IOSR Journal Of Pharmacy And Biological Sciences (IOSR-JPBS)
e-ISSN:2278-3008, p-ISSN:2319-7676. Volume 15, Issue 4 Ser. II (Jul. –Aug. 2020), PP 46-50
www.Iosrjournals.Org

Review Article to highlight of SARS-CoV2 (Covid -19) Characteristics and epidemiology

Salih Abdul Mahdi Khadim
College of Biotechnology, Al-Qasim Green University, Iraq
Corresponding author: Salih Abdul Mahdi, ORCID: 0000-0001-5909-5663

Abstract: *Recently discovered coronavirus causes coronavirus disease COVID-19 is a novel coronavirus with an outbreak of uncommon viral pneumonia which appeared in Wuhan, China and spread around the world.COVID-19is a single-stranded RNA viruses with a highly transmittable and pathogenic viral infection results in severe acute respiratory syndrome coronavirus 2 (SARS-CoV2). COVID-19 belongs to genera Beta-coronavirus. There are more one kinds of human Beta-coronaviruses are;severe acute respiratory syndrome coronavirus (SARS-CoV or SARS-CoV-1), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2 or COVID-19, andMiddle East respiratory syndrome (MERS)that are many similarities, but there is some differences in their genotypic and phenotypic structure that played critical roleintheir pathogenesis. As previously known that coronaviruses are a large family of viruses which may cause illness in animals or humans. Also some of coronaviruses are known to cause respiratory infections in human ranging from the common cold to more severe diseases such as middle east respiratory syndrome (MERS) andacute respiratory syndrome coronavirus (SARS-CoV). In the end of 2019 discovered new strain of coronavirus causes coronavirus disease COVID-19.It is containing single-stranded (positive-sense) RNA associated with a nucleoprotein within a capsid comprised of matrix protein. A typical corona viruses containstwo un-translated regions (UTRs) at the 5′ and 3′ ends and 11 open reading frames (ORFs) that encode 27 proteins in its genome. All the structural and accessory proteins are translated from the sgRNAs of CoVs. Four main structural proteins are encoded byopen reading frames (ORFs) relative to other known coronaviruses. To determine theORFs, on the one-third of the genome near the 3′-terminus. The genetic and phenotypic structure of COVID-19 in pathogenesis is very important.As of 22 June 2020, 8,860,331 confirmed cases and 465,740 confirmed deaths of COVID-19 have been reported globally among 216 countries, territories, or areas. So this article will highlight of this important strain of coronaviruses to be a modest contribution in providing the latest developments regarding COVIDReveiw-19.*

Keywords*: Coronavirus, COVID-19,,genome,vaccines.*

Date of Submission: 13-07-2020 Date of Acceptance: 28-07-2020

I. Introduction

Family of coronaviruses are a large and included spectrum of RNA related both viruses which may cause some of diseasesof animals as well as humans. Regarding humans, several types of coronaviruses are known to cause respiratory infections ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome (MERS) andsever acute respiratory syndrome coronavirus (SARS-CoV).Recently discovered coronavirus causes coronavirus disease COVID-19 [1].

Coronaviruses - CoVs (Covid -19) are enveloped single-stranded RNA viruseswith positive sense, that belong to the subfamily Coronavirinae, family Coronavirdiae, order Nidovirales. There are four genera of CoVs, namely, Alphacoronavirus (αCoV), Betacoronavirus (βCoV), Deltacoronavirus (δCoV), and Gammacoronavirus (γCoV), are distinguished.COVID-19 is an infectious disease caused by a newly discovered coronavirus. Since the start of the COVID-19 pandemic several months ago, Researchers have been puzzling over the different ways the disease manifests itself. They ranged from cases without symptoms at all to severe and acute respiratory distress syndrome, which can be fatal. What accounts for this variability? Might the answer lie in our genes[2]. Such questions have been a raised before 15 years ago. throughseveral studies in 2003 outbreak of severe acute respiratory syndrome (SARS), Ralph Baric and his colleagues at the University of North Carolina at Chapel Hill identified a gene that, when silenced by a mutation, makes mice highly susceptible to SARS-CoV, the coronavirus that causes the disease called Toll-like receptor adaptor molecule (TICAM2), the gene codes for a protein that helps activate a family of receptors, called Toll-like receptors (TLRs), that are involved in innate immunity, the first line of defense against pathogens[3,4].

Attentiveness in the present time shifted to SARS-CoV-2, the new coronavirus strain that causes COVID-19. And TLRs have once again induce researchers' interest this time to help explain the high number of

human who suffered from severe respiratory infections[4].At the end of 2019, a series of pneumonia cases of unknown cause appeared in Wuhan (Hubei, China) [5]. A few weeks later, in January 2020, deep sequencing analysis from lower respiratory tract samples identified a novel virus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) ascausative agent for that observed pneumonia cluster [5]. On February 11th, 2020, the World Health Organization (WHO) Director-General, Dr. TedrosAdhanomGhebreyesus, named the disease caused by the SARS-CoV-2 as "COVID-19", and by March 11th, 2020 when the number of countries involved was 114, with more than 118,000 cases and over 4000 deaths, the WHO declared the pandemic status [6]. In subsequent comments we will use the word COVID-19 instead of SARS-CoV-2.

for the time being the COVID-19 is became the most controversial because of its lethal behavior towards humans. SARS-CoV-1, MERS-CoV, and NL63 are the only three viral strains that are studied well, until now .The COVID-19 belongs to the nidovirales order. Positive-strand RNA genome and a rigid envelope are unique characteristics of the virus of this family so it is did not get a lot of study [6,7].

II. Covid -19 Epidemiology

The beginning of COVID-19 started from Wuhan City, Hubei province, in China. 55 % of the infected cases before one January 2020 were linked to the Huanan Seafood Wholesale Market. However, the first human-to-human case of SARS-CoV-2 infection reported on one December 2019 did not have any exposure to this market [7,8]. During January 2020, COVID-19outbreak to other towns of China because Festival travel in the Spring season. Thereafter COVID-19 was outbreakin other countries via international travelers.On13 January 2020, the first case of COVID -19 infection was reported in Thailand, and after 15 January 2020 the first with COVID-19 was confirmed in Japan. On 25 January 2020, the number of confirmed cases had risen to 2062, including 2,016 in China, Thailand, Hong Kong, Taiwan, Malaysia, Australia, France, Singapore, Japan, South Korea, the US, Vietnam, Nepal, and Sweden. On 30 January 2020, China confirmed a high rise in the number of cases with COVID-19, as well as the presence of same infection in more than eighteen countries. Therefore, WHO announced the COVID-19 outbreak to be a Public Health Emergency of International Concern [68]. Then the COVID-19 epidemic reached all parts of the world and became a global pandemic. As of 22 June 2020, 8,860,331 confirmed cases and 465,740 confirmed deaths of COVID-19 have been reported globally among 216 countries, territories, or areas. [6,9,10]

III. Coronaviruses -CoV-2 (Covid-19)Genomedescription

COVID-19 is a single stranded (positive-sense) RNA virus had been spherical or pleomorphic enveloped shapecontaining nucleoprotein within a capsid comprised of matrix protein. The envelope bears club-shaped glycoprotein projections. Some coronaviruses also contain a hemagglutinin-esterase protein (HE)[11].(Fig. 1).

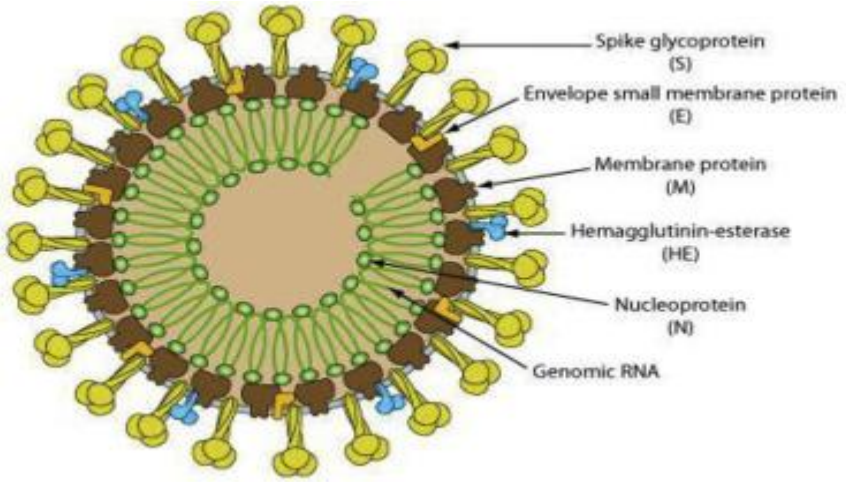

Figure no 1: Schematic diagram of COVID-19.

COVID-19has a largest genomes (26.4–31.7 kb) among all known RNA viruses, with G + C contents varying from 32% to 43%. Variable numbers of small ORFs are present between the various conserved genes (ORF1ab, spike, envelope, membrane and nucleocapsid) and, downstream to the nucleocapsid gene in different coronavirus lineages. The viral genome contains distinctive features, including a unique N-terminal fragment

within the spike protein. Genes for the major structural proteins in all coronaviruses occur in the 5′–3′ order as S, E, M, and N [12].(Fig. 2).

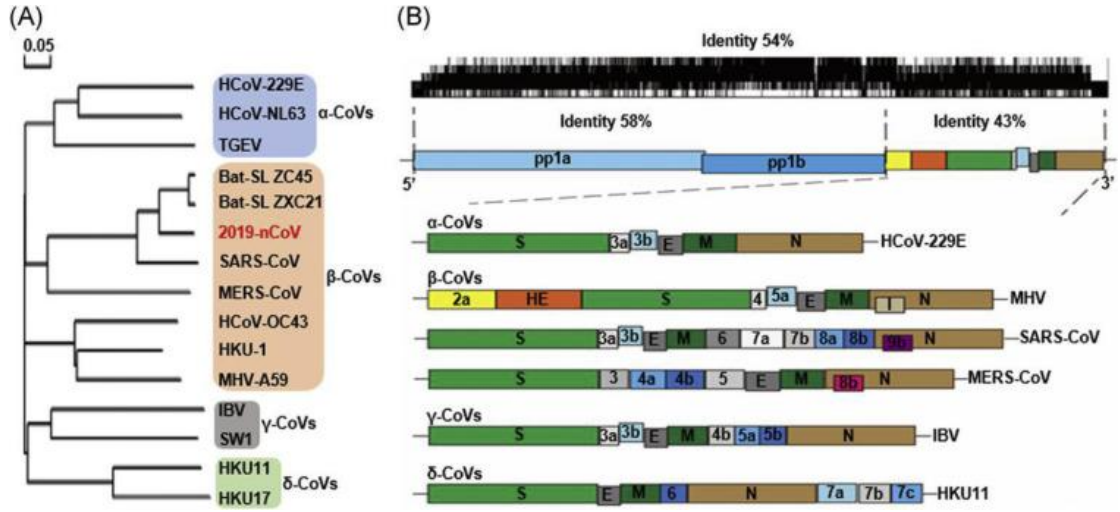

Figure no 2: The genomic structure and phylogenetic tree of coronaviruses: A, the phylogenetic tree of representative CoVs, with the new coronavirus COVID-19 shown in red. B, The genome structure of four genera of coronaviruses: two long polypeptides 16 nonstructural proteins have proceeded from Pp1a and pp1b represent. S, E, M, and N are represented of the four structural proteins spike, envelope, membrane, and nucleocapsid. COVID-19; CoVs, coronavirus; HE, hemagglutinin-esterase. Viral names: HKU, coronaviruses identified by Hong Kong University; HCoV, human coronavirus; IBV, infectious bronchitis virus; MHV, murine hepatitis virus; TGEV, transmissible gastroenteritis virus. [13].

Membrane of corona virus contained three or four proteins. The most proportion structural protein is the membrane (M) glycoprotein; it spans the membrane bilayer three times, leaving a short NH2-terminal domain outside the virus and a long COOH terminus (cytoplasmic domain) inside the virion.4 The spike protein (S) as a type I membrane glycoprotein constitutes the peplomers. In fact, the main inducer of neutralizing antibodies is S protein. Between the envelope proteins with exist a molecular interaction that probably determines the formation and composition of the coronaviral membrane. M protein plays a critical role in the intracellular formation of virus particles without requiring S. In the presence of tunicamycin coronavirus grows and produces spikeless, noninfectious virions that contain M but devoid of S.[11,12].

IV. Covid-19 life cycle

The way of entering and releasing of the Covid-19 virus into the human cell and then multiplying inside human cell, the complete entry processis mapped in Fig 2. The spike protein (S)of membrane COVID-19 attaches to the specific site that is an angiotensin converting enzyme 2 (ACE2) receptors which is found on the surface of many human cells, especially those presented on the lung cells allowing virus entry. The COVID-19 membrane Sprotein is subjected to proteolytic cleavages by host proteases (i.e. trypsin and furin), intwo sites located at the boundary between the S1 and S2 subunits (S1/S2 site). In a later stage happens the cleavage of the S2 domain (S20 site) in order to release the fusion peptide [13,14]

The attachment between virus membrane protein S willtrigger the activation of the membrane fusion mechanism then then complete the entry trip to the host cell . Therefore, the specificity of the antibody may find a foothold on the targeted part by the virus on the host cell that is utilized it to entry, which is the ACE2 receptor, such this hypothesis may be the promised goal to finding the treatment for the infection with the COVID-19 through the blocking of viral entry.Usually, COVID-19 will be ingested by human cell through process called endocytosis. But after entry of COVID-19 into the cytoplasm, it has been suggested most likely that COVID-19 used a unique method as a mechanism resistance consisted from threesteps for its membrane fusion;including receptor-binding and induced commentary changes in Spike (S) glycoprotein followed by cathepsin L proteolysis through intracellular proteases and further activation of membrane fusion mechanism within endosomes [13,14,15]. Then, the endosome opens to release virus to the cytoplasm,and uncoating of viral nucleocapsid (N) is started via proteasomes which typically can hydrolyse endogenous proteins, but they are also capable of degrading exogenous proteins such as the SARS nucleocapsid protein [14,15].

When the COVID-19virion binds to its receptor on their host cell surface through its S1 subunit and the membrane spike is split by host proteases (Hasan et al., 2020) and then itis expected the fusion at low pH

between viral and host target membranes via S2 subunit. Then the final step that , the viral single stranded RNA is fully released into the cytoplasm. There takes place the replication and transcriptionprocesses which are mediated by the so-called replication/complex (RTC). Such complex is encoded in theviral genome and it is made of non-structural proteins (nsp) [16,17]. see fig 3.

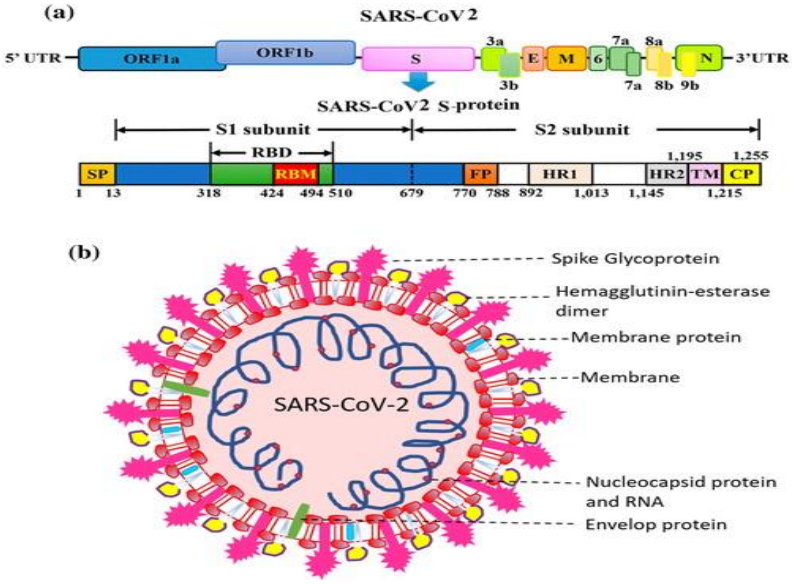

Figure no3. Schematic representation of the genome organization and functional domains of S protein for COVID-19.

Structural proteins M,S, and E of COVID-19 that are settled at cytoplasm and then inserted into the endoplasmic reticulum (ER) (Fig.4), and transfer to endoplasmic reticulum-Golgi intermediate compartment (ERGIC) [18,19]. Finally, novel virions are exported frominfected cells by transport to the cell membrane in smooth walled vesicles and then secreted via a process called exocytosis, so that can infect other cells. In the meantime, thestress of viral production on the endoplasmic reticulumeventually leads to cell death. However, the mechanism ofaction for novel COVID-19 is still complicated yet[18,20].

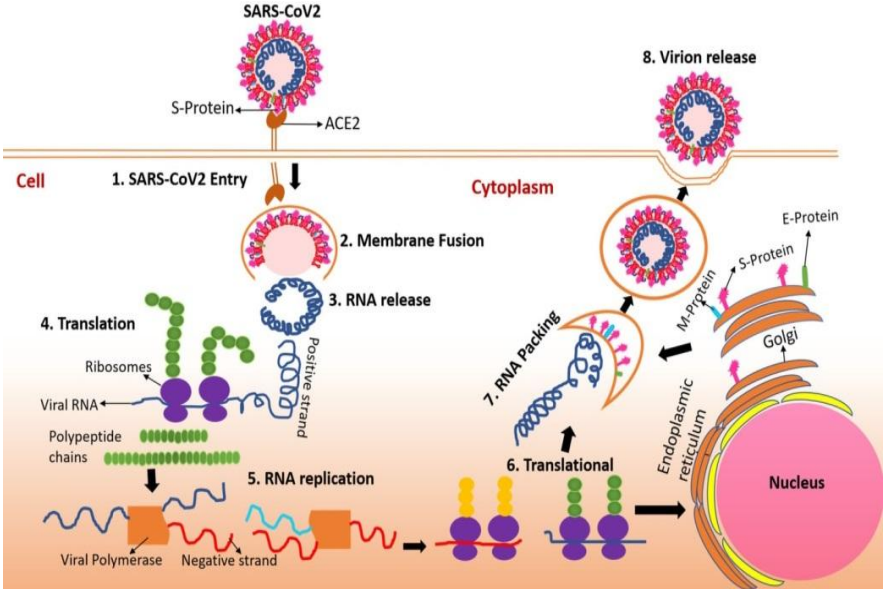

Figure no 2: The schematic diagram of the mechanism of COVID-19 entry and viral replication and viral RNA packing in the human cell.[18].

V. Covid-19 Vaccines

All Vaccines and antiviral drugs for coronaviruses that are based on membrane S protein have been previously evaluated. Du et. al. in 2009 demonstrated that several vaccines can be based on the S protein include full-length S protein, viral vector, DNA, recombinant S protein and receptor binding protein (RBD). Antiviral therapies are design based on S protein include receptor binding protein(RBD–ACE2) blockers, S cleavage inhibitors, fusion core blockers, neutralizing antibodies, protease inhibitors, S protein inhibitors, and small interfering RNAs.[21,22,23] There are some recombinant compounds such as interferon gama (IFN) with ribaverin which has only limited effects against COVID-19 infection [1]. The receptor-binding domain of SARS-CoV-2 has a higher affinity for ACE2 on humane cells, while it is a lower affinity for SARS-CoV-1, Angiotensin-converting enzyme (ACE) and its homologue ACE2, belongs to the ACE family of dipeptidylcarboxydipeptidase [23,24]. However, their physiological functions are varied. On the other hand, ACE2 serves as the binding site for COVID-19. Based on this information, Gurwitz in 2020 suggested using available angiotensin receptor 1 (AT1R) blockers, such as losartan, as therapeutics for reducing the severity of COVID-19 infections[24,25] At present therapy is based on identifying and developing monoclonal antibodies that are specific and effective against COVID-19 combines with remdesivir as a novel nucleotide analog prodrug that was used for the treatment of the Ebola virus disease.[23,24]. To understanding the transmission rate of COVID-19 spread among people, it is crucial to figure out whether COVID-19 is mutating to improve its binding to human receptors for infection considering its high mutation rate. Any adaptation in the COVID-19 sequence that might make it more efficient at transmitting among people might also boost its virulence[25,26].According to the COVID-19 properties some of some experts and specialists experts have been suspecting that COVID-19 will be less virulent through human to human transmissions due to genetic bottlenecks for RNA viruses often occur during respiratory droplet transmissions.[27]. New and rapid studies on the composition of the COVID-19 and the mechanism of immune responses may serve to produce an effective vaccine.

References

[1]. Anthony R., Fehr, Stanley Perlman. Coronaviruses, An Overview of Their Replication and Pathogenesis. Coronaviruses, 2020, pp 1-2

[2]. XiuyuanOu, Yan Liu, Xiaobo Lei, Pei Li, Dan Mi, LiliRen, Li Guo, RuixuanGuo, Ting Chen, Jiaxin Hu, Zichun Xiang, Zhixia Mu, Xing Chen, Jieyong Chen, Keping Hu, Qi Jin, Jianwei Wang, and ZhaohuiQian.Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS-CoV. Nature Communications.2020; V 11,No.1620, 60-69.

[3]. Yount B, Roberts RS, Sims AC, Deming D, Frieman MB, Sparks J, Denison MR, Davis N, Baric Ralph. S. Severe acute respiratory syndrome coronavirus group-specific open reading frames encode nonessential functions for replication in cell cultures and mice. J Virol.2005; 79(23), 14909-22.

[4]. Denison MR, Graham RL, Donaldson EF, Eckerle LD, Baric Ralph, S. (2011). Coronaviruses: an RNA proofreading machine regulates replication fidelity and diversity. RNA Biol.2011; 8(2):270-9.

[5]. Lu, H.; Stratton, C.W.; Tang, Y.W. Outbreak of pneumonia of unknown etiology in Wuhan, China: The mystery and the miracle. J. Med. Virol.2020;V.92, 401–402.

[6]. World Health Organization Director-General's Opening Remarks at the Media Briefing on COVID-19, 11 March 2020.

[7]. Amanat, F., Krammer, F. SARS-CoV-2 vaccines: status report.Immunity,2020; 52(4), 583-589.

[8]. Chu, C. M., Cheng, V. C. C., Hung, I. F. N., Wong, M. M. L., Chan, K. H.,Chan,K.S.,Yuen, K. Y. Role of lopinavir/ritonavirinthe treatment of SARS: Initial virological and clinical findings. Thorax,2004;59(3), 252–256.

[9]. Pan American Health Organization • http://www.paho.org • © PAHO/WHO, 2020.

[10]. Zhenming Jin, Xiaoyu Du, YechunXu, Yongqiang Deng, Meiqin Liu, Yao Zhao, Bing Zhang, Xiaofeng Li, Leike Zhang, YinkaiDuan, Jing Yu, Lin Wang, Kailin Yang, Fengjiang Liu, Tian You, Xiaoce Liu, Xiuna Yang, Fang Bai, Hong Liu, Xiang Liu, Luke W. Guddat, Gengfu Xiao, Chengfeng Qin, Zhengli Shi, Hualiang Jiang, ZiheRao, Haitao Yang. Structure-based drug design, virtual screening and high-throughput screening rapidly identify antiviral leads targeting COVID-19.doi: https://doi.org/10.1101/2020.02.26.964882

[11]. C.A.M. de Haan, L. Kuo, P.S. Masters, H. Vennema, P.J.M. Rottier Coronavirus particle assembly: primary structure requirements of the membrane protein. J Virol,1998; 72 (8) 6838-6850.

[12]. P.C.Y. Woo,Y. Huang, S.K.P. Lau, K.-Y. Yuen Coronavirus genomics and bioinformatics analysis. Viruses. 2010; 2 (8), 1804-1820.

[13]. Y. Chen, Q. Liu, D. Guo Emerging coronaviruses: genome structure, replication, and pathogenesis. J Med Virol.2020; 92,418-423.

[14]. Simmons, G., Gosalia, D. N., Rennekamp, A. J., Reeves, J. D., Diamond, S. L., & Bates, P. Inhibitors of cathepsin L prevent severe acute respiratory syndrome coronavirus entry. Proceedings of the National Academy of Sciences.2005; 102(33), 11876–11881.

[15]. Wang, Q., Li, C., Zhang, Q., Wang, T., Li, J., Guan, W., Yu, J., Liang, M., & Li, D. Interactions of SARS Coronavirus Nucleocapsid Protein ith the host cell proteasome subunit p42. Virology Journal. 2010; 7(1), 2010, 99–98.

[16]. Hasan, A., Paray, B. A., Hussain, A., Qadir, F. A., Attar, F., Aziz, F. M., Falahati, M. A review on the cleavage priming of the spike protein on coronavirus by angiotensin-convertingenzyme-2andfurin. Journal of Biomolecular Structure and Dynamics. 2020; 1–13.

[17]. Van Hemert, M. J., Van Den Worm, S. H. E., Knoops, K., Mommaas, A. M.,Gorbalenya, A. E., &Snijder, E. J. SARS-coronavirus replication/ transcription complexes are membrane-protected and need a host factor for activity in vitro. PLoS Pathogens. 2008; 4(5).

[18]. Masters ,P. S. The molecular biology of coronaviruses. Advancesin Virus Research.2006; 65(06), 193–292.

[19]. Song,H.C.,Seo,M.-Y.,Stadler,K.,Yoo,B.J.,Choo,Q.-L.,Coates,S.R.,Uematsu,Y.,Harada,T.,Greer,C.E.,Polo,J.M.,Pileri,P.,Eickmann,M., Rappuoli, R., Abrignani, S., Houghton, M., & Han, J. H. Synthesis and characterization of a native, oligomeric form of recombinant severe acute respiratory syndrome coronavirus spike glycoprotein. Journal of Virology.2004; 78(19), 10328–10335.

[20]. Liu C, Zhou Y, Li Y, Garner LV, Watkins Sp, Carter Lj, et al.Research and development on therapeutic agents and vaccines for COVID-19 and related human coronavirus diseases. ACS publications;2020.
[21]. Du L, He Y, Zhou Y, liu S, S. Jiang. The spike protein of SARS-CoV—a target for vaccine and therapeutic development. Nat Rev Microbiol.2009; 7 (3);226-236.
[22]. Chen Y, Q. Liu, D. GuoEmerging coronaviruses: genome structure, replication, and pathogenesis. J Med Virol, 92 2020, 418-423.
[23]. Prabakaran P, X. Xiao and D.S. Dimitrov. A model of the ACE2 structure and function as a SARS-CoV receptor. BiochemBiophys Res Commun.2004; 314 (1); 235-241.
[24]. Gurwitz D. Angiotensin receptor blockers as tentative SARS-CoV-2 therapeutics. Drug Dev Res.2020, 1-4.
[25]. SheahanT.P,sims Ac, Ghaham RL, Mencahery VD, Gralinski LE, Case JB, et al. Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic coronaviruses. SciTransl Med.2017; 9 (396).
[26]. M.A. Martinez. Compounds with therapeutic potential against novel respiratory 2019 coronavirus. Antimicrobial Agents and Chemotherapy. 2020.
[27]. Cascella M, rajnik M, Cuomo A, Dulebohn SC, Di Napoli R.Features, evaluation and treatment coronavirus (COVID-19). StatPearls [Internet];Publishing (2020).

Salih Abdul Mahdi Khadim. " Review Article to highlight of SARS-CoV2 (Covid -19) Characteristics and epidemiology." *IOSR Journal of Pharmacy and Biological Sciences (IOSR-JPBS)*, 15(4), (2020): pp. 46-50.