Drug Targets for Corona Virus (COVID-19): A Systematic Review

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Abstract

The 2019 Novel corona virus (nCoV) is a major source of disaster in the 21st century. However, the lack of specific drugs to prevent/treat an attack is a major need at this current point of time. In this regard, we conducted a systematic review to identify major drug gable targets in corona virus (CoV). We searched PubMed and RCSB database with keywords HCoV, NCoV, corona virus, SERS-CoV, MERS-CoV, 2019-nCoV, crystal structure, X-ray crystallography structure, NMR structure, target, and drug target till Feb 3, 2020. The search identified seven major targets (spike protein, envelop protein, membrane protein, protease, nucleocapsid protein, hemagglutinin esterase, and helicase) for which drug design can be considered. There are other 16 nonstructural proteins (NSPs), which can also be considered from the drug design perspective. The major structural proteins and NSPs may serve an important role from drug design perspectives. However, the occurrence of frequent recombination events is a major deterrent factor toward the development of CoV-specific vaccines/drugs.

Keywords: Corona virus, drug targets, Middle East respiratory syndrome, severe acute respiratory syndrome.

INTRODUCTION

Corona viruses (CoVs) have a single-stranded RNA genome (size range between 26.2 and 31.7 kb, positive sense), covered by an enveloped structure. The shape is either pleomorphic or spherical, and it is characterized by bears club-shaped projections of glycoproteins on its surface (diameter 80–120 nm) [1]. Among all the RNA viruses, the RNA genome of CoV is one among the largest. The number of open reading frames (ORFs) in the CoV genome ranges from six to ten [2]. CoV genetic material is susceptible for frequent recombination process, which can give rise to new strains with alteration in virulence [3]. There are seven strains of human CoVs, which include 229E, NL63, OC43, HKU1, Middle East respiratory syndrome (MERS)-CoV, severe acute respiratory syndrome (SARS)-CoV, and 2019-novel corona virus (nCoV), responsible for the infection with special reference to the involvement of the respiratory tract (both lower and upper respiratory tract), e.g., common cold, pneumonia, bronchiolitis, rhinitis, pharyngitis, sinusitis, and other system symptoms such as occasional watery and diarrhea [4]. Among these seven strains, three strains proved to be highly pathogenic (SARS-CoV, MERS-CoV, and 2019-nCoV), which caused endemic of severe CoV disease [5]. The reservoir of SARS-CoV is unknown, but bats and subsequent spread to Himalayan palm civets are hypothesized [6]. MERS-CoV also has a zoonotic origin in the Middle East, and the transmission is through camels [7]. Among these, the SARS-CoV outbreak started in 2003 in Guangdong province of China and the second outbreak of the MERS-CoV outbreak in 2012 in Saudi Arabia. Previous to these two attacks, CoV was known to cause milder disease, and these two outbreaks highlighted their adaptive potential to the changing environmental conditions and they are classified under “emerging viruses.” Knowledge about the structure, metabolic pathways of CoV, and pathophysiology of CoV-associated diseases is important to identify possible drug targets [8].

The most important structural proteins of CoV are spike (S) protein (trimeric), membrane (M) protein, envelop (E) protein, and the nucleocapsid (N) protein. Some of the viruses such as beta-CoVs also have hemagglutinin esterase (HE) glycoprotein. The RNA genome of CoV has seven genes that are conserved in the order: ORF1a, ORF1b, S, ORF3, E, M, N in 5’ to 3’ direction. The two-third part of the RNA genome is covered by the ORF1a/b, which produces the two viral replicase proteins that are polyproteins (PP1a and PP1ab) [9]. Sixteen mature nonstructural proteins (NSPs) arise from further processing of these two PPsp. These NSPs take part in different viral functions.
including the formation of the replicase transcriptase complex. The remaining genome part of the virus encodes the mRNA which produces the structural proteins, i.e., spike, envelope, membrane, and nucleocapsid, and other accessory proteins. Another important envelope-associated protein which is expressed by only some strains of CoV is the HE protein [10]. The RNA genome of CoV is packed in the nucleocapsid protein and further covered with envelope [11].

Molecular Basics of Transmission of Corona virus

In case of SARS-CoV, transmission is through droplet infection (respiratory secretions) and close person-to-person contact. It can also spread through sweat, stool, urine, and respiratory secretions. When virus enters into the body, it binds to the primary target cells such as enterocytes and pneumocytes, thereby establishing a cycle of infection and replication. Other target cells of CoV are epithelial renal tubules, tubular epithelial cells of kidney, immune cells, and cerebral neuronal cells [11-13]. CoV attaches to the target cells with the help of spike protein–host cell protein interaction (angiotensin converting enzyme-2 [ACE-2] interaction in SARS-CoV [14] and dipeptidyl peptidase-4 [DPP-4] in MERS-CoV [15]. After the receptor recognition, the virus genome with its nucleocapsid is released into the cytoplasm of the host cells. The viral genome contains ORF1a and ORF1b genes, which produce two PP's that are pp1a and pp1b which help to take command over host ribosomes for their own translation process. Both pp1a and pp1b take part in the formation of the replicase transcription complex. After processing of PP by protease, it produces 16 NSPs. All NSPs have their own specific functions such as suppression of host gene expression by NSP1 and NSP2, formation of a multidomain complex by NSP3, NSP5 which is a M protease which has role in replication, NSP4 and NSP6 which are transmembrane (TM) proteins, NSP7 and NSP8 which act as a primase, NSP9-a RNA-binding protein, the dimeric form of which is important for viral infection. Induction of disturbance to the dimerization of NSP9 can be a way to overcome CoV infection [16-20]. NSP10 acts as a cofactor for the activation of the replicative enzyme. NSP12 shows RNA-dependent RNA polymerase activity, NSP13 shows helicase activity, NSP14 shows exoribonuclease activity, NSP15 shows endoribonuclease activity, and NSP16 has methyltransferase activity. All NSPs have an important role in replication and transcription [21].

Synthesized proteins such as M, E, and S are entered into the endoplasmic reticulum (ER)-Golgi intermediate compartment (ERGIC) complex and make the structure of viral envelope. On the other hand, the replicated genome binds to N protein and forms the ribonucleoprotein (RNP) complex. The outer cover is formed by the M, E, and S proteins. Finally, the virus particle comes out of the ERGIC by making a bud-like structure. These mature virions form a vesicle, which fuses with the plasma membrane and releases the virus particles into the extracellular region [22-24]. The detailed structure of CoV and its life cycle is depicted in (Figure 1 & 2). On infection, the SARS-CoV and MERS-CoV cause a surge of pro-inflammatory cytokines and chemokines, which cause damage to lung tissue, deterioration of lung function, and then finally lung failure in some cases [25]. The S proteins of CoV binds to cellular receptor angiotensin-converting enzyme 2 (ACE2) which is followed by entry of the viral RNA genome into the host cell and translation of structural and non-structural proteins (NSP) follows. ORF1a and ORF1ab are translated to produce pp1a and pp1ab polyproteins, which are cleared by the proteases that are encoded by ORF1a to yield 16 non-structural proteins. This is followed by assembly and budding into the lumen of the ERGIC (Endoplasmic Reticulum Golgi Intermediate Compartment). Virions are then released from the infected cell through exocytosis. S: spike, E: envelope, M: membrane, N: nucleocapsid, PP: polyproteins, ORF: Open reading frame, CoV: coronavirus (Figure 1 and 2).

Currently, there is no specific antiviral drug for the treatment of CoV-associated pathologies. Most treatment strategies focus on symptomatic management and supportive therapy only [26, 27]. Some therapeutic agents that are under development or being used off-label are ribavirin, interferon (IFN)-α, and mycophenolic acid. There are many newspaper articles citing effectiveness of anti-HIV drugs: ritonavir, lopinavir, either alone or in combination with oseltamivir, remdesivir, and chloroquine and among these, ronitavir, remdesivir, and chloroquine showed efficacy at cellular level which further need experimental support and validation [28, 29]. As there is no well-defined therapy available, which specifically targets CoV, in this article, we have reviewed the possible protein structures, which could be potential targets for the development of a therapeutic approach for the treatment of CoV.

MATERIALS AND METHODS

Database Screen

We screened PubMed and RCSB database with the keywords HCoV, NCoV, corona virus, SERS-CoV, MERS-CoV, 2019-nCoV, crystal structure, X-ray crystallography structure, NMR structure, target, and drug target till Feb 3, 2020. The database files were extracted using endnote, and title and abstract screening was done using Rayyan QCRI. Full texts of these screened articles were further screened for possible inclusion in the systematic review. Articles that evaluated different druggable targets of CoV and evaluated different therapeutic measures against some identifiable target were included for further review.
RESULTS AND DISCUSSION

A total of 392 articles were found after preliminary screening of the databases. After title and abstract screening, a total of 230 articles were excluded. Full-text screening of the remaining 154 articles was done. Among these studies, after full-text screening, a total of 122 articles were included in the final review.

The PRISMA flowchart of the study is shown in (Figure-3). Thirty-two articles were excluded after full-text screen (review articles = 7, articles not specifying drug targets against CoV = 22, articles in other language other than English = 3). Details of studies with important structural and functional target proteins are summarized in (Table-1 and Flow Chart-1).
Flow Chart-1: Analysis of publications

Table-1: Details of various protein inhibitors

| PDB ID | Details | Inhibitor | IC$_{50}$ | Reference |
|--------|---------|-----------|----------|-----------|
| 4JUJ   | Interaction between PUD and NTD of N protein of HCoV-OC43 | PUD4 | - | [26] |
| 5V0P   | Structure not released | - | - | [30] |
| 4LM7   | Interactions of NTD of N protein of HCoV-OC43 with UMP | - | - | [26] |
| 4LJ4   | Interactions of NTD of N protein of HCoV-OC43 with AMP | - | - | [26] |

Protease

| PDB ID | Details | Inhibitor | IC$_{50}$ | Reference |
|--------|---------|-----------|----------|-----------|
| 4TXY   | 3CLPro of SARS-CoV with an inhibitor | 3BL | - | [27] |
| 4TXYW  | 3CLPro of SARS-CoV with an inhibitor | 41 | 63 µM | [27] |
| 4RYY3  | 3CLPro of SARS-CoV with an inhibitor | 3K8S | 249 µM | [27] |
| 4DVZ   | CoV PLPro complexed with inhibitor | PBS | 490 nM | [31] |
| 3M5U   | SARS-CoV PL$^{TM}$ complexed with inhibitor | GFM | 320 nM | [32] |
| 2FE8   | SARS-CoV PL$^{TM}$ | - | - | [33] |
| 1UK4   | SARS-CoV 3CL$^{TM}$ and its interactions with a inhibitor | Substrate analog hexapeptide DMM inhibitor IC$_{50}$ ca. 2 mM | - | [34] |
| 1UJ11  | SARS-CoV M-pro, apo-enzyme at different pH | - | - | [34] |
| 1UK3   | 1UK2 | - | - | [34] |
| 5V8B   | SARS-CoV 3CLPro in complex with O62 | O62 | 39 µM | [35] |
| 5V8B   | SARS-CoV 3CLPro with O4Z | O4Z | 1.3-4.6 µM | [35] |
| 5TLO   | HCoV-NL63 3CLPro | - | - | [36,37] |
| 5U7    | Main protease of 2019-nCoV and its complex with N3S (inhibitor) | - | - | [38] |

Spike protein

| PDB ID | Details | Inhibitor | IC$_{50}$ | Reference |
|--------|---------|-----------|----------|-----------|
| 5ZUV   | HR1 motif of HCoV-229E in complex with EK1 | Modified OG-OG-HR2P peptide (EK1) | 0.19-0.62 µM | [39] |
| 5ZVM   | EK1 in complex with SARS HR1 motif | - | - | [39] |
| 5K4G   | NTD of SARS-CoV S protein | - | - | [40] |
| 5VPR0  | SARS-CoV S protein | - | - | [41] |
| 4G05   | MERSCoV S structure in complex with Sialyl-LeRicin | - | - | [42] |
| 4AOG   | SARS-CoV S protein: ACE-2 (conformation 1) complex | - | - | [43] |
| 5A0K   | SARS-CoV S protein: ACE-2 (conformation 3) complex | - | - | [43] |
| 5SCI   | RBSD of S protein interaction with ACE-2 | - | - | [44] |

Spike Protein

The spike protein is a clove-shaped, type I-TM protein. The spike protein has three segments that are ectodomain (ED) region, TM region, and intracellular domain, which comprises the intracellular short tail part. The receptor-binding S1 domain (three S1 heads) and the membrane fusion subunit S2 (trimeric stalk) on C-terminal together comprise the ED. Spike proteins gather in the trimeric form on the outer surface of the virion, giving it the appearance of a crown, due to...
which it is called CoV. The spike protein plays an important role in virus entry into the host. Initial interactions between the S1 domain and its host receptor (ACE2 in case of SARS-CoV and PP 4 in case of MERS-CoV) and subsequent S2 segment mediated fusion of the host and viral membranes allow the CoV-RNA genome to enter inside the host cells and thus, these proteins represent as important targets from drug discovery side. The spike protein also activates the immune response of the host cell toward CoV [2, 10].

S1 Domain

The main components of the S1 domain are the N-terminal domain (NTD) and the C-terminal domain (CTD). The S1 domain acts as a major antigen on the surface of the virus [40] and has a receptor-binding domain (RBD). The 18 residues of ACE-2 interact with the RBD (contain 14 amino acids) of SARS-CoV spike protein, and for this contact, K341 of ACE-2 and R453 residue of RBD play the most important role. If point mutated on the D454 or R441 of RBD, it disturbs the binding activity with ACE-2. The S1 domain interacts with the ACE-2 or DPP-4 receptors of the host. Anti-ACE-2 antibody blocked viral entry and replication in Vero E6 cells. One another mechanism of virus for binding to host cell is using dendritic cell-specific intercellular adhesion molecule-3 grabbing non-integrin (DC-SIGN receptor) or L-SIGN in lymph nodes or in liver. S-protein has seven (109, 118, 119, 158, 227, 589, and 699) glycosylation asparagine-linked sites, which is pivotal for both L-SIGN- or DC-SIGN-based virus entry into the host [14, 25, 45-47].

S2 Subunit

The S2 subunit has two heptad repeat regions (HR 1 and 2) and hydrophobic fusion peptide. Drug designing strategies targeting S protein and its interactions. The RBD is targeted in many drug designing studies. A peptide sequence with sequence similarity to the RBD of S protein hampered S1-RBD: ACE-2 interaction and prevented entry of SARS-CoV into Vero cells (IC50 around 40 μM). A SARS-CoV RBD-specific antibody (FM6) failed to inhibit the occurrence of infection. OC43-HR2P, a peptide derived from heptad repeat 2 regions of S2 domain of HCoV-OC43 and its optimized form EK1, showed pan-CoV fusion inhibition property. The structure (protein data bank [PDB] ID 5ZUV and 5ZVM) shows as -helix bundle structure with α-HCoV and long β-HCoV-HR1 domain. Chloroquine, an antimalarial agent, inhibits SARS-CoV by elevation of endosomal pH and alters the terminal glycosylation of ACE-2, which ultimately interferes with the virus receptor binding. Other inhibitors SSA09E2 block the S-ACE2 interaction, SSA09E1 inhibits the host protease cathepsin L (which is important for viral entry), and SSA09E3 prevents fusion of host and viral cell membrane [25, 49, 50, 39, 51, 52]. Kao et al., identified 18 small molecules that targeted the S-ACE-2-mediated entry of virus into human cell. In 293T cells expressing ACE-2, one of these agents (VE607) showed a significant inhibition of SARS-pseudovirus entry. In Vero E6 cells, two other molecules tetra-O-galloyl beta-D-glucose and luteolin also inhibited SARS-pseudovirus and SARS-CoV infection. In virus-infected Vero E6 cells, a siRNA against the S sequences of SARS-CoV inhibited SARS-CoV replication [53, 54].

The S230 antibody (origin: memory B-cells of SARS-CoV-infected persons) neutralizes wide spectrum of isolates of SARS-CoV. S230 antibody Fab fragment binds to the SARS-CoV complex to neutralize it, and their structures are also available (PDB IDs: 6NB6, 6NB7, and 6NB8). The monoclonal antibody, m396, has a competitive role for RBD binding (PDB ID: 2DD8) [55, 56]. Monoclonal antibody can be generated by immunizing the spike protein of SERS-CoV (transgenic mice) or from the B-cells of CoV-infected persons. Spike-specific monoclonal antibodies 80R and CR301 block the S-ACE-2 interactions and thus neutralize infection by human SARS-CoV (HKu39849 and Tor2) and palm civet strain (SZ3). Mice vaccinated with SARS-n DNA showed T-cell immune response (both induction and proliferation), and cytotoxic T-cell response was seen against SARS-DNA-transfected alveolar epithelial cells [57].

Envelope Protein (E)

The E protein is the smallest (8.4–12 kDa size) TM structural protein of CoV. Two distinct domains comprise the E protein: the hydrophobic domain and the charged cytoplasmic tail. However, the structure is highly variable among different members of the CoV family. The E protein has a special role in viral morphogenesis, especially during assembly and egress. CoVs lacking E protein show lower viral titer, immature, and inefficient progenies. Oligomerization of E proteins leads to the formation of ion channels. However, the importance of these ion channels is still not clear. Many other studies infer that the E protein acts in coordination with other intracellular proteins and modulates the activity of those proteins. E protein also acts as a virulence factor. E protein has an important role in CoV assembly and budding formation. Apart from this, E protein found around the ER and Golgi body regions. Hexamethyleneammoniumride blocks this E protein-associated ion channel activity in the mammalian cells expressing SERS-CoV envelope protein [59-62].

Membrane Protein

Maintenance of the shape of the viral envelope is the most important function of the M protein, and the M protein performs this job by interacting with other CoV proteins, incorporation of Golgi complex into new virions, and stabilization of nucleocapsid protein. The M protein is characterized by three TM domains with C-terminal inside (long) and N-terminal (short) outside. The details of the protein structure is available in
Nucleocapsid Protein (N)

The structure of nucleocapsid protein (N protein) is conserved among different members of the CoV family. The three characteristic intrinsically disordered regions (IDRs) of the nucleocapsid (N) protein are the N-arm, central linker (CL), and the C-tail. The NTD and the CTD are the major structural and functional domain of the nucleocapsid protein. The most important function of the N protein NTD is RNA binding, while the primary job of the CTD is dimerization. As the CL region is rich in arginine and serine residue content, it also contains a large number of phosphorylation sites. The C-terminal IDRs take an important part in nucleocapsid protein oligomerization and N–M protein interactions [67]. Formation and maintenance of the RNP complex are the most important functions of the N protein. It also regulates the replication and transcription of viral RNA, and in the host, it inhibits protein translation through EF1α-mediated action, alteration of host cell metabolism, host cell cycle (N proteins are reported to inhibit CDK4), and apoptosis. In human peripheral blood, N protein inhibits cell proliferation through the inhibition of cytokinesis[66]. The NTD contains sites for RNA binding. The RNA-binding sites on the NTD of N protein were identified by observing its interactions with ribonucleoside 5’-monophosphates (AMP, UMP, CMP, and GMP). Using the information about interaction between AMP and UMP binding to the NTD of nucleocapsid protein, inhibitors of RNA binding were designed. Three-dimensional structure with all complex can see from PDB that is 4LMC, 4LM9, 4LM7, and 4LI4, respectively. One such molecule which was designed with this strategy is N-(6-oxo-5,6-dihydrophenanthridine-2-yl) (N, N dimethyl amino) (PJ34), which was designed using the HCoV-OC43 model. Binding of PJ34 on NTD affects the genome binding and replication process of CoV. The crystal structure of COV-OC43 N-NTD with inhibitor PJ34 complex is given in PDB ID: 4KX1. On the basis of interactions between PJ34 and NTD of nucleocapsid protein, another inhibitor was designed that is H3 (6-chloro-7-(2-morpholin-4-yl-ethylamino) quinoxaline-5,8-dione), which also inhibits RNA binding. This highlights the importance of NTD in RNA binding.

Other N protein-targeted peptides of importance are NP111; NP331, and NP351 [72, 73].

Proteases

The SERS-CoV genome encodes a number of proteins. The replicase gene, which is a major component of the CoV genome encoded for 16 NSPs in the form of two large PP (PP1a and PP1ab). Two types of cysteine proteases act on these PP to release the NSPs. The C-terminal end of these PP is cleaved by chymotrypsin-like cysteine protease (main protease [Mpro] or 3C-like protease [3CLpro]) and the N-terminal end is processed by the Mpro (also known as papain-like protease [PLpro]) [74]. The first three cleavage sites of the PP is cut by PLpro while the rest 11 sites are cleaved by CLpro, and this cleavage results in release of 16 NSPs [74, 75].

3C-Like Protease

The 3CLpro is present in homodimer form and has cys-his dyad on active site which shows protease activity. If mutated on the Ser139 and phe140 positions, it abolishes the dimerization of 3CLPro (PDB ID: 3F9G). This protease can cleave 11 sites in the p1 position of PP1a and PP1ab and can produce a mature protein that anchors the replication/transcription complex and also releases the mature NSPs [76-78]. N-(benzo [1, 2, 3] triazol-1-yl)-N-(benzyl) acetamido (phenyl) carboxamides are also found to be important inhibitors of CLPro. The structure of CLPro inhibitor is with ML188 (IC50 1.5 μM) is reported (CID: 46897844, PDB ID: 3V3M). Another structure with CLPro inhibitor ML300 (PDB ID: 4MDS, IC50: 6.2 μM) is reported. Some metal-conjugated and peptidomimetic compounds showed inhibitory activity against 3CLpro. Some of the small molecules also act.

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as an inhibitor that is arylboronic acids, quinolinecarboxylate derivatives, thiophenecarboxylate, and phthalhydrazide-substituted ketoglutamine analogs. Some flavonoids are also reported to inhibit Mpro [75]. GC376 also has protease inhibitor activity. A crystal structure of Mpro with small molecule inhibitor N3 is also reported (PDB ID: 2AMQ). Lopinavir and ritonavir, which are the inhibitors of HIV protease, also inhibit Mpro. In silico studies directed that among commercially available drugs, colistin, valrubicin, icatibant, bepotastine, epirubicin, epoprostenol, vapreotide, aperpitant, caspofungin, and perphenazine also bind to the lopinavir/ritonavir-binding site on CoV [79-82].

**Papain-Like Protease**

The PLpro cleaves the N-terminal region of the PP to generate three NSPs (NSP 1, 2, and 3). PLpro has a catalytic core domain that contains 316 amino acid, which is responsible for cleaving replicase substrates, and a consensus sequence LXGG was required for cleavage. Higher doses of zinc and zinc conjugates were found to inhibit both types of SARS protease (CLpro and PLpro). Benzodioxole can inhibit the PLpro enzyme. The crystal structure of interaction is shown in PDB ID: 4OVZ, 4OWZ. Through in silico approach, another new lead was identified (6577871) which was further optimized, and compound 15h (S configuration, enzyme IC50 =0.56 μM, antiviral EC50 =9.1 μM) and 15g (R configuration, enzyme IC50 =0.32 μM; antiviral EC50 =9.1 μM) were found to be the most important inhibitors. The crystalized structural details of these interactions can be visualized in the PDB database (PDB ID: 2FE8 and 3E9S) [83, 84]. Many of the protease inhibitors are being used in the treatment of COVID-19, e.g., lopinavir–ritonavir combinations [85].

**Hemagglutinin Esterase**

This HE enzyme is present in the envelope of CoV, more specifically among beta-coronaviridae. The HE is a marker of CoV and influenza virus evolution. HE mediates reversible attachment to O-acetylated-sialic-acids by acting both as lectins and as receptor-destroying enzymes. Interactions between HE in complex with sialic acid can be visualized in PDB ID: 3CL5 [86].

**NTPase/helicase**

NTPase/helicase plays an important role in the central dogma of the virus. SARS-CoV helicase enzyme is a member of the SF1. This enzyme prefers ATP, dATP, and dCTP as substrates; it also hydrolyzed all NTPs. Toxicity issues are main obstacles in the development of inhibitors of helicase, and nonspecificity of inhibitors may cause serious toxicity [87]. However, despite theoretical limitations, helicase is being increasingly recognized as a druggable target for different disease conditions [87-89]. Once entered into the host cell, the subsequent life cycle of SERS-CoV requires low pH. Inhibitors of pH-sensitive endosomal protease block CoV infection. Several different small compounds and molecules have been reported against virus infection. Amiodarone gets accumulated in the acidic organelles. Vacuoles on exposure to amiodarone shows alteration in intracellular organelles especially enlargement of late endosomes. In in-vitro environment, amiodarone inhibited coronavirus infection in Vero cells. At priori trypsin, cleavage of S protein is essential for a successful viral entry. However, trypsin cleavage also does not affect the efficacy of amiodarone [90-92].

**2019-Novel Corona virus: Challenges**

In the RCSB database, only one PDB (PDB ID: 6LU7) is there on the 2019-nCoV which is in complex with N3 (inhibitor). The complete sequence of the 2019-nCoV is available. However, it is only 95% similar to bat-SL-CoVZC45 and 88% to SIRS CoV-ZSc (nucleotide blast, NCBI). This highlights the amount of recombination processes or changes that occurred in the 2019-nCoV and changes in protein structural and functional levels [93].

**Clinical Trial Update on 2019-Ncov**

A total of 233 trials are registered till date in the Chinese Clinical Trial Registry (dated Feb 24, 2020, keywords 2019-nCoV and COVID-19). Among the pharmacotherapeutic agents evaluated, some of the highlighted agents, which are being evaluated, are high-dose Vitamin C, favipiravir, adalimumab, dihydroartemisininpiperaquine, leflunomide, dipryridamole, chloroquine or hydroxychloroquine, suramin sodium, lopinavir/ritonavir and arbidol (umifenovir) tablets, and IFN-alpha 2b. Other important agents being evaluated are Huo-Shen particles, Xiyyanping injection, Shen-Fu injection, etc., many of which are from traditional Chinese medicines background. Use of stem cells is also evaluated frequently [94].

**CONCLUSION**

Drug discovery against the CoV is a challenging job owing to frequent recombination events. The development of a vaccine is another important aspect. We need more structural biology details and details of the life cycle of the CoV, which can speed up the drug/vaccine development process against CoV. Again, as a preventive measure, strict vigilance of viral changes in different hosts for prediction of an event is important.

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