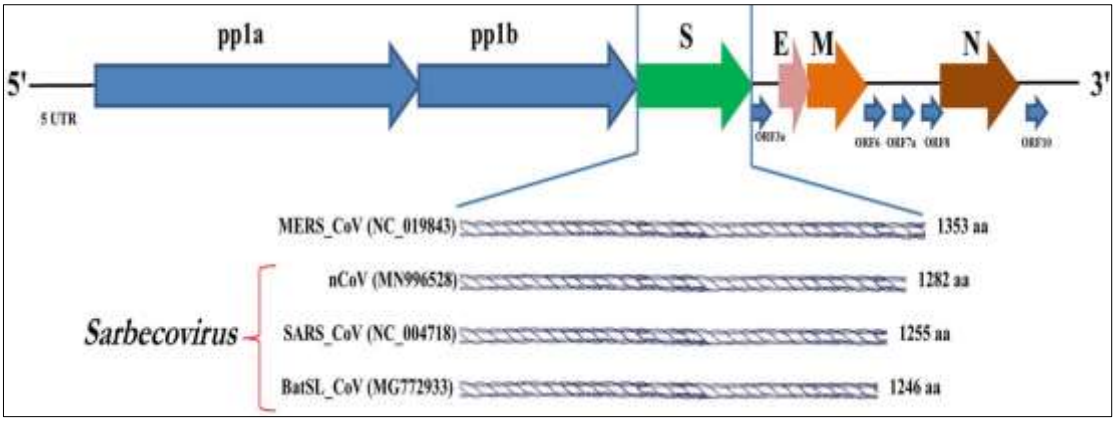

Fig. 2: Genome organization of novel coronavirus. Comparative spike (S) protein sequence length of different Beta-coronaviruses is depicted.

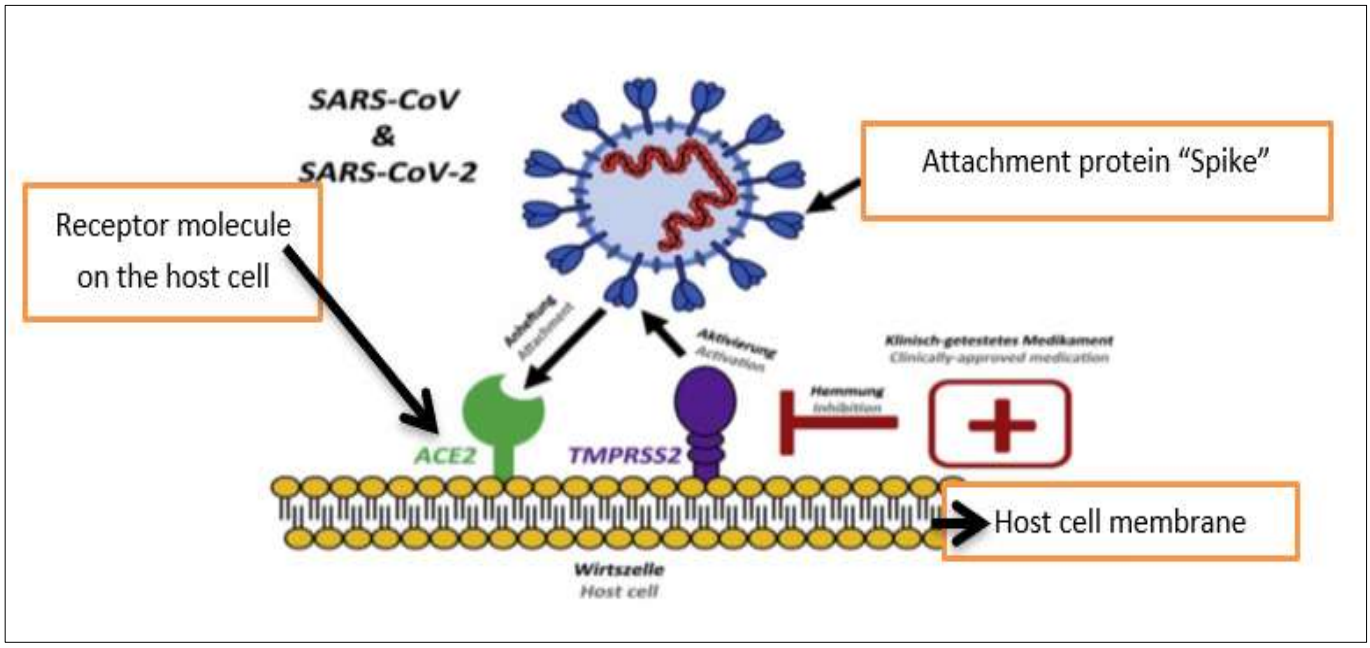

Fig. 3: The attachment protein "spike" of the new coronavirus 2019-nCoV uses cellular attachment factor (ACE2) and the cellular protease TMPRSS2 for activation.

nCoV-19 Related HCoVs

Human coronaviruses (HCoVs)) are common viral respiratory pathogens that primarily cause symptoms in the upper respiratory and gastrointestinal tracts; they have long been considered inconsequential pathogens, causing the "common cold". SARS-CoV-2 became the seventh member of the human coronaviruses (HCoVs) identified as HCoV-229E, HCoV-OC43, HCoV-NL63, HCoV-HKU1, SARS-CoV, MERS-CoV and now SARS-CoV-2 (Rabaan et al., 2020; Zhou *et al*., 2020). However, in the 21st century, 2 highly pathogenic HCoVs named as SARS-CoV and MERS-CoV emerged from animal reservoirs to cause global epidemics with alarming morbidity and mortality. Currently, four different genera exist, including *Alphacoronavirus-(α) Betacoronavirus-(β) Gammacoronavirus-(γ) and Deltacoronavirus-(δ)* where α- and β-CoV are able to infect mammals, while γ- and δ-CoV tend to infect birds; whereas, the other two known β-CoVs; SARS-CoV and MERS-CoV leads to severe and potentially fatal respiratory tract infections (Meo *et al.,* 2020; Shen *et al.,* 2019).

SARS-CoV first identified in 2002 and diagnosed in Southern China, occurred from a human CoV. Then, exactly 10 years after the SARS-CoV emergence, a new emerging Coronavirus named MERS-CoV has infected people with a high mortality rate of nearly 50% in the Middle East (Zhou *et al*., 2020).

Host Range

A wide range of species; Such as, dogs, cats, pigs, mice, bats, and humans are infected by CoVs. However, most strains of corona viruses exhibits a narrow host range (Meo *et al.,* 2020). They cause a variety of diseases in mammals and birds ranging from enteritis in cows and pigs and upper respiratory disease in chickens to potentially lethal human respiratory infections (Meo *et al.*,2020; Shen *et al.*,2019). Rarely, animal CoVs can infect humans and; as a result; may spread among humans during epidemics such as MERS, SARS, and COVID-19. Additionally, at the onset of major outbreaks caused by CoVs, palm civet has been proposed to be a natural reservoir of Human CoVs for SARS and dromedary camels for MERS. However, more advanced virological and genetic studies have shown that bats are reservoir hosts of both SARS-CoV and MERS-CoV (Shen *et al.,* 2019).

Infection and Replication

Initially for SARS-CoV-2 to replicate it starts with an infection. Infection begins when the virus enters the host cell, *via* receptors mainly by spike protein and its ligand host cell receptor called ACE2 which is found in various organs such as heart, lungs, kidneys; and gastrointestinal tract. Thus, facilitating viral entry into target cells (Shen *et al.,* 2019). Then entered-SARS-CoV-2 will subsequently release its genetic material in the cytoplasm *via* uncoating and get translated in the host nuclei (Hafeez *et al.,* 2020; Guo *et al.,* 2020). Virus-specific RNA and proteins are synthesized entirely in the cytoplasm. During this process protein synthesizing and viral expression starts with translation of two polyproteins, namely, pp1a and pp1ab, which undergo cotranslational proteolytic processing into the proteins that form the replicas complex and lastly, new virions are assembled by budding into intracellular membranes and released through vesicles by the cell secretory mechanisms (Fig. 4) (Astuti, 2020).

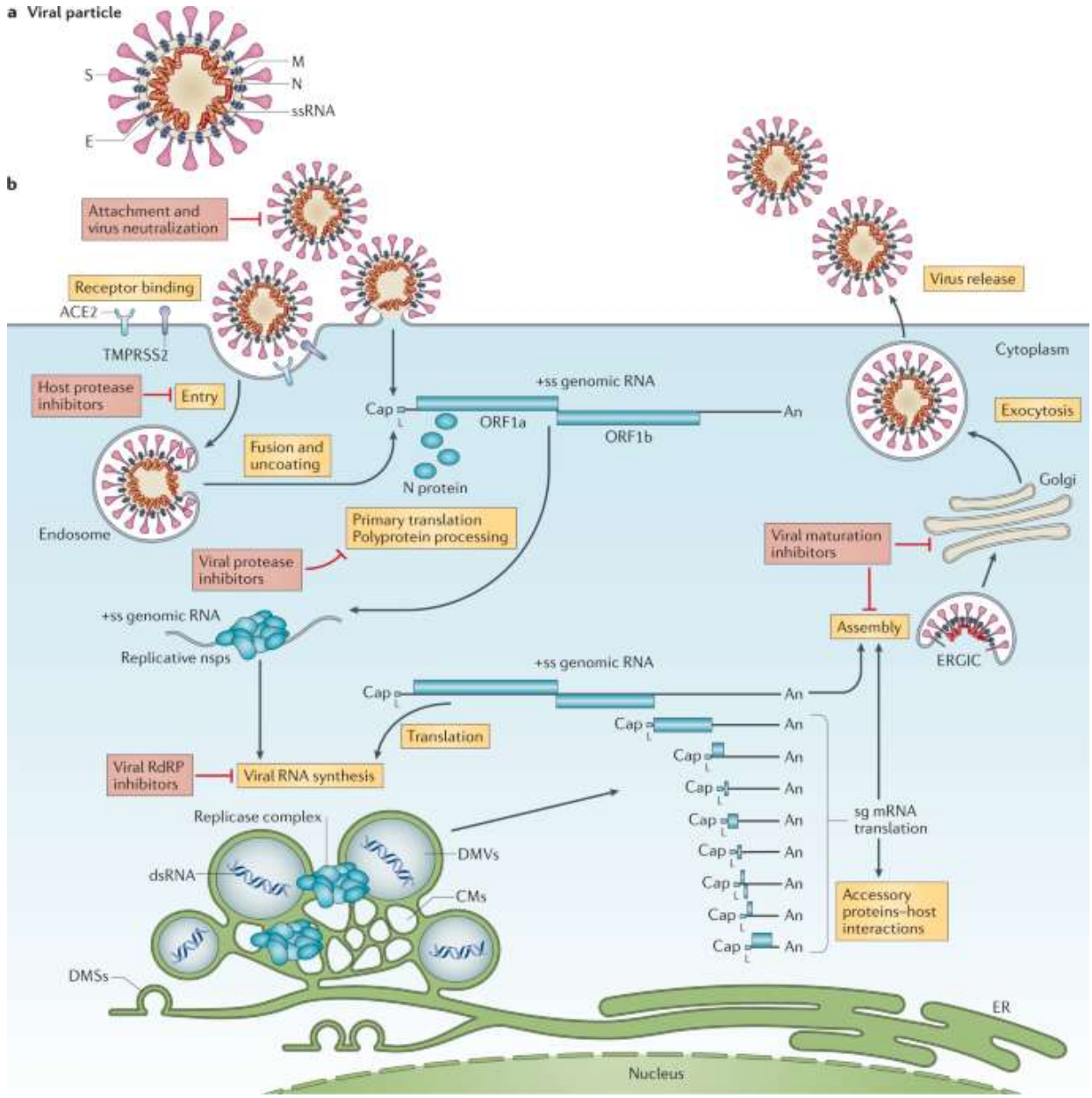

Fig. 4: Mechanism of cell entry and replication process of Severe Acute Respiratory Syndrome Coronavirus 2.

Transmission and Symptoms

In spite of the belief that 2019-nCoV was introduced into humans from an animal species (i.e. zoonotic transmission); According to the latest guidelines from Chinese health authorities human-to-human transmission is possible by three different ways ; these transmission routes includes droplets transmission, contact transmission, and aerosol transmission:- In droplets transmission viral transmission occurs when respiratory droplets produced when an infected person coughs or sneezes are ingested or inhaled by individuals nearby proximity and while during contact transmission it occurs when a subject touches a surface or object contaminated with the virus and subsequently touch their mouth, nose, or eyes; and lastly in the aerosol transmission it occurs when respiratory droplets mix into the air, forming aerosols and may cause infection when inhaled high dose of aerosols into the lungs in a relatively closed environment (Jin *et al.*, 2020). Viral incubation period ranges from 2 to 14 days with a mean day of 6.4 and the usual symptoms include fever, cough, shortness of breath, and muscle ache. In cases of some patients they may have sore throat, rhinorrhea, headache and confusion, a few days before the onset of fever. This indicates that fever is a critical symptom, but not the only initial manifestation of infection (Huang *et al.*, 2020; Tu *et al.*, 2020).

Epidemiology

According to updated world health organization (WHO) reports, the number of confirmed cases is constantly increasing worldwide even a steep increase in cases is currently being observed in low-income countries. As of 09 August 2020, based on the WHO reports; globally 19,462,112 confirmed cases and 722, 285 deaths distributed as per (Table.1) (WHO, 2020).

Table 1: COVID-19 situational report as of August 15, 2020.

Situation in numbers (by WHO Region)	Total (new cases in last 24 hours)	
Globally	21 026 758 cases (294 237)	755 786 deaths (9 985)
Africa	936 062 cases (10 765)	18 286 deaths (382)
Americas	11 271 215 cases (161 772)	410 483 deaths (7 749)
Eastern Mediterranean	1 710 272 cases (13 382)	45 361 deaths (357)
Europe	3 733 965 cases (29 260)	213 674 deaths (365)
South-East Asia	2 971 104 cases (70 757)	58 844 deaths (1 088)
Western Pacific	403 399 cases (8 301)	9 125 deaths (44)

Diagnosis

Clinical specimens used to diagnose novel coronavirus nucleic acid includes nasal secretions, sputum, lower respiratory tract secretions, blood, feces, broncho alveolar lavage (BAL) and in order to increase the positive rate of nucleic acid detection. It is recommended to take as much sample as possible; the aforementioned samples are subjected to specific serological and molecular tests specific for COVID-19 where serological tests employ enzyme linked immunosorbent assay (ELISA) or Western blots that detects specific COVID-19 proteins while molecular approaches are based on Real Time-PCR (RT-PCR) or Northern blot hybridization targeting specific COVID-19 genes. Further, viral antigens present in the clinical specimens are detected by using direct immune fluorescent assay (IFA) (Kannan *et al.*, 2020).

Treatment

SARS-CoV-2 continues to spread around the globe without any approved therapies. Researchers are urgently searching for effective prophylactic and therapeutic interventions. For instance, type I Interferons-alpha/beta (IFNs-α/β) are regulatory proteins that have broad-spectrum antiviral activities that work to directly block viral replication and support immune responses to clear virus infection "Interferons are our first line of defence against any and all viruses, but viruses such as coronaviruses have co-evolved to very specifically block an interferon response (Weiss *et al.*, 2020). However, the Current 2019-nCoV treatment strategies includes bed rest, supportive treatments, physical cooling for patients with body temperature exceeds 38.5℃, oxygen therapy like nasal catheter, mask oxygen, nasal high-flow oxygen therapy, antiviral therapy including interferon-α, favipiravir and ribavirin. In addition to this, remdesivir, galidesivir, lopinavir, and litonavir, convalescent plasma, and mAbs some situations where there is systemic inflammatory responses glucocorticoids can be used for a short period (Shen *et al.*, 2019; Li and Declercq, 2020; Li *et al.*, 2020).

Control and Prevention

Till to date, even thought, there is no clinically licensed vaccine against COVID-19, Prevention or slowing down the transmission was the first choices to reduce the pandemic. Currently, the best solution is to follow Infection preventive and control (IPC) measures that may reduce the risk of exposure. This IPC measures includes:- avoiding being exposed to the virus, case isolation, identification and follow-up of contacts, environmental disinfection, use of face masks; covering coughs and sneezes with tissues that are then safely disposed of (or, if no tissues are available, use a flexed elbow to cover the cough or sneeze); regular hand washing with soap or disinfection with hand sanitizer containing 60-80% alcohol (if soap and water are not available); avoidance of contact with infected people and maintaining an appropriate distance as much as possible; and refraining from touching eyes, nose, and mouth with unwashed hands (Ou *et al.*, 2020 ; Wei and Ren, 2020).

Conclusion

Beginning from the end of December 2019, SARS CoV 2 outbreak has challenged the economic, medical and public health infrastructure of the globe; this day, the largest challenge is being observed in low-income countries. Up to date, there is no effective treatment and vaccine; time alone will tell how the virus will impact our lives; yet there is an urgent need to develop new strategies to prevent or control infections. Therefore, the review provides an insight into the basic biological properties and increase the knowledge about the virus that helps for understanding the nature and current status of SARS-CoV-2 this plays a vital role in determining effective treatment and prevention strategies.

Authors' Contribution

All authors have contributed equally to the manuscript.

Conflict of interest

All authors declare that there exist no commercial or financial relationships that could in any way leads to a potential conflict of interest.

Acknowledgments

We Would like to thank Mr. Girum Tefera Belachew (MSc in medical Biothechnology) and Mr. Paramesh Hanumanthaiah (PhD in Biothechnology) for their Assistance in editing and commenting the document.

References

Adhikari SP, Meng S, Wu YJ, Mao YP, Ye RX, Wang QZ, *et.al*. (2020) Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease during the early outbreak period: a scoping review. *Infectious diseases of poverty* **9**(29): 1-2. DOI: 10.1186/s40249-020-00646-x

Ahn DG, Shin HJ, Kim MH, Lee S, Kim HS, Myoung J, *et.al*. (2020). Current status of epidemiology, diagnosis, therapeutics, and vaccines for novel coronavirus disease 2019 (COVID-19). *J Microbiol Biothechnol* **30**(3): 313-324. DOI: 10.4014/jmb.2003.03011

Astuti I (2020) Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2): An overview of viral structure and host response. Diabetes & Metabolic Syndrome: *Clinical Research & Reviews* **14**(4): 407-412. DOI: 10.1016/j.dsx.2020.04.020

Chen Y, Liu Q, Guo D. (2020). Emerging coronaviruses: genome structure, replication, and pathogenesis. *Journal of medical virology* **92**(4): 418-23. DOI: 10.1002/jmv.25681

Guo YR, Cao QD, Hong ZS, Tan YY, Chen SD, Jin HJ, Tan KS, Wang DY and Yan Y (2020). The origin, transmission and clinical therapies on coronavirus disease 2019 (COVID-19) outbreak–an update on the status. *Military Medical Research* 11(7): 1-10. DOI: 10.1186/s40779-020-00240-0

Hafeez A, Ahmad S, Siddqui SA, Ahmad M, Mishra S (2020) A Review of COVID-19 (Coronavirus Disease-2019) Diagnosis, Treatments and Prevention. *EJMO* **4**(2): 116–125. DOI: 10.14744/ejmo.2020.90853

Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X and Cheng Z (2020) Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *The lancet* **395**(10223): 497-506. DOI: 10.1016/S0140-6736(20)30183-5

Jin YH, Cai L, Cheng ZS, Cheng H, Deng T, Fan YP, Fang C, Huang D, Huang LQ, Huang Q and Han Y (2020) A rapid advice guideline for the diagnosis and treatment of 2019 novel coronavirus (2019-nCoV) infected pneumonia (standard version). *Military Medical Research* **7**(4): 1-23. DOI: 10.1186/s40779-020-0233-6

Kannan S, Ali PS, Sheeza A and Hemalatha K (2020). COVID-19 (Novel Coronavirus 2019)-recent trends. *Eur Rev Med Pharmacol Sci* **24**: 2006-2011.

Li F (2016) Structure, function, and evolution of coronavirus spike proteins. *Annual review of virology* **3**: 23-61. DOI: 10.1146/annurev-virology-110615-042301

Li G, De Clercq E. (2020). Therapeutic options for the 2019 novel coronavirus (2019-nCoV). *Nature Reviews Drug Discovery, Comment* **19**: 149-150. DOI: 10.1038/d41573-020-00016-0

Li H, Wang YM, Xu JY, Cao B. (2020). Potential antiviral therapeutics for 2019 Novel Coronavirus. Chinese *Journal of tuberculosis and respiratory diseases* **43**(0): E002-E003 DOI: 10.3760/cma.j.issn.1001-0939.2020.0002

Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, *et al.* (2020). Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia. *N Engl J Med* **382**:1199–1207. DOI: 10.1056/NEJMOa2001316

Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. (2020). Genomic characterization and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *The Lancet*; **395**: 565-574. DOI: 10.1016/S0140-6736(20)30251-8

Malik YS, Sircar S, Bhat S, Sharun K, Dhama K, Dadar M, Tiwari R, Chaicumpa W (2020) Emerging novel coronavirus (2019-nCoV)—current scenario, evolutionary perspective based on genome analysis and recent developments. *Veterinary quarterly* **40** (1): 68-76. DOI: 10.1080/01652176.2020.1727993

Meo SA, Alhowikan AM, Al-Khlaiwi T, Meo IM, Halepoto DM, Iqbal M, Usmani AM, Hajjar W, Ahmed N (2020) Novel coronavirus 2019-nCoV: prevalence, biological and clinical characteristics comparison with SARS-CoV and MERS-CoV. *Eur Rev Med Pharmacol Sci* 24:2012-9.

Mousavizadeh L and Ghasemi S (2020) Genotype and phenotype of COVID-19: Their roles in pathogenesis. *Journal of Microbiology. Immunology and Infection*, article in press DOI: 10.1016/j.jmii.2020.03.022

Ou F, Wu H, Yang Y, Tan W, Zhang J, Gu J (2020) Countermeasures for rapid spread of new coronavirus pneumonia in Wuhan. *Chinese General Practicing Nursing*.002.

Rabaan AA, Al-Ahmed SH, Sah R, Tiwari R, Yatoo MI, Patel SK, Pathak M, Malik YS, Dhama K, Singh KP, Bonilla-Aldana DK (2020) SARS-CoV-2/COVID-19 and Advances in Developing Potential Therapeutics and Vaccines to Counter this Emerging Pandemic Virus **19**(40): 1-37. DOI: 10.1186/s12941-020-00384-w

Sahin AR, Erdogan A, Agaoglu PM, Dineri Y, Cakirci AY, Senel ME, Okyay RA, Tasdogan AM (2020). 2019 novel coronavirus (COVID-19) outbreak: a review of the current literature. *EJMO* **4**(1): 1-7. DOI: 10.14744/ejmo.2020.12220

Schoeman D and Fielding BC (2019). Coronavirus envelope protein: current knowledge. *Virology Journal* **16**: 1-22. DOI: 10.1186/s12985-019-1182-0

Shen K, Yang Y, Wang T, Zhao D, Jiang Y, Jin R, Zheng Y, Xu B, Xie Z, Lin L, Shang Y. (2020). Diagnosis, treatment, and prevention of 2019 novel coronavirus infection in children: experts' consensus statement. *World journal of pediatrics* **16**: 223-231. DOI: 10.1007/s12519-020-00343-7

Singhal T. (2020). A review of coronavirus disease-2019 (COVID-19). *The Indian Journal of Pediatrics* **87**(4): 281-286. DOI: 10.1007/s12098-020-03263-6

Tok TT, Tatar G. (2017). Structures and functions of coronavirus proteins: Molecular modeling of viral nucleoprotein. *Int J Virol Infect Dis* **2**(1): 001-007.

Tu YF, Chien CS, Yarmishyn AA, Lin YY, Luo YH, Lin YT, Lai WY, Yang DM, Chou SJ, Yang YP and Wang ML. (2020). A review of SARS-CoV-2 and the ongoing clinical trials. *International journal of molecular sciences* **21**(7): 2657 DOI: 10.3390/ijms21072657

V'kovski P, Kratzel A, Steiner S, Stalder H and Thiel V (2020) Coronavirus biology and replication: implications for SARS-CoV-2. *Nature Reviews Microbiology* 155-170. DOI: 10.1038/s41579-020-00468-6

Wei Q and Ren Z (2020) Disinfection measures for pneumonia foci infected by novel coronavirus in 2019. *Chin J Disinfect* **37**: 59-62

Weiss SR and Navas-Martin S (2005) Coronavirus pathogenesis and the emerging pathogen severe acute respiratory syndrome coronavirus. *Microbiology and molecular biology reviews* **69**(4): 635-664. DOI**:** 10.1128/MMBR.69.4.635-664.2005

World Health Organization (2020) Coronavirus disease (COVID-2019) situation reports. 2020. Available on: https://www.WHO. Int/docs/default. Source/coronaviruses/ situation reports /20200221-sitrep-32-covid.;19.

Zhang J, Zeng H, Gu J, Li H, Zheng L and Zou Q (2020) Progress and prospects on vaccine development against SARS-CoV-2. *Vaccines* **8**(2): 153. DOI: 10.3390/vaccines8020153

Zhou H, Chen X, Hu T, Li J, Song H, Liu Y, Wang P, Liu D, Yang J, Holmes EC and Hughes AC (2020) A novel bat coronavirus closely related to SARS-CoV-2 contains natural insertions at the S1/S2 cleavage site of the spike protein. *Current Biology* **30**(11): 2196–2203. DOI: 10.1016/j.cub.2020.05.023