A brief molecular insight of COVID-19: epidemiology, clinical manifestation, molecular mechanism, cellular tropism and immuno-pathogenesis

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Abstract

In December 2019, the emergence and expansion of novel and infectious respiratory virus SARS-CoV-2 originated from Wuhan, China caused an unprecedented threat to the public health and became a global pandemic. SARS-CoV-2 is an enveloped, positive sense and single stranded RNA virus belonging to genera betacoronavirus, of Coronaviridae family. The viral genome sequencing studies revealed 75–80% similarity with SARS-CoV. SARS-CoV-2 mainly affects the lower respiratory system and may progress to pneumonia and Acute Respiratory Distress Syndrome (ARDS). Apart from life-threatening situations and burden on the global healthcare system, the COVID-19 pandemic has imposed several challenges on the worldwide economics and livelihood. The novel pathogen is highly virulent, rapidly mutating and has a tendency to cross the species boundaries such as from bats to humans through the evolution and natural selection from intermediate host. In this review we tried to summarize the overall picture of SARS-CoV-2 including origin/ emergence, epidemiology, pathogenesis, genome organization, comparative analysis with other CoVs, infection and replication mechanism along with cellular tropism and immunopathogenesis which will provide a brief panoramic view about the virus and disease.

Keywords SARS-CoV-2 · COVID-19 · Pandemic · Infection · Pathogenesis

Introduction

Recent mysterious pneumonia that spread worldwide and known to have an origin at the seafood and animal market, in Wuhan, China has become global pandemic and given the name "2019-nCoV" by World Health Organization (WHO). Further, the International Committee of Virus Taxonomy classified this new virus as SARS-CoV-2 (Severe Acute Respiratory Syndrome coronavirus) based on standard practice, pathology, phylogeny and taxonomy [1]. SARS-CoV-2 known to be originated from bat coronavirus and transmitted to humans due to its ability to cross species barrier from bats to humans [2]. In the past two decades, coronaviruses are responsible for the three epidemics namely COVID-19, SARS and MERS. This novel SARS-CoV-2 is a zoonotic virus, belong to Coronaviridae family of Nidovirales order [3]. This family got its name "coronavirus" because of the crown-like appearance of its spike protein. The Coronavirus family is composed of four subgroups i.e. alpha (α), beta (β), gamma (γ) and delta (δ). Two subgroups the alpha (α), beta (β), mainly affect mammalians, whereas the other two subgroups, gamma (γ) and delta (δ) primarily affect birds [4]. Till date, seven kinds of human coronavirus have been identified out of which two belongs to alpha (α), HCoV-NL63 and HCoV-229E and five belongs to beta (β) HCoV-OC43, HCoV-HKU1, SARS-CoV (severe acute respiratory syndrome corona virus), MERS-CoV (Middle East respiratory syndrome coronavirus) and SARS-CoV2. The size of

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corona viruses range from 65 to 125 nm in diameter with a crown-like feature on the exterior surface. Genetically, Coronavirus is single-stranded positive-sense RNA with a relatively larger genome composition of 26 to 32kbs. Its genome composed of 6–10 open reading frames (ORFs), in which first ORF constitutes largest part of genome and other ORFs encode accessory and structural proteins. SARS-CoV-2 is different from SARS-CoV as seen in phylogenetic report and genomic sequencing. During last one year, it has become more virulent by undergoing frequent mutation thereby making it difficult to associate a particular strain with the severity of the disease. The binding of virus to host cell is the main determinant for the viral pathogenesis and designing of any antiviral therapy. Angiotensin-converting enzyme (ACE2) a Type 1 membrane glycoprotein which is highly up-regulated in the lungs and endothelial cells acts as a primary receptor for the viral entry and physiologically important in the progression of COVID-19 disease and illness [5]. This virus mainly affects the lower respiratory system and causes pneumonia similar to other beta coronaviruses SARS-CoV and MERS-CoV. Apart from the lower respiratory system it is also affecting gastrointestinal system, liver, heart, and kidney and leading to multiple organ failure [6, 7]. The extra pulmonary manifestations such as diarrhoea, impaired liver function, chronic renal disease etc. suggests viral tropism/affinity for the non-pulmonary tissues [5].

Epidemiology

The novel coronavirus, SARS-CoV-2 outbreak that started from Wuhan, China in December has been globally spread and imposed a severe threat to the people's health. China, the epicenter of the COVID-19 pandemic reported 4653 deaths and 89,000 confirmed cases. As per WHO latest report, more than 200 countries are threatened with more than 146 Million confirmed cases and over 3.1 Million deaths globally (Fig. 1) while more than one billion patients have given vaccine doses (232 Million fully vaccinated). Apart from life-threatening situations and huge burden on the global healthcare system, the COVID-19 pandemic has imposed several other challenges on economy, livelihood, individual freedom and social life. Besides confirmed cases; millions people were in quarantine/isolation for several months. To combat the pandemic, several countries have posed nationwide/statewide lockdown. Still several countries and states are in lockdown or under some sort of curb/curfew as world is witnessing second/third wave. Worldwide lockdown has
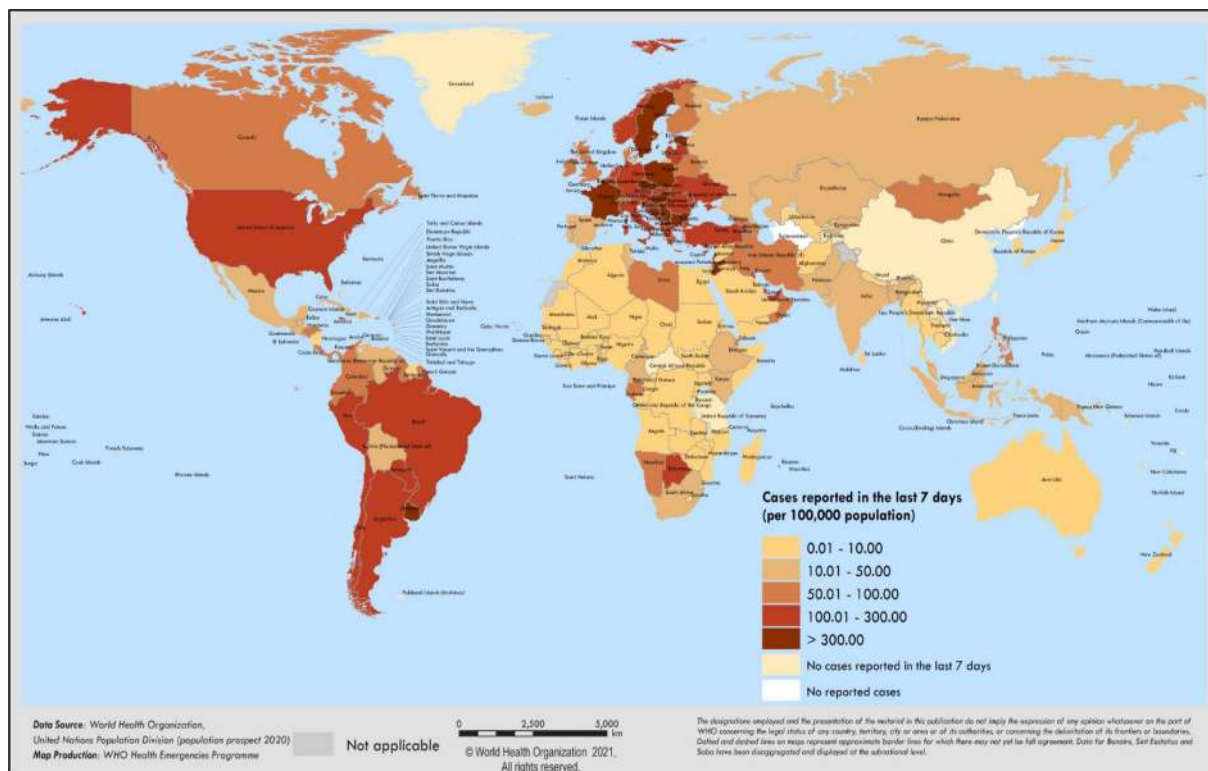
Fig. 1 Countries, territories or areas with reported confirmed cases of COVID-19, 30 March 2021 (Source: www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-reports)

imposed different kinds of psychological challenges among people and also affected the livelihood of millions.
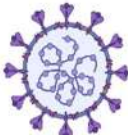
Symptoms, age, sex and CFR

The recent outbreak of pandemic COVID-19 is known as a respiratory disease caused by SARS-CoV-2 (https://www.who.int/westernpacific/emergencies/COVID-19). Chinese Centre for Disease Control and Prevention (China CDC) published a detailed analysis of 44,672 confirmed cases on February 14th. The clinical manifestations of COVID-19 could be both asymptomatic and symptomatic that include fever, sore throat, dry cough, tiredness, shortness of breath, ARDS (Acute respiratory distress syndrome), and pneumonia with varying degrees of severity. Complaints of gastrointestinal symptoms such as diarrhoea, nausea and vomiting, and myalgia or fatigue are also seen during illness [8–14]. The estimated CFR (case fatality rate) for COVID-19 is 3.4% up to March which is much higher than the flu (Fig. 2). As per the China CDC, 14% of patients were severe while 81% of patients showed only mild symptoms i.e. non-pneumonia and mild pneumonia, and no death was reported in this case [15]. 49.0% CFR was reported in 5% critically ill with respiratory failure, septic shock, and multiple organ failure. Total CFR was 2.3% while out of total fatality only 2.2% of patients were below 20 years. As per various reports children appeared to be at lower risk. CFR in the age group 70–79 was 8% while it was 14% in the age group 80 and above. Higher CFR was reported among the patient with pre-existing chronic ailments such as cardiovascular disease (10.5%), diabetes (7.3%), chronic respiratory disease (6.3%) and hypertension (6%). Variable CFR has been seen based of region/country. Variable CFR has been seen based of region/country. Variability in CFR would be very common as its depends on many factors such as socioeconomic condition, healthcare infrastructure, level of preparedness, population, co morbidity in population, testing capacity per million etc. in the particular country.

Till the date, no sex-disaggregated data on SARS-CoV-2 susceptibility towards infection and both males and females are equally infected with COVID-19. However, there is few reports on sex disaggregated data on mortality and vulnerability towards the disease that suggest that male mortality is higher than female. As per one report published in Lancet, male to female ratio was found to be 80% to 20% (median age of 79·9 years for men and women for 83·4 years for women) [16]. Another report stated that male patient were more severely affected than female ($P = 0.035$) and mortality of male were 2.4 times higher than female (70.3 vs. 29.7%, $P = 0.016$) [17].

Low rate mortality in women could be due to sex-based immunity, low smoking, and drinking as compared to men. However, there is no conclusive understanding yet as sex-disaggregated data are insufficient and it would be too early to conclude anything at this stage.

Disease	Flu	COVID-19	SARS	MERS
Disease Causing Pathogen	Influenza virus	SARS-CoV-2	SARS-CoV	MERS-CoV
R_0 Basic Reproductive Number	1.3	2.0 - 2.5 *	3	0.3 - 0.8
CFR Case Fatality Rate	0.05 - 0.1%	~3.4% *	9.6 - 11%	34.4%
Incubation Time	1 - 4 days	4 - 14 days *	2 - 7 days	6 days
Hospitalization Rate	2%	~19% *	Most cases	Most cases
Community Attack Rate	10 - 20%	30 - 40% *	10 - 60%	4 - 13%
Annual Infected (global)	~ 1 billion	N/A (ongoing)	8098 (in 2003)	420

* COVID-19 data as of March 2020.

Fig. 2 Epidemiological comparison of respiratory viral infections

Incubation period

The incubation period is crucial information for active healthcare monitoring and taking proactive measures to stop the spreading. One of the very first reports estimated a mean incubation period of 5.2 days based on ten confirmed cases [18]. Another report claimed the median incubation period of 4.75 (interquartile range: 3–7.2) days based on the study of 125 patients with confirm exposure [19]. A study based on 158 confirmed cases reported a median incubation period of 5.0 days (CI, 4.4 to 5.6 days) [20]. However, estimation on incubation period based large sample size suggested only 3.0 days median incubation period and could be as long as 24 days [21]. There is strong possibility that this RNA virus invades the host innate immune system, a first-line host defence, to evade immune detection. Also, genetic variation plays an important role in the variable host immune response. These may be the reasons behind the long and variable incubation period. There is a possibility that a high incubation period plays a role in the degree of pathogenicity.

A study performed on 1099 patients to determine the viral load and transmission potential during the incubation period in both symptomatic and asymptomatic patients found to be higher soon after the onset of symptoms similar to influenza [22]. Viral load in both symptomatic and asymptomatic patients was quite similar indicating the transmission potential of both asymptomatic patients as well as symptomatic patients 2–3 days prior to the onset of symptoms. The role of asymptomatic patients in the transmission of infection is yet to be defined. Larger cohorts data will be needed to understand the disease and transmission dynamics. However, primary reports/studies led countries to strategies different measures such as quarantine, isolation and tracing/testing to minimize the transmission.

Origin and reservoir

Recent genomic data indicate that the most closely related virus to SARS-CoV-2 originated from bats [23–25]. Genomic sequence of sampled virus from bat from Yunnan province approximately 1500 km away from epicentre Wuhan showed 96%–97% similarity with SARS-CoV-2. Practically these viruses will take almost 15–20 year to evolve to SARS-CoV-2 which suggests the possibility of multiple intermediate hosts. Current findings suggest that bats are most anticipated reservoir hosts for SARS-CoV-2, but there is a strong possibility of 'intermediate' host that augmented SARS-CoV-2 to acquire some desired

mutations to become virulent to human transmission as it happened in case of MERS and SARS where camels and civets were intermediate hosts, respectively. MERS-CoV was supposed to be present in camels for almost a decade and through multiple cross-species transmission, it appeared in humans. A strong possibility is that these animals could be true reservoir hosts of SARS-CoV-2 [26].

Another intriguing finding is that none of bat corona virus sequenced from Hubei province was found close to SARS-CoV-2 in phylogenetic trees. [27] One interesting report revealed that the virus found in Malayan pangolins (*Manis javanica*) is closely related to SARS-CoV-2 and showed strong similarity to the RBD sequence of SARS-CoV-2 along with six key residues important for ACE2 receptor binding. However, the rest of the genome of SARS-CoV-2 was distant from this pangolin-associated coronavirus. This study suggests that pangolins could be another possible intermediate host in the rise of novel SARS-CoV-2 outbreak. Closest bat CoV RaTG13 virus genomic sequence showed 96–97% similarity with SARS-CoV-2 though spike protein diverges in bat virus. Natural selection is currently the most probable answer for the origin of SARS-CoV-2 infecting a primary and intermediate hosts and finally reaching to humans. However, current findings and research are not sufficient to provide complete information on natural host or intermediate host of SARS-CoV-2.

Peculiar features, mutation and insertion in SARS-COV-2 genome

Genome Organization and predisposition

SARS CoV-2 as other corona viruses belong to the order Nidovirales and family Coronaviridae of the betacoronavirus genera [28]. SARS-CoV-2 is a single stranded positive sense virus having 29,891 nucleotides (G+C=38%) encoding 9860 amino acids. Its genome contains two untranslated region (UTR) and one long open reading frame (ORF) that codes for the polyprotein. S protein of SARS-CoV-2 is also distinct from other coronavirus in the subgenus Sarbeco virus [29]. S protein of SARS-CoV-2 possess a size of 1273 amino acids while it is 1255 amino acids and 1245–1269 amino acids in case of SARS-CoV and bat SARS-CoV. In term of sequence similarity, SARS-CoV-2 S protein has 76–77% similarity from civet and human but surprisingly higher similarity 90.7–92.6% with pangolin coronavirus [30].

The sequential arrangement of genes from 5′-3′ is ORF1a, ORF1b, S, ORF3, E, M, and N in SARS-CoV-2 which is distinct in its genera [31] (Fig. 3). Also, SARS-COV-2 lacks the hemagglutinin esterase gene which is present as a component of the structural gene in SARS-CoV
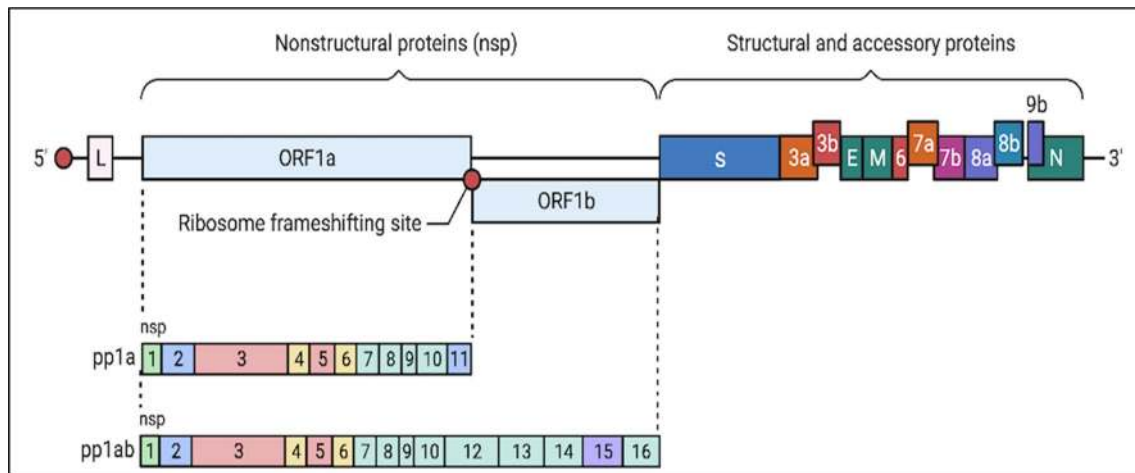
Fig. 3 Genome organization of SARS-CoV-2

Table 1 Comparison of proteins of SARS-CoV and SARS-CoV-2

Proteins	SARS-CoV	SARS-CoV-2
8a	Present	Absent
8b	Shorter, 84aa	Longer, 121aa
3b	Longer, 154aa	Shorter, 22aa

and MERS-CoV [29]. There are no major differences in the nsps and ORFs of SARS-CoV-2 and SARS-CoV except at some particular proteins [32]. Recent works reported 116 mutations along with three common mutations in the ORF1ab gene at C8782T, in the ORF8 gene at T28144 C and in the N gene at C29095T based on bioinformatics analysis of 95 complete genomic sequence of SAR-CoV-2 available till 05 April 2020 [33]. Pb1ab is the first ORF starting from 5′ end which encodes a nonstructural protein of size 29844 bp, 29751 bp, and 30119 bp in SARS-CoV-2, SARS-CoV and MERS-CoV respectively. The length of spike protein is significantly different in CoVs. The length of spike protein at the 3′ in SARS-CoV-2 is 1273aa while 21493aa and 1270aa in SARS-CoV and MERS-CoV respectively [31].

A comparative analytical study of the transmembrane region of SARS-CoV-2 nsp2 and nsp3 with SARS-CoV revealed that mutation occurs at 723aa (glycine to serine) and 1010aa (isoleucine to proline) positions [34]. The functional significance of these changes is still unknown but these are mostly related to the virulence of the virus.

Nsp7, nsp13, E protein, and accessory proteins p6, 8b do not show any mutation. As evident by the genomic similarity of SARS-CoV-2 with SARS-CoV, the amino acid organization is also quite similar except some notable differences in the accessory proteins present at the 3′end [35] (Table 1).

High affinity to angiotensin converting enzyme 2 (ACE-2)

The crystal structure revealed that SARS-CoV RBD is composed of two major structures: a core structure and a receptor-binding motif (RBM) that binds to the outer surface of the ACE2 receptor [36]. Further, another study demonstrated that SARS-COV-2 bound strongly to human and bat ACE-2 and even inhibited the binding of SARS-COV to ACE2. [37]. Sequence alignment studies of the amino acid (aa) of SARS-CoV-2 S protein with SARS-CoV S protein revealed [38, 39] the complete structural and functional domain in SARS-CoV-2 S protein. S1 segment (aa14–685) consists of N-terminal domain (aa14–305), RBD (aa319–541) along with RBM (aa437–508)) and S2 segment (aa686–1273) consists of fusion domain (aa788–806), HR1 (aa912–984), HR2 (aa1163–1213), TM domain (aa1214–1237) and cytoplasmic domain (aa1238–1273) [40]. Residues from 318 to 510 in the S1 region are enough for high-affinity binding to the peptidase domain of ACE2 [41]. Sequence alignment study between SARS-CoV-2 and SARS-CoV spike has revealed that they share 76% to 78% identity in the whole spike protein and approximately 73% to 76% identity in the receptor binding domain and around 50% to 53% similarity in RBM. [36].

A total of 27 amino acid substitutions have been discovered in spike protein which comprises of 1273 amino acids. Six amino acid residues L455, F486, Q493, S494, N501 and Y505 in SARS-CoV-2 which corresponds to Y442, L472, N479, D480, T487 and Y491 in SARS-CoV RBD, are crucial for ACE2 receptor binding. Out of six crucial amino acid residues five are substituted in SARS-CoV-2 [37, 42–44]. Detailed analysis of S protein indicates longer capping loop (responsible for electrostatic interaction) and greater protein–protein contact result in the enhanced

binding capability of SARS-CoV-2 (− 15.7 kcal/mol) in comparison to SARS-CoV (− 14.1 kcal/mol) [45]. These amino acid substitution and greater protein contact found in the hotspot area of the spike protein may indicate the effect of natural selection in increasing the affinity of the SARS-CoV-2 toward human ACE2[46].

Other six substitutions in the amino acid residue 569–655 of the SD segment present in S1 subunit have been discovered. Host range and affinity of RBD are critically determined by six RBD amino acids. Four notable substitutions have been seen in two peptides that were served as antigen in C-terminal in S1subunit (Q560L, S570A, F572T, and S575A) [35, 47].

Very recent work based on the isolate from 11 random patients, observed total 33 mutations out of which 19 were new and not reported before including six mutations in the spike S protein. Further, it showed that these mutations lead more cytopathogenicity and viral load in the Vero-E6 cells. This finding suggests that the virus is capable of varying its pathogenicity and virulence in a short time frame [48].

Presence of polybasic furin cleavage site and N-glycan shielding

Another unique feature of the SARS-COV-2 genome is the insertion of a polybasic furin cleavage site at the S1/S2 interface of spike protein which is missing in all other SARS/SARS-CoV [42, 49]. Furin is a proteolytic enzyme that is responsible for the cleavage of basic amino acids. Activation and priming by furin-like proteases are the signatures of several pathogenic viruses [50]. Addition of a polybasic cleavage site helps in the cell–cell fusion without altering the viral entry into the cell [50].

Amino acid alignment-based bioinformatics study of the S glycoprotein of SARS-CoV-2 revealed the insertion of furin cleavage sites in the sequence. Surprisingly, the most closely related bat CoV, RaTG-13 doesn't have the furin cleavage site [51] Since, furin proteases are abundant in the respiratory tract, it is hypothesized that SARS-CoV-2 S glycoprotein is separated upon exit from the epithelial cells and therefore can effectively target different cells and can increase the virulence.

Glycan shielding is a critical feature of SARS-CoV-2 having great importance in the context of vaccine designing. Virus uses glycan shielding strategy to evade the host immune system by masking the spike glycoprotein (S protein) through extensive glycosylation. Thick coating of carbohydrate on highly immunogenic epitope of the virus is a classic example of escaping from the host immune responses [52, 53]. Glycosylation pattern of SARS-CoV and SARS-CoV-2 is different from other RNA virus such as HIV in having greater concentration of N-glycan in comparison to O-glycans [54]. SARS-CoV-2 has 22 speculated

glycoprotein sites per promoter on the spike protein out of which 17 have been proved to be already preoccupied [54].

## Mechanism of virus invasion in host cell

The viral proteins that mediates SARS-CoV-2 entry and fusion and replication into host cells share a similar structure with those of SARS-CoV. Sequencing of COVID-19 shows 79.5% sequence similarity to SARS-CoV, 51.8% with MERS-CoV, and shares 96% structural identity across the whole genome to a bat coronavirus [38, 55].

Virus attachment and fusion

SARS-CoV-2 has the conventional coronavirus structure with spike glycoprotein, nucleocapsid protein, envelope glycoprotein, membrane glycoprotein, lipid bilayer, and genomic RNA. The CoV spike (S), which is classified as type I viral fusion protein [56], synthesized as 1300 amino acids containing single-chain precursor followed by folding and trimerization [56], plays pivotal role in viral attachment, fusion, and entry to the host cell. The binding between RBD of the spike protein of the SARS-CoV-2 to host ACE2 receptor (angiotensin-converting enzyme 2), is important for viral entry into the host body similar to SARS-CoV [55].

There are two domains of viral S glycoprotein that recognize a variety of host receptors leading to viral attachment (S1) and fusion (S2) domain to host cell. The spike protein, an anchor machinery, present on the surface of coronavirus as homotrimers protruding from the viral surface mediates its entry into the host cell through receptor binding domain (RBD) in S1 subunit. [57] It is reported in many studies on CoVs that S is cleaved at the host surface between the S1 and S2 subunits before fusion, however they remain noncovalently bounded and this confirmation is considered as closed prefusion conformation. [58–62] Further, host proteases cleave S protein, at S2 site, very close and upstream to fusion peptide [63, 64] that lead to activation the protein for membrane fusion through irreversible fusion favourable conformational changes [60, 61, 65–67]. Virus entry into the host cell is complex and orchestrated between both viral and host cell (Fig. 4).

RBD in S1 of SARS-CoV-2 spike protein strongly binds to human ACE 2 and is a key player of virus host range and cellular tropism. Recent evidences by Cryo-Electron Microscopy have affirmed that SARS-CoV-2 S protein binding affinity to ACE2 is approximately 10–20 times greater than those of SARS-CoV S protein. [41, 68] The other subunit of S protein i.e., S2 is enriched with alpha helices and mediates viral-host cell membrane fusion by two tandem domains naming heptads repeats 1 (HR1) and 2 (HR2). The fusion domain contains a fusion peptide composed of 15–25
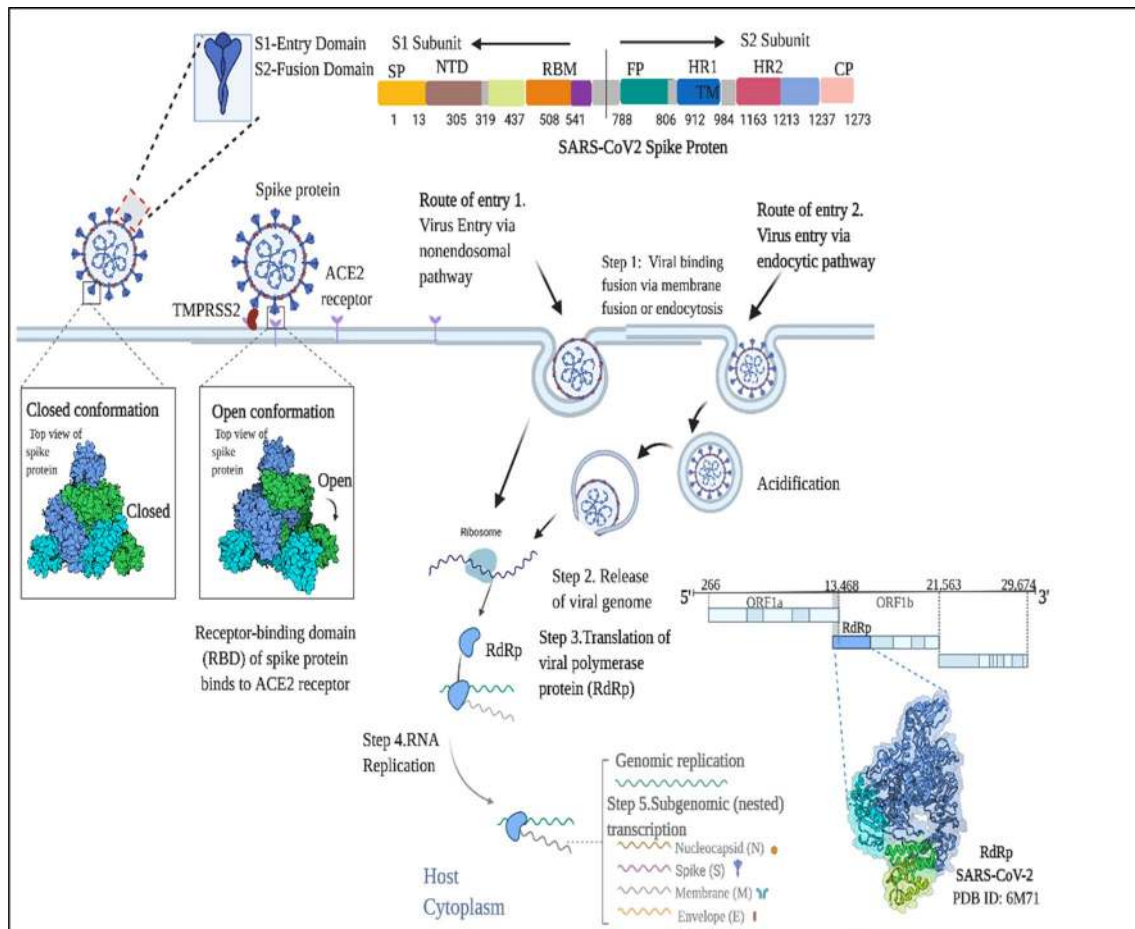
Fig. 4 SARS-CoV-2 Spike protein conformation, entry, fusion and replication. *1* SARS-CoV-2 interacts with host's ACE2 receptors and transmembrane protease serine 2 protein (TMPRSS2) through the spike protein. *2* It is followed by two entry pathways either A. non-endosomal or B. endocytic pathway or both to enter the host cell. *3.* Soon after its entry into host cell, it releases its genome and overtake protein synthesis machinery of host cell and start the translation of RdRp *4* Afterward SARS-CoV-2 replication and transcription are catalyzed by RdRp

hydrophobic amino acids. There are two distinct structural conformations of spike protein, before and post fusion which indicates the presence of some triggering mechanism for transition of confirmation.

The second step of viral infection is fusion with the host cellular membrane. Based on structure and function viral fusion proteins are classified into three types (I, II, and III). [69, 70] Based on structural features of fusion domain and requirement of protease cleavage to form fusogenic conformation and presence of HR1 and HR2 to form 6-HB, the coronavirus S protein is classified as class I fusion protein [56]. Fusion machinery, S2, is enriched with alpha helices and mediates viral-cell membrane fusion with the help of two tandem domains naming heptads repeats 1 (HR1) and 2 (HR2) and S2 subunits of SARS-CoV-2 and SARS-CoV shows 88% sequence identity. HR1 and HR2 domain of S2 subunit interact with each other that lead to the formation of 6-helix bundle (6-HB) fusion core, which brings viral and

host cellular membranes in close proximity for fusion and subsequently leads to the entry of virus in host cells. Four conformational changes happen throughout fusion process (1) Pre-fusion structural conformations (2) pre-fusion meta-stable conformation (3) pre hair-pin confirmation (4) post fusion stable state, which indicates the presence of some triggering mechanism for transition of confirmation. It is reported in many studies on CoVs that S protein is cleaved at host surface with protease between the S1 and S2 subunits before fusion however, they remain non-covalently bounded and this confirmation is considered as closed meta-stable prefusion conformation. [56, 59–64] Host proteases cleave S protein, at S2′, very close and upstream to fusion peptide [64, 65] that lead the activation of the protein for membrane insertion through pre-hairpin intermediate state an irreversible fusion favourable conformation [59, 62, 63, 66, 67]. A recent study demonstrates that priming of SARS-CoV-2 S proteins by host cell serine protease TMPRSS2 and

endosomal cysteine proteases CatB/L, vital for viral entry into host cells, mediate through S protein cleavage at S2′ site at S1/S2 interface. [71] After insertion of the FP domain, the HR1 regions rearranged to form coiled trimer and facilitate the binding hydrophobic grooves with three HR2 regions antiparallelly [72]. This rearrangement of HR1 and HR2 forms fusion core 6-HB, which leads to viral and host cell membranes into close proximity for fusion and forms the last stable post-fusion state. The last step of fusion process happens through two stages hemi-fusion stage and pore formation. [73] In a nutshell, virus entry into the host cell is complex and orchestrated between both viral and host cell. Presence and availability proteases involve in priming on target cells play a key role in determining whether CoVs penetrate inside cells through the plasma membrane or endocytosis pathway.

Replication

Replication machinery has a conserved organization at 5′ end (including nonstructural protein) and 3′ end (including structural protein). The viral replication is initiated when S protein binds to the ACE2 receptor inducing a conformational change which results in the endocytosis of the virus causing the release of viral ssRNA genome into the host cytoplasm [67].

The corona virus replication process could be divided into three parts: (1) translation of viral genome (ssRNA) to make necessary protein for genome synthesis (2) Simultaneous transcription and translation process (3) Assembly of viral genome and protein (Fig. 4). The SARS-CoV-2 replicase gene present on the 5′ end make around 2/3 of the genome and consists of two 2 ORF, ORF1 and ORF2 which further code for two co- terminal polyproteins pp1a and pp1a respectively [29, 74]. For the expression of these two polyproteins, slippery sequence (5-UUUAAAC-3) and RNA pseudoknot is essential for ribosomal frameshifting from the rep1a reading frame into rep1b ORF. These polyproteins are subsequently cleaved in distinctive nonstructural protein (nsp). Cleavage of giant polyprotein mainly done by two proteases, papain-like (PLpro or nsp3) and chymotrypsin like (3CLpro or nsp5) into 16 nsp. ORF1a encode nsp1 to nsp11 and ORF1b encodes nsp12 to nsp16. The 3′ part of the genome encode for 13 ORF's which include 4 structural proteins and 13 accessory proteins.

The second step is the organization of nsp 7, 8, and 9 at 3′end of genomic RNA to form membrane-associated replicase–transcriptase complex (RTC) where nps8 primase initiate RNA synthesis that finally leads to change in confirmation of 3′RNA (BSL to PK). This conformation change recognized by RdRp and helicase (nsp13) and other related factors like processing (nsp7 and nsp8), proofreading (nps10 and nps14)) and allow the synthesis of negative stranded RNA to replication and translation of genomic and subgenomic RNA. Further, this negative strand RNA can take two pathways 1. Replication into genomic positive sense RNA or 2. Discontinuous transcription into several subgenomic mRNA that can be translated into different proteins [75].

In discontinuous transcription small subgenomic RNA are transcribed through premature termination during the synthesis of the negative-strand RNAs when preceding viral gene, TRS-B, jump and bind to the TRS-L of parent RNA. Long distant interaction TRS-B of preceding gene and 5′ TRS-L of parent RNA is mediated through RNA–protein complex as complex bring them in close proximity. [76–78]. This whole process of replication happens in DMV (double membrane vesicle) and CM (convoluted membrane). SARS-CoV electron tomography analysis demonstrated that it forms a unique reticulovesicular network with which both viral replicase subunits and ssRNA were associated [79].

Recent studies reveal that DMVs are originated from ER and nps4 and nps6 play a key role in DMVs formation by inserting their hydrophobic transmembrane domain into ER. Further after replication of genomic and subgenomic RNA in RTC complex start translation of accessory proteins, structural (S, E, M proteins), and nonstructural proteins.

In the third step assembly of virion takes place. After the synthesis of these proteins, they are inserted into the endoplasmic reticulum, then move through the secretory pathway (ER-Golgi intermediate compartment [80, 81]. In this compartment, the viral genome is encapsulated by N protein forming the mature virion containing vesicles [82]. Further, virions packed in the vesicle are carried to the cell surface and delivered by membrane fusion and exocytosis. How transportation of virion happens exactly, not clear yet. Either it happens through large cargo from Golgi or virus follow different, novel exit pathway.

Cellular tropism

Both SARS-CoV and SARS-CoV-2 known to use human ACE2 receptor to take entry inside the cell [83]. SARS-CoV-2 mainly affects respiratory tract however there are several evidences that show broader cell tropism. Clinical manifestations of SARS-CoV-2 have been well defined and genome of SARS-CoV-2 is fully sequenced. However, much of the cellular tropism and its manifestation is still unclear and limited data on tissue and cellular tropism are available as of now. ACE2 receptors expression was significantly seen in alveolar, type II epithelial cells, heart, kidney, brain and gastrointestinal tract (especially in small and large intestines). The single cell RNA sequencing studies showed the presence of ACE2 mRNA in different cells of various organs such as lung epithelial cells, myocytes, kidney tubular cells,

oesophageal epithelial, urothelial cells [84–86]. Greater binding affinity with ACE2 might facilitate virus entry into pulmonary cells leading to higher transmission among people through various direct and indirect contacts with the patients [44]. The robust replicative property of coronavirus in bronchial as well as alveolar epithelium also describes the higher transmissibility of SARS-CoV-2 as compared to other CoVs. SARS-CoV-2 and SARS-CoV have shown significant replication in various cell lines that manifest their abilities to cause lower respiratory tract infection. Reports have shown replication competence and cellular tropism of SARS-CoV-2 in respiratory tract and extra pulmonary cells. SARS-CoV shown significant replication levels in both Calu3 (pulmonary cells) and Caco2 (intestinal cell) which indicated lower respiratory tract and gastrointestinal infection in COVID-19 patients [87].

Cardiovascular system

Cardiovascular manifestations are also one of the prominent consequences due to SARS-CoV-2 infection. This includes various cardiac injuries, stroke, coronary arterial ischemia, pulmonary embolism, arterial thrombosis etc. [88]. In a cohort study consisting of 2 groups (29 patients) infected with SARS-CoV-2, 30-fold increase in Kawasaki like disease were observed. [89] SARS-CoV-2 infection seems to be correlated with higher incidences of cardiac dysfunction and macrophage activation syndrome. [89].

Endothelial cell

Recent studies shown viral infection and inflammation in endothelial cell in COVID-19 infected patient due to presence of same ACE2 receptor on the surface of endothelial cells. Other than this, endothelial dysfunction has also been seen because of the recruitment of different immune cells by various direct and indirect infection caused by SARS-CoV-2, which is associated with cell death and multiple organ failure. [90].

Gastrointestinal tract and liver

Evidence from several studies indicated that coronavirus has a tropism to the gastrointestinal tract due to the presence of ACE2 receptor. Different cohort studies showed diarrhoea vomiting and other gastrointestinal problems [91–96]. Liver injury was also reported in the blood test reports of COVID-19 patients [97]. Elevated levels of alanine aminotransferase (ALT) and aspartate aminotransferase (AST) were also detected in cohort studies of infected patients [91, 92]. There was abnormal elevation of bilirubin during the infection. However, there was no severe damage observed in liver function, but the patients having severe viral infection

seems to have higher level of liver injury. Similar infection of colorectal carcinoma epithelial cell line shown replication of virus in gastrointestinal tract that hints possibility of oral-faecal transmission. These multiple routes of transmission might explain the rapid spread of COVID-19 worldwide.

Kidney

Cellular tropism for kidney was observed even in the patients who do not have any history of chronic renal disease. mRNA sequencing studies revealed that ACE2, TMPRSS, Cathepsin genes are present in kidney cells that facilitate the entry and infection of SARS-CoV-2 causing various kidney injuries [98]. Chronic kidney injuries are one of the strongest risk factors for COVID-19 related death [99, 100]. In the cohort study consisting post-mortem report of 63 patients, out of this SARS-CoV-2 RNA was found in 60% of the patients with kidney injuries. Renal tropism also shown to be associated with disease severity and kidney injury that leads to premature death [101].

Brain

SARS-CoV-2 also infects extra pulmonary tissue including CNS and PNS, mechanism of which is still not known. It is hypothesized that virus crosses the blood brain barrier to invade the brain that leads to various neurological manifestations including headache, dizziness, seizures, loss of consciousness. Reports have shown that SARS-CoV-2 can also cause viral encephalitis, meningitis, encephalopathy etc. Mao et. al [102] shown ischemic and haemorrhagic stroke as one of the neurological manifestations seen in 3% of infected patients.

Eyes

There are evidence showing conjunctival epithelium and conducting airways as potential portal of infection for SARS-CoV-2. Infection in conjunctiva suggests eye as additional route of infection [103].

Immunomodulation by SARS CoV-2

Innate immunity presents the first barrier for virus invasion. Pattern recognizing receptor (PRR) recognizes the molecular patterns associated with the virus and initiate a cascade of downstream signaling to release a burst of cytokines known as cytokine storm (Fig. 5). This include both Th_1 and Th_2 associated cytokines including IL1, IFNγ, IL10 etc. [104]. IL6 which is known to play an important antiviral role in case of influenza and herpex simplex virus (HSV) [105, 106] and its higher level is
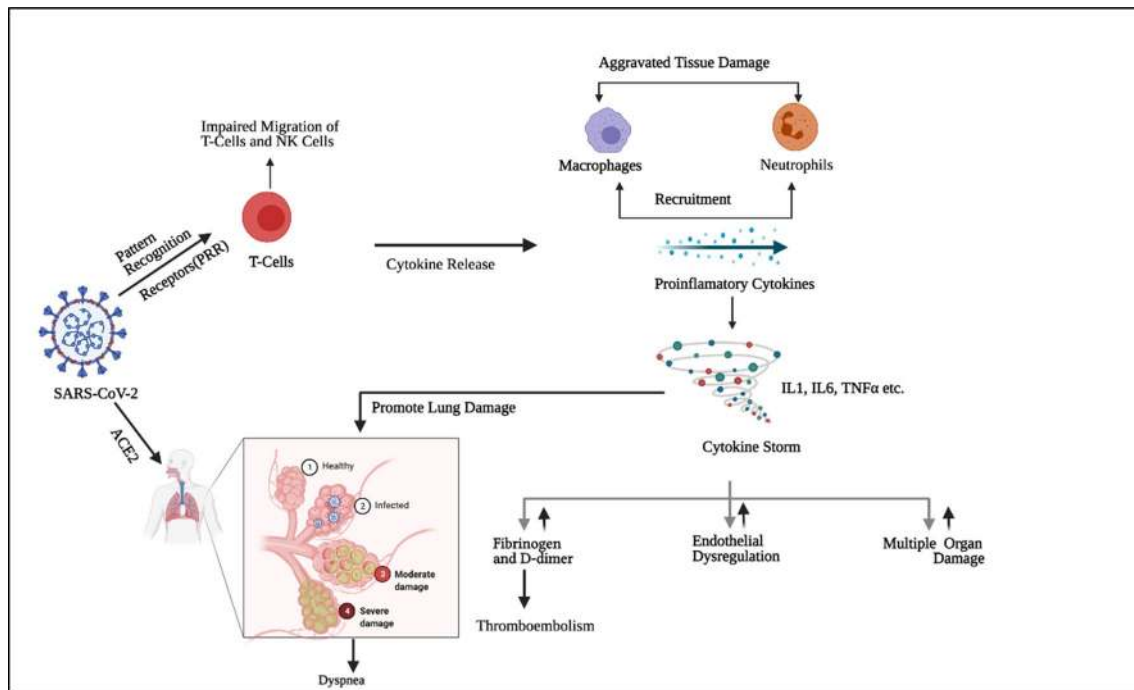
Fig. 5 Overview of immunological aspect of COVID-19 indicating the viral induced immune modulation in the infected host tissues. SARS-CoV-2 is recognised by the pattern recognising receptors by the T cells which in turn initiates a cascade of events particularly

cytokine storm, recruitment of inflammatory cells etc., ultimately resulting in multiple organ damage and the development of symptoms that are associated with the progression of COVID-19 disease

correlated with the severe progression of the disease and mortality in SARS-CoV and SARS-CoV-2. [107, 108] IL6 can be induced directly or indirectly by SARS. Studies found out that indirect stimulation happens when the virus bind to the toll like receptor 4 (TLR4) and induces IL6 expression through NF-κB pathway [109]. Direct stimulation of IL6 occurs when structural protein (N protein) of SARS-CoV bind to the NF-κB regulatory portion in the promoter region of IL6 [110]. IFNγ 1 pre-injection or early presence can limit or stop the virus associated damage with much more potency than in SARS-CoV [111]. Adaptive immune response in viral infected patient are drastically affected as helper T cells and cytotoxic T cells are significantly reduced in the peripheral circulation in moderate and severe cases of COVID-19 [112]. Number of CD8 memory T cells exceeds the CD4 memory T cells in the SARS-CoV survivor and virus specific T cells present in the blood for at least 6–11 years [113]. IFNγ and TNFα that are upregulated in the infected patient are responsible for the retention and binding of T cells to the epithelium in the lymphoid organs that may result in overall reduction in peripheral blood circulation. [114] Lavage fluid collected from the COVID-19 patients showed the clonal expansion of CD8 cells suggesting that T cell migration to the infected site that results in the overall lower peripheral counts. [115].

Immuno-pathogenesis

A study of 99 hospitalized patients in china showed that 12% had thrombocytopenia, 36% had elevated D dimer and proinflammatory cytokines, 5% show increase prothrombin and four others suffered from septic shock [116]. As already discussed, SARS-CoV-2 induced a burst of proinflammatory cytokines in the infected site. The higher level of these cytokines in the serum may be correlated with the lung lesion as these cytokines promoted the massive migration of immune cells to the infected site (Fig. 5). Also, type II alveolar cells of the lung express high level of ACE2 receptor, thus lung is one of the most susceptible organ to viral attack [117]. These lung lesion may be correlated with the dyspnea, a common symptom associated with COVID-19 [118]. Lung Natural killer (NK) cells doesn't possess the ACE2 receptor, exhibit CD16^{+}KIR^{+} phenotype thus virus can't directly target these cells but studies found that after infection CD16^{+} NK cell significantly decreased in the peripheral blood suggesting defective migration or maturation process of NK cells [119, 120]. Thrombocytopenia is also normally observed symptom in the patients suffering from COVID-19. One hypothesis could be that virus may bind to CD13, a marker present on bone marrow cells and platelets and then induces apoptosis of the megakaryocytes thus resulting in decrease number of platelets [121]. Another hypothesis is

that SARS-CoV-2 bind the liver cells via ACE2 receptor and induces its damage. Liver cells produce thrombopoietin required for the differentiation and maturation of megarkaryocytes in to the platelets [122, 123]. Also, lung damage induced by the proinflammatory cytokines reduces the capillary bed in the lung which may result in lower pulmonary recirculation and ultimate result is thrombocytopenia. [124, 125]. Further, increase in proinflammatory cytokine particularly IL6 induces fibrinogen and D dimer which may indicate a direct link between cytokine storm and procoagulation/thromboembolism in the virus infected persons [126–128].

Dysgensia (loss of taste) and Hyposmia (loss of smell) are an early indicator of SARS-CoV-2 infection [129]. Salivary gland and neural cells of olfactory epithelium express ACE2 receptors thus serves as a target of SARS-CoV-2. Infected salivary glands may produce less quantity and quality of saliva, thus resulting in dysgensia. [130] Damage to neuronal cells of olfactory epithelium, expressing high amount of ACE2 receptor may be a reason behind the partial loss of smell associated with the viral infection. [131].

Conclusion and future direction

This short review provides brief overview of available information of SARS-COV-2 origin, infectivity, biology, brief molecular insight of disease pathogenesis and progression. It also includes concise description of peculiar mutations, genome organization, cell tropism and immunomodulation/immunopathogenesis caused by SARS-CoV-2. Current pandemic caused by SARS-CoV-2 is the deadliest pandemic of twenty first century that took whole world on storm. Despite of our best effort and frenetic search of therapeutic we are not able to find the cure of COVID-19 even after more than one year since outbreak. Since last century we have witnessed several virus outbreaks i.e., Swine Flu, Ebola, Zika and so on. Even after much efforts pathogenic virus outbreaks keep happening and huge scientific advancement is not enough to combat such pandemics. The disease keeps spreading and taking toll on lives and economy despite of huge efforts and there are emergence of second and third wave across the globe. Researchers are unfolding mysteries around corona virus every day in all dimensions i.e., infectivity, clinical manifestation, drug trials and failures and vaccine development. Coronaviruses emergence is very rapid, repetitive and unpredictable. However, disease pathogenesis and involvement of several human receptors/proteins such ACE2, Cathepsine, and viral protein such as PLpro, CLpro and other accessary protein involved in disease progression are explored well now and can provides better insight for screening of new lead molecules for antiviral drug development. But, we need integrated approach involving computational biology, genome analysis, immunology, proteomics studies, and systems biology along with various animal models for in depth information of disease progression and manifestation. To be better prepared to mitigate this kind of pandemic in future, it is very necessary to have multidisciplinary international consortium including virologist, molecular biologist, pathophysiologist, chemist, statistician and clinician. Considering the threat imposed by SARS-CoV-2, there is dire need to take virus research at deeper level for better understanding of pathogenesis from molecular to clinical level and to develop the advance therapeutic strategies to tackle COVID-19 like infection in future.

Current outbreak not only necessitates development of the broad spectrum antiviral drug but also the more robust, sustainable and responsive global public healthcare preparedness than ever. SARS-CoV-2 is far more infectious and widespread than earlier CoVs. There are challenges not only associated with virus but with patients as it imposes several issues like wide range of symptoms, severity and clinical manifestations. The disease need to be understood on various parameters such as heterogeneity in infected population, genetic makeup, co-morbidity/pre-existing medication for clear and comprehensive understanding for effective treatment. Immune- triggered response are worsening the treatment outcome and hampering the disease understanding. Drug repurposing has surfaced as life and time saver, cost effective alternative during COVID-19 pandemic. Currently, repurposed drugs are used to treat critical patients. However, there are challenges associated with drug repurposing such as dose optimization and dose associated toxicity that need to be addressed carefully. Virus affect the host immune response as well as organ function and repurposed drug can cause adverse pharmacological effect on ailing patients. Another important aspect which should be taken into consideration while using repurposed is pharmacogenomics which is overlooked due to extenuating situation to treat the critical patients. Pharmacogenomics is key parameter to establish for long term efficacy and safety of the drugs.

More so, zoonotic origin virus and pathogens outbreaks are inevitable and likely to continue in future so concerted and cohesive efforts considering all aspect are required to minimise the health care burden and death toll in future.

Authors Contribution The named two authors with equal contribution participated equally in designing the study, writing, and editing of the manuscript.

Compliance with ethical standards

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