

Review Article

SARS-COV-2/COVID-19: EVOLVING REALITY, GLOBAL RESPONSE, KNOWLEDGE GAPS, AND OPPORTUNITIES

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ABSTRACT—Approximately 3 billion people around the world have gone into some form of social separation to mitigate the current severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic. The uncontrolled influx of patients in need of emergency care has rapidly brought several national health systems to near-collapse with deadly consequences to those afflicted by Coronavirus Disease 2019 (COVID-19) and other critical diseases associated with COVID-19. Solid scientific evidence regarding SARS-CoV-2/COVID-19 remains scarce; there is an urgent need to expand our understanding of the SARS-CoV-2 pathophysiology to facilitate precise and targeted treatments. The capacity for rapid information dissemination has emerged as a double-edged sword; the existing gap of high-quality data is frequently filled by anecdotal reports, contradictory statements, and misinformation. This review addresses several important aspects unique to the SARS-CoV-2/COVID-19 pandemic highlighting the most relevant knowledge gaps and existing windows-of-opportunity. Specifically, focus is given on SARS-CoV-2 immunopathogenesis in the context of experimental therapies and preclinical evidence and their applicability in supporting efficacious clinical trial planning. The review discusses the existing challenges of SARS-CoV-2 diagnostics and the potential application of translational technology for epidemiological predictions, patient monitoring, and treatment decision-making in COVID-19. Furthermore, solutions for enhancing international strategies in translational research, cooperative networks, and regulatory partnerships are contemplated.

KEYWORDS—Acute respiratory distress syndrome, animal models, clinical trials, immuno-modulation, pandemic, pneumonia

INTRODUCTION

In late 2019, a novel human coronavirus, termed severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged in Wuhan, China. SARS-CoV-2 quickly spread in several Chinese provinces producing a high incidence of acute respiratory illness (1). Following its further spread, the World Health Organization (WHO) has coined this global illness Coronavirus Disease 2019 (COVID-19) and has declared the outbreak to be a Public Health Emergency of International Concern on January 30, 2020. SARS-CoV-2 infections quickly escalated to a pandemic with virtually all continents reporting COVID-19 cases (2). The SARS-CoV-2 infections appeared to have spread in China over several weeks prior to the first delayed reports of patients suffering from severe pneumonia in late December 2019. Since then, the number of confirmed cases has

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exponentially increased, first in China, subsequently across other continents with almost five million people affected (3). The countries currently most affected by this pandemic are the United States (US) as well as Russia, the UK, Spain, Italy and France in Europe, and the UK in Europe accounting for more than 70% of the entire global death toll (3). According to the WHO, the April spike of SARS-CoV-2 infections in Africa positions this continent as the next epicenter with dire consequences for its population. In May 2020, the US recorded the highest number of known coronavirus cases (with new cases continuously increasing) compared to any other country with one-and-half million cases. However, an enormous variability in testing and data reporting (deaths usually not confirmed through autopsy) exist, which impedes precise estimations. The yet known global propagation pathways of SARS-CoV-2 based on its genetic fingerprinting are displayed in Figure 1 (4).

Given that the initial containment was often delayed and insufficient (5, 6), the most affected countries have introduced a range of restrictive mitigation mechanisms such as social distancing, border closures, and travel/business restrictions. On March 18, 2020, more than 250 million people went into lockdown in Europe. The enormous and uncontrolled influx of patients in need of specialized medical care has rapidly brought several national health systems to near-collapse. Adhering to

the WHO call (7), the healthcare systems worldwide rapidly increased hospital capacities and adapted to the specific needs of COVID-19 patients as a fundamental response measure. These adaptation mechanisms, however, are difficult (impossible) to achieve in many underprivileged regions/countries with an under-developed health infrastructure putting those populations at much higher risk.

SARS-CoV-2 is assumed to be mainly spread via small droplets produced at coughing/sneezing in close contact (up to 2 m) although longer distances cannot be ruled out (8). Experimental evidence shows that SARS-CoV-2 may remain viable in aerosols up to 3 h and up to 72 h on various surfaces such as plastic, steel, copper, and cardboard (9). Of note, the American Centers for Disease Control and Prevention (CDC) reported that SARS-CoV-2 RNA was identified on cabin surfaces of a cruise ship 17 days after cabins had been vacated; it is unclear whether the material remained infectious (10). High viral load and active shedding in the upper respiratory tract that peaks during the first week of symptoms, suggests that SARS-CoV-2 is most contagious in already symptomatic subjects although some spread is likely before occurrence of symptoms (11). The SARS-CoV-2 infection may be asymptomatic in some people; analysis of the “Diamond Princess” cruise ship cohort indicated that approximately 19% of the infected

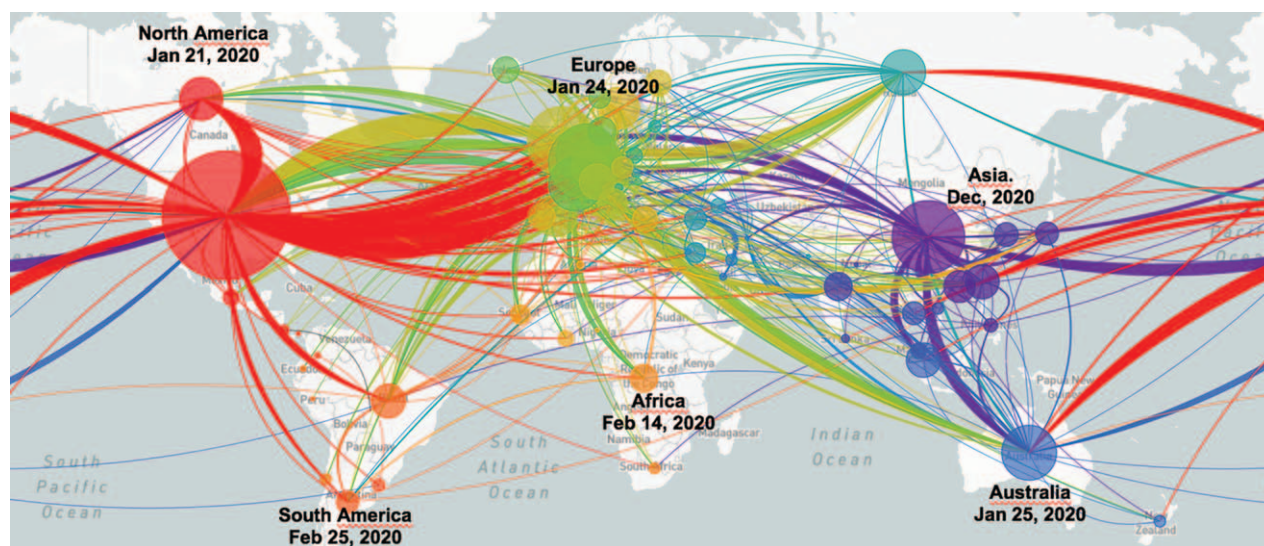


FIG. 1. Phylogeny, evolutionary relationships, global propagation pathways, and timeline of SARS-CoV-2 viruses from the ongoing COVID-19 pandemic. Despite relatively clear genetic relationships among sampled viruses, an uncertainty for specific transmission dates and the reconstruction of the geographic spread remains. Note that the specific inferred transmission patterns (connecting lines) are only hypothetical (4). Thousands of complete genomes are available and increase on a daily basis. The visualization is based upon sub-sampled available genome data (see more under: <https://nextstrain.org/ncov>). As the pathogen replicates and spreads, its genome is replicated and random mutations/errors accumulate in the genome. Such random mutations allow tracking of the SARS-CoV-2 spread inferences regarding its transmission routes and dynamics. The colors indicate the origin/source of the various viral strains, while circle diameters reflect the size of the transmission clusters. The initial SARS-CoV-2/COVID-19 emergence occurred in Wuhan, China, in November and December 2019, with the first (officially announced) COVID-19-related death on January 11, 2020. The phylogeny is rooted relative to early samples obtained from Wuhan, China. Thereafter, a sustained human-to-human transmission with the first case outside of China (Thailand) was confirmed on January 13, 2020. On January 21, 2020 the first case was confirmed in North America (Wash, USA) and 4 days later in Australia (Victoria). The first three cases in Europe were reported in France on January 24, 2020 (first death on February 15, 2020 France). COVID-19 surveillance was implemented by the European CDC and WHO in the European Region on January 27, 2020, 3 days later the WHO declared SARS-CoV-2 a global emergency. On February 14, 2020 the first case in Africa (Egypt) was confirmed. On February 21, 2020 nine European countries (Belgium, Finland, France, Germany, Italy, Russia, Spain, Sweden, and UK) reported SARS-CoV-2/COVID-19 cases. On February 25, 2020 SARS-CoV-2 reached South America (São Paulo, Brazil). On March 11, 2020 the WHO declared SARS-CoV-2 a pandemic and 2 days later Europe was announced the active pandemic center; on 17 March 2020, all European countries reported confirmed SARS-CoV-2/COVID-19 cases. On March 31, 2020 the number of COVID-19-related deaths (>3,500) in the US surpassed those (officially reported) in China. The highest worldwide daily death toll of 10,761 was recorded on April 27, 2020; as of May 18, 2020, 4,727,625 confirmed cases in 213 countries/territories and two international conveyances with 315,389 deaths were reported (www.worldometers.info). Graphic modified based on <https://nextstrain.org/ncov> (accessed on April 27, 2020). COVID-19 indicates coronavirus disease 2019; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

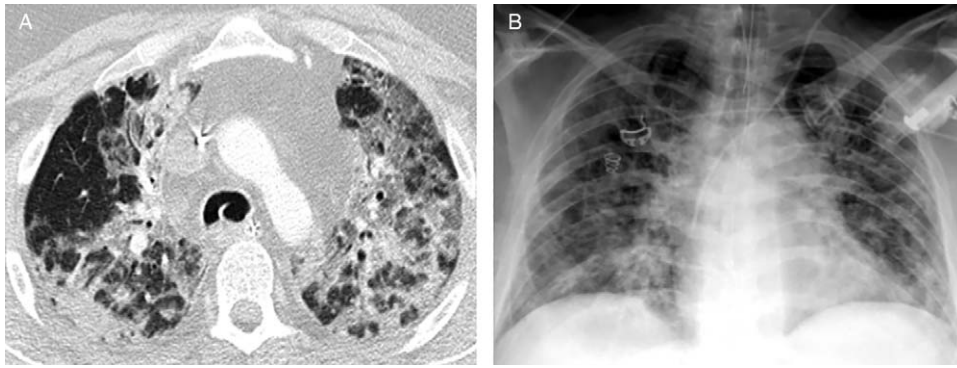


FIG. 2. A pulmonary presentation of SARS-CoV-2 infection in a severely ill, intubated, and mechanically ventilated COVID-19 patient by computed tomography (CT; panel A) and plain chest x-ray imaging (panel B). The CT shows characteristic milk-glass like opacities with consolidations in both upper lobes (A). CT findings may be unspecific and the primary diagnosis of SARS-CoV-2 remains laboratory-based. However, if indicated, imaging studies are helpful in assessing the severity and the course of COVID-19 pneumonia. A CT score can be used to evaluate the severity of the disease (15). The risks of an in-hospital transfer and potential contamination need to be considered. (Source: Axel Gossmann (MD), Department of Radiology, Cologne-Merheim Medical Center (CMMC), Cologne, Germany). COVID-19 indicates coronavirus disease 2019; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

passengers remained clinically healthy (12). The viral load in asymptomatic patients may reach a level comparable to the one seen in symptomatic patients; preliminary evidence demonstrates that asymptomatic patients may transmit the virus but the transmission pathways and timing are yet to be identified (13, 14). The percentage of patients who remain truly asymptomatic for the course of their infection is unknown; it is likewise unclear what percentage of individuals who initially present with an asymptomatic infection subsequently progress into clinical disease.

Clinical features of COVID-19 are nonspecific and are hardly distinguishable from other causes of severe community and hospital-acquired pneumonia. While approximately 80% of cases follow a relatively mild trajectory, the elderly and/or patients with comorbidities (e.g., chronic lung conditions, hypertension, diabetes, and obesity) are at risk for severe COVID-19 course with pneumonia as the typical manifestation (Fig. 2) (15). Not infrequently, patients may show a disproportionate extent of radiographic pulmonary involvement compared to the mild level of hypoxemia. Some of these patients suddenly deteriorate to severe respiratory failure followed by intubation and mechanical ventilation requirement. Deaths appear to be dominated by severe respiratory failure, fulminant myocarditis (leading to heart failure), thrombo-embolic events (stroke, infarcts, embolism), and late secondary sepsis with severe single or multiorgan dysfunction (typically involving the liver and kidneys) (16–18). Renal dysfunction may be an early sign for later deterioration. Emerging data suggest that severe COVID-19 phenotypes are associated with a significant (hyper-) coagulopathy that correlates with disease severity (19–21). Direct viral infection of the endothelial cells and diffuse endothelial inflammation with a shift of the vascular equilibrium toward enhanced vasoconstriction (with subsequent organ ischemia), inflammation with an associated tissue edema, and a pro-coagulant state may constitute the main underpinnings of the severe clinical phenotypes (22, 23). Studies confirm the high rate of comorbidities among deceased SARS-CoV-2/COVID-19 patients, but serial (and better powered) studies are needed to precisely identify the cause(s) of death in the most severe cases (24).

With most of the world in lockdown, an ongoing SARS-CoV-2 spread and new infection waves expected, the pandemic will continue to represent a major global threat (25). As solid scientific evidence remains scarce, there is an urgent need to expand our understanding of the SARS-CoV-2 evolving epidemiology, its infectivity and body site-specific replication as well as COVID-19 immuno-inflammatory characteristics and treatment strategies against it (25). The existing gap of high-quality, reproducible evidence-based data is frequently filled by anecdotal reports, contradictory statements (26), and misinformation. The present review addresses several important aspects unique to the SARS-CoV-2/COVID-19 pandemic highlighting the newest evidence, most relevant knowledge gaps, and windows-of-opportunity.

COMPARISON OF COVID-19 TO THE RECENT VIRAL PANDEMICS

COVID-19 is the fourth viral pandemic of the last two decades following the SARS virus in 2002/2003, the influenza A virus H1N1 in 2009, and the Middle East Respiratory Syndrome (MERS) virus in 2012 (Table 1). All these viruses are enveloped by a host cell-derived membrane and contain a single RNA as genome. Many of the RNA viruses possess the capacity to induce zoonotic infections. Wild birds are a reservoir for influenza A viruses that may be transmitted to swine, human, and other mammals (27). SARS-CoV and SARS-CoV-2 have high similarity to coronaviruses (CoV) in bats and likely have been transmitted from bats to humans via an intermediate host (civet for SARS-CoV; possibly pangolin for SARS-CoV-2) (28–30). MERS-CoV was transmitted from camels to humans, with limited human-to-human transmission capacity (but high pathogenicity; (31)). Due to the tight contact between camels and humans, in some communities, MERS-CoV continues to circulate and temporal disease clusters arise.

H1N1 (and other influenza viruses) belong to the *Orthomyxoviridae* and induce upper respiratory tract infections. Influenza A virus enters the host via the viral hemagglutinin attaching to sialic acid residues present on upper respiratory tract cells with an average incubation time of 2 days (32). The 2009 pandemic H1N1 virus integrated gene segments from

TABLE 1. Main differences between COVID-19 and previous viral pandemics

	COVID-19 2019–present*	MERS 2012–2019	Flu (H1N1) 2009	SARS 2002/03
Confirmed cases/ deaths worldwide	>4.7 Mill./ >315,000 in 213 countries	2,494/858 in 28 countries	3–5 Mill./200,000 (estimated values)	8,098/774 in 29 countries
Origin	bat →?	bat → camel	pig	bat → civet
Median incubation time	5 days	5 days	2 days	5 days
Human-to-human transmission	++	-/+	++	+
Receptor used for host cell entry	ACE2	DPP4	Sialic acid residues	ACE2
Estimated case fatality ratio (CFR)	1.38%–3.8% [†]	34.4%	<0.3%	9.6%
R ₀	1.4–5.7	0.3–0.8	1.4–1.6	2–5
Vaccination	No	No	Yes	No
Availability of therapeutic drugs	No	No	Yes	No

*As of May 18, 2020.

[†]Remains to be determined; CFR currently low in Germany, Taiwan, Singapore; high in Brazil, Italy, France, Spain, USA.

ACE indicates angiotensin-converting enzyme; DPP4, dipeptidyl peptidase 4; R₀, basic reproduction rate; COVID-19, coronavirus disease 2019.

multiple avian and mammalian strains thereby forming a novel virus unrecognizable by any pre-existing immunity (27). Despite relatively efficient vaccines and antiviral drugs, the flu continues to kill >200,000 people worldwide per year (33).

SARS, MERS, and the novel COVID-19 are caused by CoV that are widely distributed, highly infectious and responsible for the symptoms associated with common cold in humans, i.e., the strains NL63, OC43, 229E, and HKU1. For their entry into the human cells, SARS-CoV and SARS-CoV-2 use a spike protein that binds to the angiotensin-converting enzyme (ACE) 2 on alveolar type II cells in the lung (also airways mucosa) (34). The expression of ACE2 in the liver, heart, and gastrointestinal tract (Table 2) may explain why some infected patients also develop liver injury, fulminant myocarditis with subsequent heart failure, and diarrhea in addition to severe pneumonia (35–38). In contrast to SARS-CoV, MERS-CoV uses the enzyme dipeptidyl peptidase (DPP) 4 as receptor for host cell entry (39). The median incubation time for CoV infections is 5 days but up to 2 weeks incubation time is not uncommon.

The extraordinarily high spread and the number of SARS-CoV-2 infections indicate that its infectivity is higher compared to SARS-CoV, with a basic reproductive number (R₀) at approximately 3 (40, 41); a recent estimate by the CDC defines the SARS-CoV-2 R₀ at approximately 5.7 (42). This may be explained by an improved virus entry due to a molecular change of the receptor-binding domain and the insertion of a furin-cleavage site in the spike protein of SARS-CoV-2; this enables a 10-fold increased binding affinity to ACE2 and fusion with the host cell membrane (43). SARS-CoV-2 may additionally infect epithelial cells in the upper respiratory tract, thereby facilitating transmission of the shed virus via respiratory droplets. Presently, it appears that SARS-CoV-2 is more pathogenic than the influenza A virus but less pathogenic than SARS-CoV (44); the reported overall case fatality ratio of SARS-CoV-2 ranges between 1.38 and 3.8 (1, 25, 45). Notably, wide testing and identification of asymptomatic carriers versus focal testing restricted to the hospitalized (symptomatic) patients may either underestimate or overestimate the CFR.

IMMUNOPATHOGENESIS OF SARS-CoV-2

Given the vague COVID-19 pathogenesis, references to the earlier SARS/MERS-CoV pandemics are inevitable. While

useful given the similar CoV origin, this is not ideal as several significant immunological differences among the three diseases are apparent (Table 2).

Upon infection, virus internalization typically evokes intracellular pattern-recognition receptors signaling likely via RIG-I, OAS (46), and TLR-7 inducing interferons (IFN) I/III (and IFN-stimulated genes; IFGs) subsequently triggering a local immune response. In uncomplicated COVID-19, an increase in circulating follicular helper T cells and antibody secreting B cells was observed (47) concurrent with an upregulation of activation markers on CD14⁺ and CD8⁺-T cells. In contrast, there was a reduction of circulating CD14⁺CD16⁺ monocytes. Interestingly, the systemic cytokine response has been typically negligible in mild COVID-19, while rarely soaring in severe COVID-19 cases (48–50). Such a scenario reflects an optimal orchestration of the immune system and a balance between the inflammatory response and disease tolerance leading to uneventful pathogen eradication. Unfortunately, in a subgroup of patients developing life-threatening COVID-19 phenotype this balance is deranged. In the following sections, Table 2 and Figure 3 summarize the rudimentarily understood dynamics of the immuno-inflammatory processes in patients with varying COVID-19 severity and phenotype.

Viral load

In adults, viral load was found to correlate with COVID-19 severity and has been suggested as a potential mechanism responsible for the disease progression (51). However, the role of the viral load is unclear since it may reflect failure of the immune response and a high viral load can also be the result of immuno-evasion (SARS-CoV-2 poorly upregulates IFN I and III) (46). Endocytosis of the virions bounded to ACE2 decreases activity of this enzyme which can skew the angiotensin II/angiotensin (1–3, 5–8) balance by increasing ACE1 activity (52). It remains to be verified whether the increase in angiotensin II indeed contributes to propagation of the inflammation and impaired hypoxic vasoconstriction in COVID-19 patients. In human alveolar epithelial cells, SARS-CoV-2 induces cytopathic effects (53). SARS-CoV-2 appears to be very cytotoxic; infection of epithelial Vero-E6 cells with a patient-isolated SARS-CoV-2 strain was highly cytopathic after 48 h (M. Ranawak, personal communication). It can only be

TABLE 2. Comparison of selected aspects of immune response to SARS-CoV, MERS, and SARS-CoV-2*

Item	SARS-CoV	MERS	SARS-CoV-2
Receptor abundance	ACE2: Lung and intestine epithelium Endothelium Cardiomyocytes Central nervous system	Dipeptidyl peptidase 4 - DPP4 (CD26): T-helper cells Two receptor types High expression in the placenta, kidney; moderate expression in the kidney, lung, liver Low expression of 4.2 kb mRNA only in the skeletal muscle, heart, brain, pancreas	ACE2: Lung and intestine epithelium Endothelium Cardiomyocytes Central nervous system Macrophages Presumably CD147
Antibody: protection and dynamics	Protection conferred - 304 B cell epitopes Seroconversion as early as (d4) found in most patients by day 14 Long-lasting IgG and neutralizing antibody up to 2 years postinfection	Protection conferred MERS-CoV reinfection can occur in seropositive camels, Transitory antibody response in mild disease	Protection likely conferred Common cross-reactivity in antibody binding to the spike protein Rare cross-neutralization of the live viruses Highly variable neutralization capacity across patients Presence of non-neutralizing antibody response to conserved spike epitopes
Lymphocytes	Prominent lymphopenia (68%–85% cases)	Lymphopenia (35% cases)	Lymphopenia (75% cases)
T-cell mediated immunity: role and dynamics	Plays an important role in recovery 959 T cell epitopes T cell responses correlate with neutralizing ab Human memory T-cell responses specific for SARS-CoV N protein persist for 2 years in the absence of antigen Airway memory CD4+ T cells mediate protective immunity	Plays an important role in recovery Robust virus-specific CD8 T-cell responses Late CD4 T-cell responses Long-lasting T-cell immunity (≥2 years) T cell apoptosis present Airway memory CD4+ T cells mediate protective immunity	Unclear; under investigation Activation of follicular T cells in resolving infection Signs of activation of memory CD8+ T cells in resolution phase
Macrophages and dendritic cells: innate immunity	Low/no viral replication in macrophages, DCs Innate immunity able to control SARS-CoV in the absence of CD4/8 T cells and antibodies	Increased neutrophil and monocyte- macrophages influx in severe/ lethal disease	Unclear; under investigation Increase in CD14 ⁺ CD16 ⁺ monocytes in severe cases
Cytokine production and dynamics	PBMCs expressing high level of inflammatory cytokines Large production in the lungs	Systemic elevation of IL-17 and IFN I No direct evidence for the involvement of pro-inflammatory cytokines and chemokines in lung pathology during SARS and MERS, correlative evidence from patients with severe disease suggests a role for hyper- inflammatory responses in hCoV pathogenesis	Mild/medium cytokine response IL-6 and monocyte-related chemokines are elevated in the peripheral blood
Interferon production	No type I IFN responses in cell culture No IFN α/β induction in patients	Therapeutic IFN-I administration protective in mice Therapeutic IFN- β treatment ineffective in inhibiting viral replication in mice	Sensitive to <i>in vitro</i> type I IFN pretreatment Weak induction of IFN I and III <i>in vitro</i>
Immune evasion	Anti-type I IFN strategies preventing its production and its effects	Anti-type I IFN strategies preventing its production and its effects	Unclear; under investigation

*Due to the similar origin and genome, the immune response to human coronaviruses shares several confirmed and assumed aspects but numerous differences have already been reported. The characterized immune responses are of relevance to their pathophysiology and treatment (36–38). ACE indicates angiotensin-converting enzyme; CoV, coronavirus; DC, dendritic cell; IFN, interferon; IL, interleukin; MERS, Middle East Respiratory Syndrome; PBMC, peripheral blood mononuclear cell; SARS, Severe Acute Respiratory Syndrome.

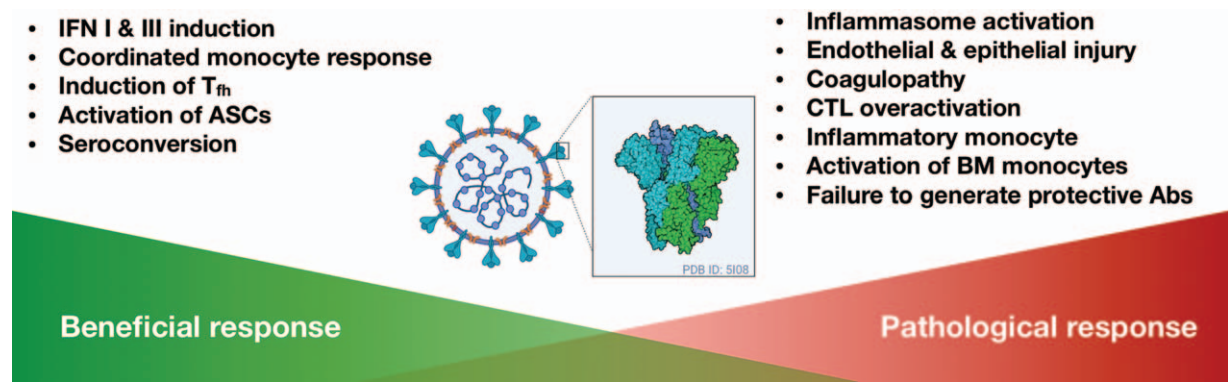


FIG. 3. Summary of potentially protective and harmful host responses during the SARS-CoV2 infection based on the currently available data. ASC indicates antibody secreting cells; BM, bone marrow; CTL, cytotoxic T-cells; IFN, interferon; T_{fh}, follicular helper T-cells; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

hypothesized that, similarly to SARS-CoV, SARS-CoV-2 activates the NLRP3 inflammasome leading to pyroptotic cell death (54); an abundant serum lactate dehydrogenase release in severe COVID-19 supports this notion (55). Interestingly, in bats, MERS-CoV poorly activates the inflammasome which contributes to their disease tolerance (56).

Innate immunity

Even in severe COVID-19, a mild neutrophilia is typically observed (48, 49), while circulating monocyte counts typically remain unaltered (49). An increased fraction of CD14⁺CD16⁺ cells was reported in severe cases (57) and several groups found blood monocytes IL-1β⁺, IL-6⁺ with IFGs expression (57, 58). Monocytes in COVID-19 were found to reduce their Human Leukocyte Antigen – DR isotype expression but the magnitude and time course of that reduction remains to be determined (59, 60). This suggests a pathological role of inflammatory monocytes in the immune response to SARS-CoV-2. Moreover, transcriptomic analysis of peripheral blood mononuclear cells (PBMCs) revealed upregulation of complement-related genes and increase in C-C motif ligand (CCL)2, C-X-C motif ligand10, CCL3, and CCL4 chemokines expression (61). Importantly, the CD169⁺ macrophages can be stimulated and infected by the virus up-regulating IL-6 (62). In some severe COVID-19 patients, high circulating ferritin was reported suggestive of hemophagocytosis by activated macrophages (48, 60).

Adaptive immunity

Severe cases of COVID-19 are characterized by peripheral lymphopenia attributable to the loss of T-cells, while B and NK cells remain only marginally affected (48, 49). Mechanisms of the T-cell lymphopenia remain mostly hypothetical but upregulation of pro-apoptotic genes expression has been suggested (61). Hallmarks of apoptosis and necrosis were present in lymph nodes and spleens in three autopsied COVID-19 patients (62). Alternatively, lymphopenia may be due to a robust lung infiltration and tissue homing (of circulating lymphocytes) which needs to be verified in further autopsy studies. Differentiating between these two mechanisms is key for understanding the pathophysiology and potential treatments. The circulating CD4⁺ and CD8⁺ T-cells are activated, but there is discrepancy

in the available reports regarding their ability to produce IFN-γ (49, 63). Notably, in aged mice, CD4⁺ but not CD8⁺ T-cells were crucial in controlling interstitial inflammation and clearing SARS-CoV-infection (64). One group reported an increased frequency of central memory with a decrease in naive T-cells subpopulations and clonal expansion of cytotoxic CD8⁺ T cells (58), while another group showed a rise in the frequency of naive CD4⁺ T-cells (49). It can be hypothesized that an uncontrolled “bystander activation” (in a cytokine-dependent manner) of the cytotoxic T-cells and their tissue sequestration are among the major pathogenic events which is supported by activation markers in severe cases (63). Interestingly, only in the ICU-admitted patients the pathogenic GM-CSF⁺IFN-γ⁺CD4⁺-T cells were found (57). Simultaneously, the regulatory T cells decrease (49) suggesting an impairment of the immune regulation. A single-cell analysis revealed an increase in memory B and plasma cells, which maintained activation and antibody production (with IgA overrepresentation) (58). Most antibody-related findings indicate that specific anti-SARS-CoV-2 immunoglobulins possess a neutralizing potential *in vitro* (65). However, the role of antispike protein antibodies should be further evaluated as these molecules may aggravate COVID-19 by promoting proinflammatory monocyte activation (66) and enable infection of immune cells (67). Those cellular changes were accompanied by seroconversion and appearance of Immunoglobulin G (IgG) and Immunoglobulin M (IgM) immunoglobulins. However, seroconversion takes from 5 to 9 days (68–70). Whether this humoral immunity is fully protective or could also contribute to antibody-dependent immunopathology (71, 72) remains to be established. Nevertheless, when studied *in vitro*, a correlation was reported between antibody titers and neutralization properties. At present, several studies investigate convalescent plasma-containing antibodies for treatment (73, 74).

Cytokines

Despite evidence of the so-called “cytokine storm” in SARS and MERS (75, 76), recent data suggest that this is not necessarily the case in SARS-CoV-2 infection (48, 51). Conflicting viewpoints backed by yet insufficient data have emerged fueling controversy about this concept (77, 78). Circulating cytokines (both pro- and anti-inflammatory)

increase in COVID-19 patients; however, only some of them (e.g., IL-2, IL-7, IL-10, G-CSF, MCP1, TNF α) are relatively robustly increased in severely (ICU-admitted) ill patients when compared with moderate/mild cases (48, 51). Compared with hyperreactive responses recorded in bacterial septic patients (79) and after noninfectious triggers (80), the cytokine upregulation in COVID-19 appears to be at least one log of magnitude lower. Many controversies arise regarding IL-6 as this cytokine was shown to be slightly increased in some severely ill (51), while it was also markedly up-regulated in non-survivors (81) and critically ill COVID-19 patients (82). Others found IL-6 predictive of mechanical ventilation requirement at a cutoff of 80 pg/mL (83). Of note, the expression of IL-6R in bronchoalveolar lavage fluid cells was downregulated and unchanged in PBMCs, suggesting that this pathway may not be crucial for COVID-19 pathophysiology (61). The current rationale to inhibit IL-6 is also controversial as IL-6 promotes antibodies formation (84), regeneration of airway ciliated cells from basal stem cells (85) and protects against H1N1 influenza (86). An indiscriminate application of IL-6 (and other) blockers has potential for harm, especially when done in a “blind” fashion in a heterogeneous population of COVID-19 patients.

The interferons

The precise role of IFNs in SARS-CoV-2 infection is yet unclear and requires further investigation. It is unclear whether patients by default produce amounts of interferon like certain mammals (87) or low IFN concentrations may reflect the coronaviruses' capacity to prevent/reduce its production and action (88–95). The latter may be plausible given that CoV are well capable of preventing NF- κ B activation (96) and protein translation (97). It is also important to define the specific role played by IFN- ϵ in the mucosa; this may explain differences between humans versus bats/pangolins regarding their response to a CoV infection (98–100). Better understanding of the crosstalk between SARS-CoV-2 and IFNs will offer insights into the COVID-19 immunopathogenesis. Some data suggest that the strategy of a very early administration of type I IFN could be considered (101–103). However, the negative effect of a late exposure to IFNs must also be considered; a study combining single-cell RNA-sequencing data and *in vitro* analysis showed that ACE2 is upregulated by type I and II IFNs in human and primate airway epithelial cells (104). Furthermore, IFN-inducible genes are highly expressed in cells from broncho-alveolar lavage fluid of COVID-19 patients and exhibited pathogenic potential with overrepresentation of genes involved in inflammation (105). Of note, the National Institute of Health (NIH) recommends against the use of IFNs for the treatment of COVID-19 outside of clinical trials (<https://www.covid19treatmentguidelines.nih.gov/therapeutic-options-under-investigation/host-modifiers-immunotherapy/>). Carefully designed trials will hopefully inform on the potential of the type I interferon application (106).

Coagulopathy and endotheliopathy

Coagulopathy appears to be a critical element in the context of severe COVID-19 courses. Elevation of D-dimers (fibrin degradation products) has been frequently observed in severe cases

and identified as a significant risk factor (107). One study revealed presence of a procoagulant state even during the early COVID-19 stage (21) and disseminated intravascular coagulation has been diagnosed in most critically ill patients (108). Moreover, the incidence of thromboembolic events is high (comparable to sepsis) and most likely underdiagnosed (109). It can be hypothesized that there is dominant local pulmonary vessel microthrombosis which correlates with the severity of hypoxemia and high compliance (110) and stays in accordance with fibrin accumulation found in the lungs (110, 111). Presumably, there are several pathways which may contribute to the clinical coagulopathy observed. Direct infection of the endothelium, thereby triggering endothelial injury, inflammation, and cell death (22), can directly activate the coagulation cascade. Pyroptosis and inflammasome-released mediators are other potent coagulation cascade activators (112, 113). Histopathological examination revealed deposition of activated complement complexes that may propel microvascular injury and subsequent activation of the clotting pathway (114). Neutrophilic infiltrates can also activate coagulation through the generation of neutrophil extracellular traps (115) and a recent anecdotal study confirmed the presence of antiphospholipid antibodies in three COVID-19 patients with severe coagulopathy (116). An analysis of over 3,500 genes (differentially expressed in the lungs) following murine SARS-CoV infection identified various procoagulatory factors (especially urokinase) to be strongly associated with mortality (116). Urokinase activity results in the generation of plasmin and in turn in fibrinolysis with elevated D-dimers manifested by alveolar coagulopathy and pulmonary hemorrhage. Furthermore, serpin1 knockout mice confirmed an enhanced pulmonary expression of procoagulatory and profibrinolytic proteins and clinical susceptibility to SARS-CoV (117). Apart from cytokine effects on the pulmonary endothelium, it has also been proposed that disruptions of the kallikrein-bradykin axis can increase microvascular permeability and cause angioedema (118).

EXPERIMENTAL THERAPIES AND PRECLINICAL EVIDENCE

The number of proposed therapeutic strategies against COVID-19 grows weekly; presently, there are over 50 substances considered as potential remedies including brand new (Small interfering RNA) (119)) as well as well-known/repurposed chemicals (chloroquin, interferons, remdesivir). Yet, the currently available pre- and clinical evidence supportive of the experimental therapies is suggestive at best. Several substances with different targets have been proposed based on sparse peer-reviewed publications (Table 3) (120–143); some based on non-peer-reviewed (medRxiv and bioRxiv) preprints and/or anecdotal evidence only. As of May 19, 2020, there is only one peer-reviewed study (140) that tested an anti-COVID-19 candidate drug in a relevant SARS-CoV-2 animal model (Table 3); many drugs have not yet been directly tested against SARS-CoV-2 *in vitro*. Except a single case (140), the only available animal model-based evidence stems from MERS/SARS-CoV studies (Table 3), but these diseases are not identical to COVID-19 (Table 2).

TABLE 3. Preclinically tested therapeutics against SARS-CoV, MERS-CoV, and SARS-CoV-2 and related illness*

Area of activity	Substance administered	Corona virus type	Findings	Animal/cell model(s)
Viral replication	Remdesivir	1. MERS-CoV	1. Prophylactic/therapeutic; viral replication inhibition, reduced lung lesions	1. NHP (120)
		2. MERS/SARS-CoV, human CoV, batCoV	2. Prophylactic/therapeutic; viral replication inhibition, improved respiratory function	2. pHAEC, pHLC, mouse (121)
		3. MERS-CoV	3. Prophylactic/therapeutic; reduced viral replication and ALI, prevented mortality	3. Mouse, Calu-3 cells (122)
		4. SARS-CoV-2	4. Pre-/co-/post-treatment; blocked cell entry, reduced viral replication	4. Vero E6 (123, 124)
	siRNA	SARS-CoV	Prophylactic/therapeutic; viral replication inhibition, reduced lung lesions	NHP (125, 126)
	NHC (cells)	1. MERS-CoV	1. Prophylactic/therapeutic; reduced viral replication, increased viral mutation rates (cells), reduced lung lesions and improved respiratory function (mouse)	1. Calu-3, pHAEC cells, mouse (127)
	NHC prodrug (mouse)	2. SARS-CoV	2. Prophylactic/therapeutic; viral replication inhibition (cells and mouse), improved respiratory function and reduced lung lesions (mouse)	2. Calu-3, pHAEC cells, mouse (127)
		3. SARS-CoV-2	3. Reduced viral replication	3. Calu-3, Vero, pHAEC cells (127)
Cell/nuclear entry	Chloroquine (CQ) and hydroxychloroquine (HCQ)	1. SARS-CoV-2	1. Pre-/post-treatment; blocked/reduced cell entry, reduced viral replication, inhibitory efficiency HCQ>CQ	1. Vero E6 (123, 128, 129)
		2. SARS-CoV	2. Therapeutic; no effect on viral replication	2. mouse (130)
	camostat mesylate	SARS-CoV-2	Pre-treatment; reduced cell entry	Calu-3 cells (131)
	Ivermectin	SARS-CoV-2	Post-treatment; reduced viral replication	Vero/hSLAM (in press)
Immuno-inflammatory-modulation	Mycophenolic acid	MERS-CoV	1. Therapeutic; viral replication and mortality exacerbation	1. NHP (132)
		SARS-CoV	Prophylactic/therapeutic; prevented mortality, reduced lung lesions and pro-inflammatory markers	Mouse (133)
		SARS-CoV	Therapeutic; no effect on viral replication	Mouse (130)
		1–3. SARS-CoV	1. Prophylactic/therapeutic; viral infection inhibition, reduced lung lesions	1. Mouse (134)
		4. MERS-CoV	2. Prophylactic; viral infection inhibition	2. Hamster (135)
			3. Prophylactic/therapeutic; reduced viral load and lung lesions	3. NHP (136)
			4. Prophylactic/co-application; reduced viral replication, lung/spleen lesions and pro-inflammatory markers	4. Mouse (137, 138)
	Interferon (α / β 1b)	1. SARS-CoV	1. Prophylactic/therapeutic; viral replication inhibition, reduced lung lesions	1. NHP (139)
		2. MERS-CoV	2. Therapeutic; viral replication inhibition, improved survival	2. NHP (132)
		3. SARS-CoV	3. Therapeutic; viral replication inhibition	3. Mouse (130)
Other compounds	1. Lianhuaqingwen 2. Pudilan xiaoyan	SARS-CoV-2	1. co-/post-treatment; reduced viral replication (Vero E6), reduced pro-inflammatory markers (Huh-7)	1. Vero E6 and Huh-7 (124)
			2. therapeutic; reduced viral load & lung lesions	2. Mouse (140)
Combinations	1. Lopinavir/ritonavir 2. Lopinavir/ritonavir/IFN β 3. IFN- α 2b and ribavirin	MERS-CoV (1–3),	1. Therapeutic (NHP); viral replication inhibition, improved survival. Cotreatment (FRhK-4); reduced cytotoxicity	1. NHP (132), FRhK-4 (141)
		SARS-CoV (1&3)	2. Prophylactic/therapeutic; minimal effects	2. Mouse, Calu-3 cells (122)
			3. Therapeutic; reduced lung lesions, improved respiratory function, reduced pro-inflammatory markers	3. NHP, Vero and LLC-MK2 cells (142, 143)

*Data on the following coronaviruses are included: MERS-CoV, SARS-CoV, SARS-CoV-2, human CoV, bat CoV. Complete *in vitro* record is provided for SARS-CoV-2 only. Only peer-reviewed publications are included (May 19, 2020).

FKrH-4 indicates fetal rhesus kidney cells; Huh-7, hepatocyte derived cellular carcinoma cell; LLC-MK2, rhesus monkey kidney epithelial cells; MERS, Middle East Respiratory Syndrome; NHC, N4-hydroxycytidine; NHP, non-human primate; pHAEC, primary human airway epithelial cell; pHLC, primary human lung cells; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2; siRNA, Small interfering RNA. Prophylactic administration: before virus inoculum, therapeutic administration: after virus inoculum.

Mechanistically, we are only at the very beginning to understand how SARS-CoV-2 infects, targets the lungs (and other organs), and causes severe vascular and tissue damage. Despite the aforementioned limitations, the existing experimental findings warrant a well-organized, collaborative verification of therapeutics aiming at clearing the virus load, modulating the inflammatory response, protecting/repairing damaged tissues (e.g., endothelium), and ameliorating vascular coagulopathy. The mechanisms of pulmonary and remote organ response to SARS-CoV-2 present an additional level of complexity; any pathophysiological (and subsequently therapeutic) leads remain mostly speculative and require adequate modeling and experimental verification. This is currently difficult to achieve given that (mostly non-peer-reviewed) evidence suggests the only animal models suitable for studying SARS-CoV-2/COVID-19 include non-human primates, ferrets, and transgenic mice. The WHO asserts high reproducibility of SARS-CoV-2 infection in Rhesus macaques and ferrets (144). *Macaca mulatta* was the most susceptible to SARS-CoV-2 (compared with *M. fascicularis* and *C. jacchus*) displaying a wide array of clinical-like COVID-19 symptoms (145). In another study, six macaques developed infection and pneumonia but remained asymptomatic (120). Kim et al. (146) demonstrated ferrets as an apt model both for SARS-CoV-2 infection and transmission; animals were symptomatic (e.g., fever, cough), displayed high viral RNA in the lungs and upper respiratory tract and shedded virus via multiple routes. The disease phenotype in ferrets was reproduced by another study (147) and there is unpublished evidence from the Australian Centre for Disease Preparedness, Geelong, Victoria.

However, small laboratory animals remain the most accessible and cost-effective model to study. Transgenic human ACE2 mice (both sexes) infected with the HB-01 strain developed COVID-19-like interstitial pneumonia, high viral load, and produced high specific IgG titer but the disease was generally mild (148). The most recent study largely reproduced this phenotype in hACE2 mice (149). Syrian hamsters constitute another potential option; two groups recently recapitulated a mild but widely symptomatic COVID-19 phenotype (150, 151). In contrast, species such as pigs, chickens, and ducks were virus-free when either inoculated or exposed to the virus, cats were asymptomatic despite postexposure infection whereas dogs were minimally susceptible to SARS-CoV-2 exposure (152). Experimental drugs will soon be tested in the newly emerging COVID-19 models. While modeling of SARS-CoV-2 infection in healthy and young animals will be informative, it is important to consider that the most severe COVID-19 phenotypes appear in aged patients with comorbidities—the animal models should reflect this to maximize their translational capability for pathophysiology studies and drug testing. The most recent macaque experiment attests to that; 15-year-old animals developed an exacerbated COVID-19 phenotype while the young ones did not (153). Another important element in preclinical modeling is to promote study designs that allow drug testing in divergent, precisely defined and relatively homogeneous COVID-19 phenotypes (provided they can be recapitulated in animals). It is likely that a given therapeutic may be either beneficial or detrimental contingent upon the timing of its administration and/or specific COVID-19

pathophysiological characteristic. Compared with patients, animal studies present a relatively cheap and safe platform to establish such relationships.

The yet limited evidence derived from preclinical studies coupled with the emerging clinical data as discussed previously indicates that SARS-CoV-2-induced coagulopathy may be one of the key interests for experimental studies (116). In this context, another less apparent but interesting target for potential COVID-19 therapy is the complement activation pathway. Genetic absence of the complement C3 component was associated with reduced pulmonary/systemic inflammation and improved lung function (154). MERS-CoV-infected mice displayed elevated complement component C5a in the lungs and blood and blockade of the C5aR receptor attenuated inflammation in the lungs and spleen and reduced pulmonary viral replication (137). As aforementioned, adaptive immunity cells activation is prerequisite for eradication of the virus. Whether specific cell types of adaptive immune cells may help to induce pulmonary healing processes in SARS-CoV is currently unclear. Mechanistically, the large surface area of the alveolar capillary endothelium appears as a key target organ; protection and repair of the dysfunctional air–blood barriers (through reduction of endothelial swelling, damage, boosting epithelial regeneration) and endothelium-derived coagulopathy (e.g., formation of microthrombi) could be life-saving in COVID-19 patients, especially in those with advanced pulmonary damage and severe respiratory failure. Unfortunately, these postulates remain largely speculative and valid SARS-CoV-2/COVID-19 models are needed for verification.

An application of experimental (unlicensed) therapeutics via the compassionate use protocol (CUP) while justified as last resort (155) should not be reflexively overexpanded in the context of SARS-CoV-2/COVID-19 infection; CUP rarely provides reliable efficacy data given multiple confounding factors and inobjectivity. Whereas the magnitude of pandemic may justify extraordinary measures to save patients' lives, these measures must be counterbalanced by an extraordinary analytical rigor and resistance to overoptimistic interpretation of the daily-emerging *in vitro/silico*, animal and clinical data. In a disease with a relatively low mortality and rudimentary understanding of its pathophysiology, potential risks for life-threatening side effects by unproven therapeutics must not be ignored in a pursuit of the desired benefits. The hazards of adverse effects are additionally aggravated by the typically advanced age of COVID-19 patients, who frequently present with various comorbidities and comedications (156). Properly designed animal experiments and clinical studies will gradually reveal the cons and pros of the experimental therapeutics.

CLINICAL MANAGEMENT AND TRIALS

With the exception of remdesivir, which has received an emergency use authorization by the US Food and Drug Administration (FDA) for the treatment of hospitalized COVID-19 patients on May 1, 2020, (European Medical Agency (EMA) announced on May 18, an upcoming conditional marketing authorization), there are no drugs yet approved by any professional authority to prevent and treat COVID-19; results from any large-scale clinical trials are not yet available. The WHO,

EMA, and CDC strongly discourage the application of any unlicensed therapeutics outside of adequately designed clinical trials (<https://www.cdc.gov/coronavirus/2019-ncov/hcp/therapeutic-options.html#r8>; <https://apps.who.int/iris/bitstream/handle/10665/331446/WHO-2019-nCoV-clinical-2020.4-eng.pdf?sequence=1&isAllowed=y>; <https://apps.who.int/iris/handle/10665/330680>). The most reliable strategies continue to rest on supportive ICU care practices including supplemental oxygen, mechanical ventilation, and, *in extremis*, extracorporeal membrane oxygenation. However, traditional ventilation protocols used in acute respiratory distress syndrome (ARDS) may not be adequate for all COVID-19 patients. Interim guidelines to inform clinicians how to care for patients with COVID-19 have been released by the NIH (<https://covid19treatmentguidelines.nih.gov/introduction/>) and by the Surviving Sepsis Campaign as an initiative supported by the Society of Critical Care Medicine and the European Society of Intensive Medicine (SCCM/ESICM, (157)). Health professionals from the European Respiratory Society partner societies have compiled an international directory of guidelines and best practice recommendations documents intended to help share COVID-19 expertise around the world (<https://www.ersnet.org/covid-19-guidelines-and-recommendations-directory>). However, the guidelines are based upon current limited evidence and will require rapid updates to account for any new and compelling evidence; the NIH guidelines are conceptualized as living guidelines (158). Some of the more prominent, currently investigated therapies include antimalarials, antivirals, immunotherapeutics, and corticosteroids (158).

Antimalarials

The trial-based evidence has been fluctuating very dynamically since the dawn of the SARS-CoV-2 pandemic. Initially, it was proposed to treat severely ill Chinese COVID-19 patients with chloroquine phosphate (159). Following these observations, a combination of oral hydroxychloroquine and azithromycin was proposed in patients with signs of lower respiratory tract involvement. This was based on a small-scale open-label clinical trial, in which 36 patients were allocated to treatment with hydroxychloroquine ($n = 20$) or left untreated ($n = 16$). Hydroxychloroquine was associated with virological cure on days 3, 4, and 5 in 50%, 60%, and 70%, respectively, compared with 6.3%, 25%, and 12.5% of untreated controls (azithromycin co-administration in six patients further improved it to 83%) (160). This French study was further confirmed by the same team on 80 patients (161). These studies were heavily criticized by the MRC-NIHR Trials Methodology Research Partnership for numerous shortcomings (160). The two subsequent studies with hydroxychloroquine indicated no improvement (162, 163). The most recent reports emphasize risks associated with chloroquine-based trials; due to adverse cardiac reactions, chloroquine treatment (with and without azithromycin) was stopped in Brazilian (164) and French (165) trials; and several hospitals in Sweden stopped administering hydroxychloroquine to COVID-19 patients based on similar findings (166). A recent preprint article that retrospectively analyzed hydroxychloroquine use in hospitalized US veterans found an association of increased overall mortality with its use (167).

Antivirals

Other suggested alternatives have been antiviral treatments with remdesivir and lopinavir-ritonavir. The most recent remdesivir CUP study was performed in 53 patients with severe COVID-19 and the median follow-up showed an improvement in oxygen support in 36 patients (68%) including 17 of 30 patients (57%) with mechanical ventilation that were successfully extubated (168). However, the study has been widely questioned as no comparator group was involved (<https://www.sciencemediacentre.org/expert-reaction-to-a-study-about-compassionate-use-of-remdesivir-for-patients-with-severe-covid-19/>). Another open-label randomized trial in 199 COVID-19 patients showed that lopinavir-ritonavir failed to accelerate clinical improvement, reduce mortality, and diminish viral RNA detectability (169). Nearly 14% of patients in the lopinavir-ritonavir arm could not complete the full 14-day treatment course due to gastrointestinal adverse events. Remdesivir and (hydroxy) chloroquine are both under evaluation in the largest international trial in severe COVID-19 patients launched by the WHO and partners. The “SOLIDARITY” trial compares four options: local standard of care (LSC), or LSC plus either remdesivir, chloroquine/hydroxychloroquine, lopinavir with ritonavir, or lopinavir with ritonavir plus IFN β -1a. As of May 18, 2020, over 90 countries are active participants to this trial (<https://www.who.int/emergencies/diseases/novel-coronavirus-2019/global-research-on-novel-coronavirus-2019-ncov/solidarity-clinical-trial-for-covid-19-treatments>). As the most recent development, results of two different randomized, placebo-controlled, multicenter studies testing remdesivir were released on April 29, 2020: the Chinese trial (NCT04257656; 237 patients; (170)) demonstrated no statistical benefit, whereas an official announcement (apnews.com) stated that an NIH-led trial (NCT04280705; 460 patients at interim analysis) shortened the time to recovery to 31%. Two days later, on May 1, 2020, the FDA approved remdesivir for emergency use to treat COVID-19 patients based upon the belief that “*the known and potential benefits of [remdesivir] outweigh the known and potential risks of the drug for the treatment of patients hospitalized with severe COVID-19*” (<https://www.fda.gov/media/137564/download>).

Immuno-inflammatory modulation

Various strategies aiming to modulate the immune response in critically ill COVID-19 patients have been proposed. Specific examples include the transfusion of convalescent plasma and targeted anti-inflammatory treatments. In two case-series critically ill COVID-19 patients (171, 172) received compatible transfusions of 250 mL to 400 mL of convalescent plasma. In the first case-series (171), all five patients were under co-administration of methylprednisolone and antivirals (mainly lopinavir/ritonavir). After 12 days from transfusion, an improvement was noted in the Sequential Organ Failure Assessment score, an increase of the partial oxygen to fraction of inspired oxygen (pO $_2$ /FiO $_2$) ratio along with virological cure was observed (172). In the second case-series, clinical improvement was not observed in the 10 enrolled patients but all patients experienced virological cure (172). Three trials testing convalescent plasma in COVID-19 patients are currently recruiting patients (NCT04321421; NCT04343755; NCT04355897).

The idea of modulating the immune response of the host originates from the observed alterations of various cytokines in the blood of COVID-19 patients (49, 60, 172). For example, circulating cytokines were compared between 286 severe and 166 non-severe COVID-19 patients; TNF α , IL-2 receptor, IL-6, IL-8, and IL-10 were significantly higher in the severe versus non-severe patients. Another recent study analyzed immune characteristics of 54 COVID-19 patients with (n = 28) or without (n = 26) mechanical ventilation requirement suggesting two divergent dysregulation patterns: a generalized immune hyperactivation and dysregulation associated with a decreased Human Leukocyte Antigen – DR isotype expression (60). Several clinical trials are currently testing a range of inflammatory modulators; four medium-size trials investigate the efficacy of biologically targeting the IL-1 and the IL-6 pathway: recombinant IL-1 receptor antagonist anakinra (NCT04330638/COV-AID, 342 patients), IL-6 receptor antagonists tocilizumab (NCT04330638/COV-AID, 342 patients; NCT04320615/COVACTA, 330 patients), and sarilumab (NCT04320615/CORIMUNO-SARI, 240 patients). Mortality, ventilator-free days, and the change of the respiratory ratio are the most common endpoints. Smaller-scale trials also aim (not yet recruiting) to investigate the impact of immunostimulants like PD-1 blockers thymosine (NCT04268537; 120 patients) and novilumab (NCT04343144/CORIMUNO-NIVO, 92 patients), and Treg stimulant human recombinant IL-2 (NCT04357444/LILIADE-COVID, 30 patients). However, these strategies are not controversy-free given that there is no clear consensus as to what extent the magnitude of the inflammatory response generated by SARS-CoV-2 is detrimental to COVID-19 patients (hence favoring cytokine inhibition) or necessary for eradication of the virus and host defense (hence discouraging their blockage and/or favoring immuno-supportive interventions).

Corticosteroids

The use of corticosteroids in the acute respiratory distress syndrome (ARDS) of COVID-19 remains also a matter of debate as no evidence of their efficacy currently exists. In a recent report in 84 COVID-19 patients with ARDS, the administration of methylprednisolone (dosage similar to the SCCM/ESICM recommendations (173)) was associated with a reduced risk of death (0.38; 95% CI, 0.20–0.72) (107). Although opinions vary on the administration of corticosteroids in COVID-19 patients, the two largest studies on H1N1 and SARS (n = 7568) were supportive to their use (174, 175). However, the WHO interim ([https://www.who.int/publications-detail/clinical-management-of-severe-acute-respiratory-infection-when-novel-coronavirus-\(ncov\)-infection-is-suspected](https://www.who.int/publications-detail/clinical-management-of-severe-acute-respiratory-infection-when-novel-coronavirus-(ncov)-infection-is-suspected)) and NIH (<https://covid19treatmentguidelines.nih.gov/introduction/>) guidelines do not recommend corticosteroids in viral pneumonia outside of clinical trials. There is preliminary information from China and Italy, suggesting that the use of corticosteroids in COVID-19-associated ARDS could be considered (176) but such anecdotal evidence is burdened by bias and should not be used as reference for altering treatment practices. The WHO has prioritized the evaluation of corticosteroids in COVID-19 with five running randomized controlled trials. At present, no definite conclusion can be drawn from the available experimental and clinical data to assess the acute and long-term effects of corticosteroids for the resolution of the local and systemic inflammatory response in COVID-19 and/or the development of fibrotic complications.

Coordinating clinical trials

An overwhelming number of clinical trials has emerged (Fig. 4) aiming to assess therapies ranging from antivirals, immune-therapeutics, and host-directed therapies, vitamins, gases, mesenchymal stem cells to Traditional Chinese Medicine—all in the bid to save lives of COVID-19 patients. As of May 18,

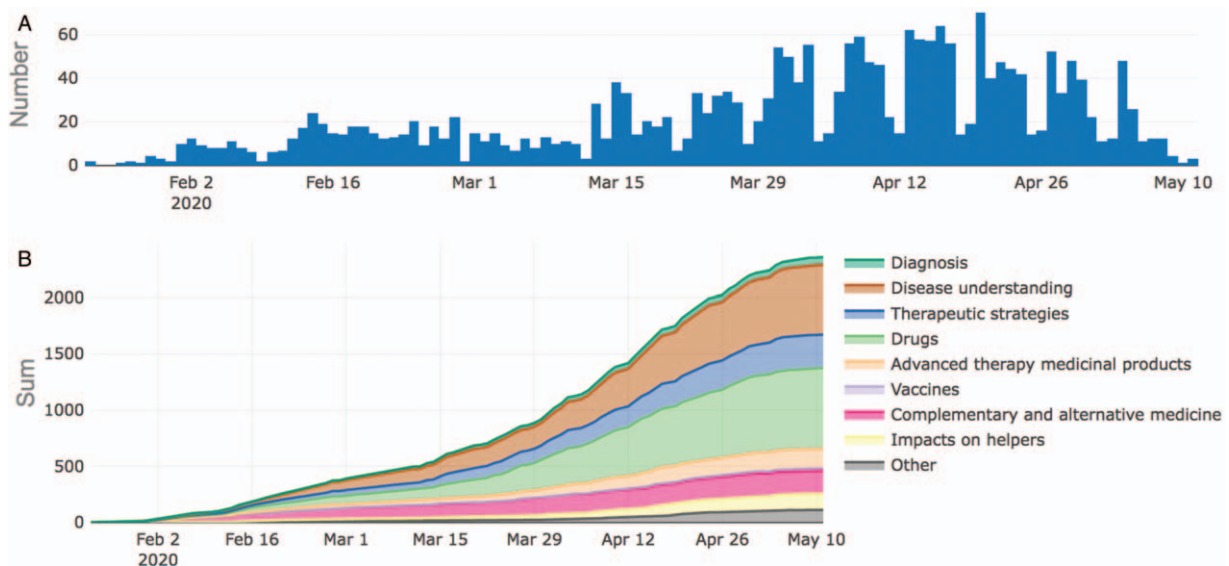


FIG. 4. **Global clinical research activities on SARS-CoV2/COVID-19 based upon trial registration data.** A, Registration of COVID-19 clinical trials for each day. B, The cumulative number of registered COVID-19 clinical trials exceeds 1,500. Information based on data from the WHO Clinical Trials Search Portal (<https://apps.who.int/trialsearch/>) for COVID-19-related clinical trials as of May 18, 2020. This portal allows access to a central database containing the trial registration data sets provided by international registries. The WHO portal is updated every Friday by six important registries and every 4 weeks by additional registries (https://covid-19.heigit.org/clinical_trials.html; COVID-19-Karte der Hoffnung; Universität Heidelberg; May 18, 2020). COVID-19 indicates coronavirus disease 2019; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

2020, the cumulative number of registered COVID-19 clinical trials according to the WHO Clinical Trials Portal was 2356 (<https://www.who.int/ictrp/en/>). The trial count grows daily and is frequently updated. The deluge of trials scheduled to recruit simultaneously may create a realistic “traffic jam” risk for under-enrolment and is perceived as chaotic (177). An additional major concern of many ongoing COVID-19 trials is their relatively low power to detect significant differences in meaningful outcomes. Low-powered trials rarely provide unequivocal evidence justifying the use of tested therapeutics. In this respect, pandemics provide a unique window of opportunity for large-scale collaborative initiatives, thus, enabling networks to jointly generate and address common goals as well as to standardize data collection in large patient volumes. The WHO recommends the development of “Master Protocols” for high-powered, adequately-designed trials as a tool for the most rapid and reliable evaluation of investigational therapeutics and vaccines (<https://www.who.int/blueprint/priority-diseases/key-action/novel-coronavirus/en/>). The five ongoing global clinical trials SOLIDARITY (<https://www.who.int/emergencies/diseases/novel-coronavirus-2019/global-research-on-novel-coronavirus-2019-ncov/solidarity-clinical-trial-for-covid-19-treatments>), REMAP-CAP (A Randomised, Embedded, Multifactorial, Adaptive Platform Trial for Community-Acquired Pneumonia; (NCT02735707; [remapcap.org](https://www.remapcap.org) (178)), RECOVER (Randomized Evaluation of COVID-19 Therapy; <https://www.recoverytrial.net/>; <https://doi.org/10.1186/ISRCTN50189673>) and PRINCIPLE (Platform Randomized trial of Interventions against COVID-19 in older people; ISRCTN86534580 (179)), and Trial of Treatments for COVID-19 in Hospitalized Adults (DisCoVeRy) (<https://clinicaltrials.gov/ct2/show/NCT04315948> (180)) exemplify such an approach.

Vaccines

Finding a safe and effective vaccine to prevent infection with SARS-CoV-2 has become an urgent public health priority and a number of legacy drug-makers and startups have begun to develop vaccines (and treatments) that target SARS-CoV-2. At present, the global COVID-19 vaccine R&D landscape includes 115 vaccine candidates, of which 78 are confirmed as active and 37 are unconfirmed ((181), <https://clinicaltrials.gov/>). Of the 78 confirmed active projects, 73 are currently at exploratory or preclinical stages. The most advanced candidates have recently been moved into clinical development, including mRNA-1273, Ad5-nCoV, INO-4800, LV-SMENP-DC, and pathogen-specific aAPC (181). On March 16, 2020, the first-ever injection of an investigational vaccine for SARS-CoV-2 (mRNA-1273) was administered to four volunteers participating in an open-label phase 1 clinical trial in the United States. The study is expected to conclude June 1, 2021. Multiple other vaccine developers have communicated plans to initiate human testing within this year.

SARS-CoV-2 DIAGNOSIS AND OPTIMIZATION OF TESTING

The differentiation of the SARS-CoV-2-positive cases from the healthy is among the main clinical challenges. Many asymptomatic persons are a source of infection despite being

considered healthy prior to a positive test result (182). The prevalence of asymptomatic (SARS-CoV-2 positive) patients ranges between 1.5% and 30% (182–184). Non-test-based COVID-19 diagnosis is difficult given that the most common clinical symptoms, e.g., fever, fatigue, dry cough, myalgia, and dyspnea (51, 185) are unspecific and overlap with other viral diseases (185). Several hematologic and immuno-inflammatory abnormalities observed in SARS-CoV-2-positive patients resemble MERS/SARS-CoV infection symptoms (185). To reduce the transmission risk, aggressive containment, mitigation, and treatment strategies must be combined and rapid and accurate testing is key. A few countries/territories such as Taiwan, Hong Kong, Singapore, and South Korea have rapidly implemented aggressive testing (186); South Korea has performed >300,000 tests (5,829 tests/million population) within the 9 weeks after the first SARS-CoV-2 case was identified, effectively containing the SARS-CoV-2 spread (187, 188). The majority of other countries have been struggling with tests approval, availability, and/or operationalization of high-throughput testing, which was accompanied by substantial differences in reported numbers.

The current recommendation of many professional radiological associations and societies is that imaging should not be employed as a screening nor diagnostic tool for COVID-19 but reserved for the evaluation of complications. Although used frequently in early reports with some characteristic features described ((4), Fig. 2), imaging has limited sensitivity for COVID-19 and the definitive test for SARS-CoV-2 remains laboratory-based. A wider evaluation of the CT value in COVID-19 patients is further complicated by its different use among different countries (e.g., frequent in China, infrequent in Europe, sporadic in the US).

As of March 9, 2020, the WHO recommends testing based on clinical and epidemiological factors contingent on the likelihood of SARS-CoV-2 infection and/or exposure (189). Similarly, the CDC has established a priority system for diagnostic testing for SARS-CoV-2 infection based on the availability of tests; the CDC testing guidance is updated periodically (<https://covid19-treatmentguidelines.nih.gov/overview/>). In asymptomatic or mildly symptomatic subjects who were in contact with SARS-CoV-2/COVID-19, virus nucleic acid amplification tests (NAAT), such as RT-PCR, is typically recommended (189). Given that NAAT recommendations are difficult to meet in many countries due to limited testing resources and/or excessive demand, the WHO suggests adopting screening protocols tailored to the local situation and provides reference laboratories for confirmatory testing (<https://www.ecdc.europa.eu/en/novel-coronavirus/laboratory-support>) as well as shipment instructions if local testing is unavailable (190). As co-infections and false-negative diagnoses occur, testing for other respiratory pathogens should be also performed utilizing routine laboratory procedures (189). Currently, two types of diagnostic kits for SARS-CoV-2 are available: genomic (RNA-based, long, precise) and serological (IgM/IgG-based; fast, relatively imprecise).

Nucleic acid amplification test (NAAT)

The WHO recommends a RT-PCR test for SARS-CoV-2 detection (185, 189); RT-PCR was the first established and

rapidly commercialized diagnostic method in the SARS-CoV-2 pandemic (191, 192). The WHO testing recommendations differ depending on the SARS-CoV-2 prevalence. In the virus-free areas, a positive NAAT for at least two target SARS-CoV-2 genes is considered reliable; in areas with SARS-CoV-2 presence, a confirmation of a single discriminatory target is sufficient (185, 189). The Chinese National Institute for Viral Disease Control and Prevention recommends a cycle threshold value (Ct-value) below 37 as positive, Ct-value >40 as negative test (193), and (40) <Ct-value < 40 requiring retesting. The intermediate values have frequently been associated with reported false-negative rates (194). Therefore, a negative RT-PCR result does not necessarily rule out the possibility of SARS-CoV-2 infection (194). The WHO quotes several culprit factors including a poor specimen quality, timing of specimen collection, specimen handling, and/or shipping and various technical problems (189). A small Chinese study demonstrated that some COVID-19 patients who met criteria for hospital discharge and/or quarantine discontinuation (free of clinical symptoms, radiological abnormalities and with two negative RT-PCR tests) were tested positive (by RT-PCR) 5 to 13 days later (195). A South Korean study reported that two out of 10 negative COVID-19 cases by RT-PCR were later confirmed as positive (196). In a large study, the second RT-PCR test was positive in 12.5% of initially negative 384 patients (197). Thus, the detection of SARS-CoV-2 is highly specific (no false positives) but the sensitivity is not ideal (198). These findings reveal limitations of RT-PCR testing and indicate that some recovered patients may continue to be virus carriers (195). This phenomenon, if confirmed on a larger scale, may force changes in the current criteria for hospital discharge and quarantine discontinuation. Furthermore, the SARS-CoV-2 diagnostics should account for clinical findings; preliminary data from China showed that isolated patients (with presumed COVID-19) with initially negative RT-PCR but with typical clinical and radiological COVID-19 symptoms were confirmed as SARS-CoV-2-positive after repeated swab testing (194). Thus, a combination of repeated RT-PCR testing and radiological imaging may be helpful in determining suspected false-negative cases.

Although the RT-PCR constitutes the current diagnostic standard, the test kits suffer considerable limitations. In 610 patients, in the first all-patient test, 27.5% cases were positive, 0.2% weakly positive, 9.3% dubious, and 63% were negative (197). Among the patients with initial negative results, the second test was positive in 12.5%, dubious in 7% patients, negative in 73% patients, and results were not available for 7.6% patients (197). The false-negative readouts are also contingent on the workflow for molecular detection (e.g., and isolation method with/without commercial kit) (194, 195, 199). Additionally, RT-PCR has long turnaround times, requires certified laboratories, expensive equipment, and trained personnel. Due to these limitations, RT-PCR may not be practical as a rapid and simple diagnostic and/or screening tool. There is an urgent need for a fast, sensitive, accurate, and simple test to process a large number of suspected and asymptomatic carriers. Moreover, there is a pressing need for rapid, digital analyses of viral load as the field moves forward.

Serological testing

Serologic detection of specific IgM/IgG antibodies constitutes a rapid, simple, and cost-effective complementation to NAAT (170). The WHO continues to evaluate and update all available immunodiagnostic tests for COVID-19 (200). One of the newest point-of-care tools is the lateral flow immunoassay test able to detect IgM and IgG in the blood sample within 15 min (201). Since the IgG concentration begins to rise as IgM levels start to drop, the dynamic pattern in COVID-19 patients is consistent with an acute viral infection (202).

The serological SARS-CoV-2 testing with an average sensitivity of 88.7% and a specificity of 90.6% faces the risks of both false-positive and false-negative readouts (201). The key testing limitations include low antibody concentrations, differences in individual immune responses and antibody production, and quick changes in the IgM/IgG ratio (201); possible cross-reactivity with other corona and flu viruses cannot be excluded (203, 204). The above shortcomings practically preclude defining the exact infection time-point and the length of infection. Over 500 commercial SARS-CoV-2 tests are currently available or under development ((205); <https://www.finddx.org/covid-19/pipeline/>); however, their efficacy remains limited and the validation of their clinical performance and quality constitutes a global priority (200). As of April 8, 2020, the WHO does not recommend the use of antibody-detecting rapid diagnostic tests for direct patient assessment; their application is encouraged for COVID-19 surveillance and epidemiological research (200).

MODELING AND TRANSLATIONAL TECHNOLOGY FOR MONITORING AND THERAPEUTIC STRATEGIES

The knowledge gaps in our understanding of COVID-19 pathophysiology and the complexity of treatment validation are major limitations for the current standard of care. One possible strategy to overcome this is to engage complex statistical and physiological modeling. *In silico* models devoted to big data analysis and encompassing systems biology and precision medicine concepts have been introduced to inflammation, trauma, and sepsis research as a new complementary tool supporting translational applications (206–208). Similarly, advanced data analysis techniques constitute a potential support in the interpretation of different clinical COVID-19 presentations, in the timely identification of infected subjects prone to ARDS, and in the prediction of patient trajectories and their complication risks while on the ICU.

Artificial intelligence (AI) has been already introduced into the fight against SARS-CoV-2 (209). Despite the poor quality and inhomogeneity of the available data (that affect the modeling robustness and accuracy), AI may hold potential for the prediction and monitoring of SARS-CoV-2 outbreak hot-spots, transmission, and spread. For example, the analysis of big data from the commercial aviation industry was used to predict patterns of the international SARS-CoV-2 spread (210). Given the suboptimally coordinated response to the original outbreak, it is advisable that transnational organizations such as the WHO as well as national governments and local health systems

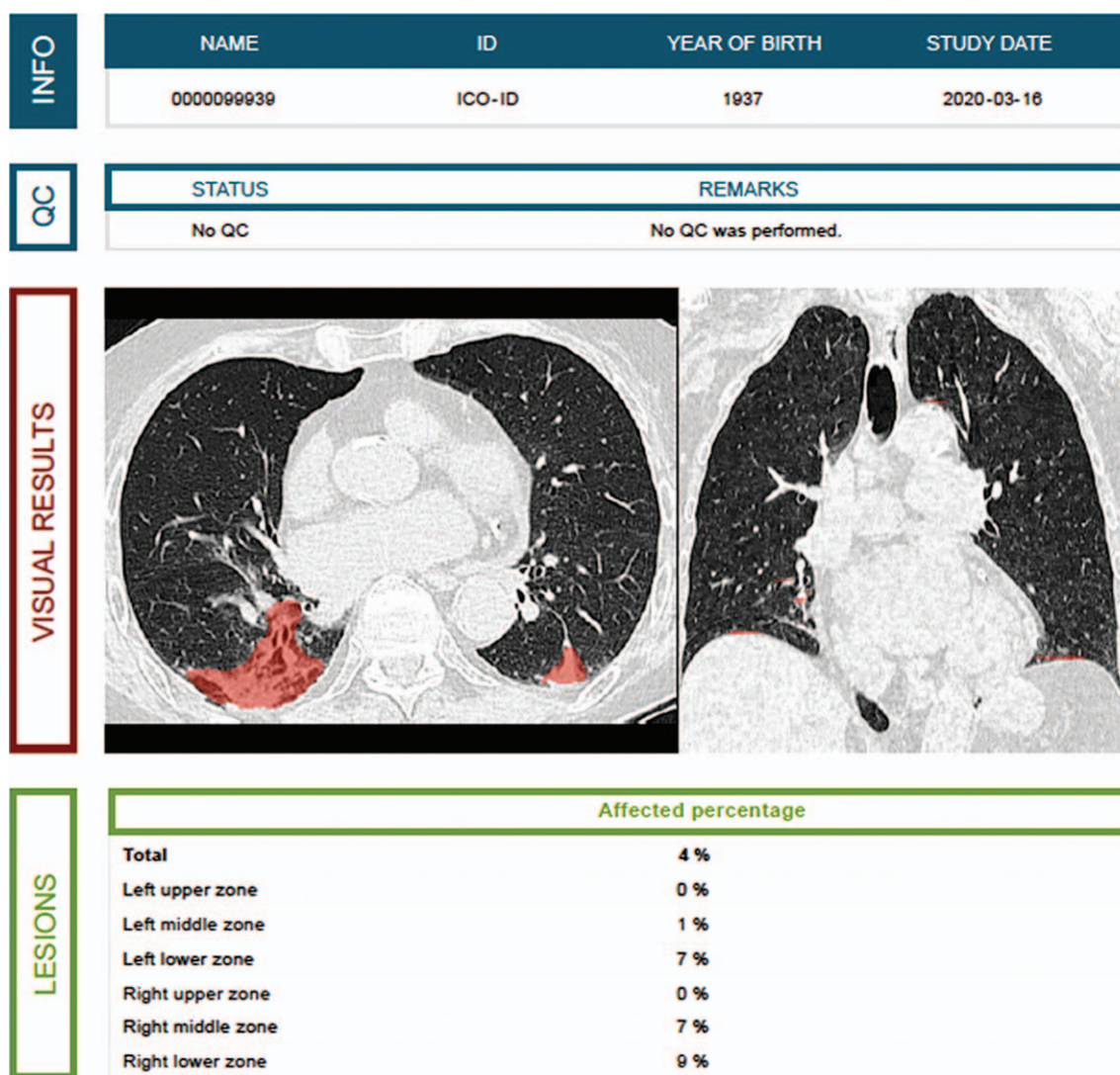


FIG. 5. Example of a fully automated assessment of the total and lobar disease burden in COVID-19 pneumonia based upon an AI algorithm. Evaluating the type, pattern, and extent of lung pathology on chest CT can help in the assessment, triage, and follow-up of COVID-19 patients. (Source: Jan Verheyden, icometrix (icolung), Leuven, Belgium). COVID-19 indicates coronavirus disease 2019; CT, computed tomography; AI, artificial intelligence.

integrate AI-based analyses to support their decision-making in: the design and implementation of lockdown and post-lockdown strategies and the early identification and prevention of second infection waves. Such applications have already been proposed to predict the preparedness and vulnerability to SARS-CoV-2 in Africa (211) and could be expanded to other continents/regions around the globe. Artificial intelligence can be also used in a cluster fashion in individual clinics. For example, AI-powered automated analysis of chest X-rays and CT scans effectively reduced the workload of radiologists (212–215); AI identified COVID-19-induced airway injury and pneumonia of varying magnitude as accurately as human operators. Thus, AI applications appear as a time- and resource-saving alternative in diagnosing COVID-19 in mildly symptomatic individuals. Recently, a multidisciplinary global initiative to leverage AI in the fight against COVID-19 was launched in Belgium together with hospitals and organizations worldwide (icometrix/icolung, Leuven (Belgium), Chicago). This multinational collaboration resulted in the development of an

AI solution for rapid and objective quantification of lung pathology on chest CT scans in admitted COVID-19 patients (Fig. 5).

Despite its epidemiological and diagnostic potential, it is premature to expect AI to be a game-changer in real-time patient monitoring (216). It is unclear whether AI can precisely prognosticate, and its usefulness has been modest in the context of therapy design. Even though AI algorithms have been used to predict the efficacy of existing drugs repurposed to treat COVID-19 (217, 218), the candidate drugs (and pharmacological targets) still require experimental validation before translating them to bedside and into clinical practice. Interestingly, promising results were obtained from the analysis of high-throughput data on the interaction between SARS-CoV-2 and ACE2 receptors encouraging research on interventions preventing the internalization of SARS-CoV-2 (131, 219).

The contribution of data-driven models in the improvement of patient monitoring and in the design of new therapeutic approaches critically depends on the quality of the available

data; it is key to ensure the best possible consistency and homogeneity across databases. Initiatives such as the COVID-19 data portal by the European Molecular Biology Laboratory—European Bioinformatics Institute (EMBL-EBI) (<https://www.covid19dataportal.org/about>) and the COVID-19 (COVID-19 Open Research Dataset) by the Allen Institute for AI (Seattle, Wash) and collaborators (<https://allenai.org/data/covid-19>) exemplify this paradigm and support the development of knowledge-based models to formulate and test hypotheses on the desired pathological mechanisms of interest, and characterize and interpret the dynamics of the disease progression in real time. Physiological models will likely benefit from the integration of data from different levels of the biological scale. In particular, high-throughput, multi-omics data have been increasingly used in acute illness (220–226) to investigate disease pathways and their molecular signatures, and to search for novel diagnostic biomarkers and therapeutic targets. The use of multiscale models in COVID-19 research could shed light on the complexity of phenotypes and enhance the design of combinatorial treatments not limited to a single drug or intervention. A recent study (227) used a multi-omic approach and machine learning algorithms to analyze COVID-19 signatures; the data showed that COVID-19 severity was associated with distinct profiles in the serum proteome and metabolome, implicating massive metabolic suppression, macrophage dysregulation, platelet degranulation, and complement system imbalance. Multilevel data integration, including the -omics, hemodynamic, biochemical, and clinical readouts, could further advance our understanding of the relationships among various COVID-19 phenotypes such as bilateral pneumonia/ARDS requiring mechanical ventilation (228), shock requiring vasopressor support (229, 230), cardiomyopathy (231), and neurological manifestations (232).

Retrospective studies will be necessary to build and validate physiological multiscale models. The success of this effort will rely on the availability of well-annotated, cohesive, and consistent databases and corresponding biobanks. The integration of statistical (data-driven) modeling and physiological (knowledge-based) modeling should be pursued to enhance the translational potential of computational analytics for: diagnostics and monitoring, the design of novel, more effective treatments, the guidance of therapy by decision support systems.

DISSEMINATION OF DATA AND LARGE-SCALE TRANSLATIONAL RESEARCH NETWORKS

The SARS-CoV-2 outbreak has triggered an unprecedented cooperative activity worldwide, yet with varying perception and outcomes. Major funding agencies including the European Commission with dedicated emergency funding action under the Horizon 2020 Framework Program, the National Institutes of Health and other funding agencies such as the Department of Defense among others, and numerous national agencies have mobilized funds to facilitate rapid basic and clinical research on the SARS-CoV-2 pathogenesis and COVID-19 treatments. While this greatly supports COVID-19-oriented research, it simultaneously puts other important research areas at risk of slowdown and under-funding. To enable an uninhibited and rapid

exchange of emerging knowledge, major publishers such as Elsevier (<https://www.elsevier.com/connect/coronavirus-information-center>), Springer Nature (<https://www.springernature.com/gp/researchers/campaigns/coronavirus>) JAMA, (<https://ja.ma/covidyt>), The Lancet, The New England Journal of Medicine, and Science, among others, have gone open-access covering multiple SARS-CoV-2/COVID-19-related topics. The video/audio knowledge exchange has been at its finest; the JAMA Update podcast with Dr. M Cecconi (March 3, 2020) from the Italian COVID-19 frontline was followed by over million viewers (233) and the 7 h-long COVID-19 Marathon Webinar organized by ESICM (March 23, 2020) gathered expert-speakers from 15 countries and four continents (<https://esicm-tv.org/covid19/>). However, perception of the rapid data dissemination by the preprint servers (e.g., bioRxiv.org; medRxiv.org) is less favorable. There has been a growing concern that such a steep growth of unscrutinized scientific evidence (3718 bio/medRxiv.org articles on SARS-CoV-2/COVID-19; accessed May 19, 2020) rather provokes more confusion than meritorious guidance and indiscriminately selected pieces of the preprinted data are recurrently sensationalized by the lay press.

While the majority of above activities are effective (and impressive), there is an important gap: the lack of a functional translational-research collaborative network on the SARS-CoV-2/COVID-19 pandemic. Although clinical studies are costly and organizationally challenging, clinical centers can join them with relative ease and without a need for additional and/or specialized core facilities. This is in sharp contrast to basic and translational studies. While the progress in modern basic science can be made using online resources like sequencing and structural data, e.g., enabling *in silico* modeling (234), translational studies require work with live SARS viruses and animal models at biosafety level (BSL)-3 facilities (<https://www.cdc.gov/sars/guidance/f-lab/app5.html>). The availability of SARS-CoV-2-susceptible animals and BSL-3 labs is limited. Therefore, efforts should be undertaken to enhance cooperation among existing centers by creating international collaborative research platforms able to simultaneously investigate multiple hypotheses/aims. This can be achieved by implementing three key objectives: to galvanize an open-access scientific exchange and tools (e.g., models, protocols) among laboratories, to facilitate a multilateral data flow among basic science researchers in an organized, standardized fashion, and to improve the validity of preclinical treatment studies by introduction of multicenter animal testing. Encouraging examples of such strategies exist; beginning with China (2020/01/21), hCoV-19 genome sequences have been rapidly and freely shared by the international scientific community (virological.org; GenBank; www.gisaid.org/), some SARS-CoV-2-related findings are published patent-free (235) and first multicenter animal studies have shown a superior reproducibility and validity (236). A few of such preclinical collaborative networks have also been found in the area of critical care medicine; Operation Brain Trauma Therapy is a fully operational US-based multicenter drug and biomarker screening consortium for traumatic brain injury (237), whereas the international Wiggers-Bernard Initiative is in the process of forming a multicenter preclinical RCT in mouse sepsis (<https://wiggers-bernard.org/2019-topic/>).

In the context of COVID-19, especially the trials performed in non-human primates would highly benefit from a multicenter coordinated approach given that single-center studies are typically limited to very low numbers ($n=4-6$) of animals (120, 238, 239). The translational research community should also learn from the clinical examples that employ additional, more advanced designs: for example, the REMAP-CAP trial enables multicenter large-scale and adaptive-design treatment testing. Adaptation and utilization of the above strategies in preclinical research will likely save time and resources, increase rigor of the findings, and enhance the bidirectional flow of data between the laboratories and clinic (and vice versa) given their tighter alignment.

Another key element is to strengthen regulatory partnerships among institutions and countries that would directly complement large-scale multicenter preclinical and clinical studies, through initiatives such as creation of shared data repositories and associated biobanks with patient or animal samples for future retrospective studies. A Dutch-based (private-government-academic) Molecular Diagnosis and Risk Stratification of Sepsis consortium (<https://consortiapedia.fastercures.org/consortia/mars/>) exemplifies such an approach; organized in four complementary working packages brings together several international partners and integrates clinical, discovery, and technology data-sharing platforms. Similarly, the largest existing military registry for combat-related trauma patients (with data on combat casualty care epidemiology, treatments, and longitudinal outcomes) has been created by the US Department of Defense Joint Trauma System (<https://jts.amedd.army.mil/>). On April 20, 2020 the European Commission, in cooperation with the EMBL-EBI, deployed a data platform specifically dedicated to COVID-19 to collect and share scientific evidence (<https://www.covid19dataportal.org>). The availability of diverse data types from different clinical centers can enhance the validation of both data-driven and knowledge-based models, leading to a faster introduction of diagnostic and patient monitoring tools as well as decision support systems.

CONCLUSIONS

COVID-19 represents a major global health challenge for the up-coming months and years. SARS-CoV-2 infection likely presents in various phenotypes reflected by differential immunopathogenesis. While many derangements contribute to the pathophysiology of COVID-19, particularly damage to the endothelium along with altered hemostasis appear to be the key driver and link between the different phenotypes. Despite many similarities, the SARS-CoV2/COVID-19 is not identical to MERS and SARS-CoV and should be contemplated as a novel and independent disease entity. Reliable scientific evidence regarding SARS-CoV-2/COVID-19 epidemiology, infectivity, host response, as well as clinical assessment and treatments needs to be generated through a verified, orchestrated, large-scale transnational, and interdisciplinary effort rather than anecdotal, idiosyncratic preclinical studies and multiple small-scale, low-powered clinical trials. It is imperative that the currently contemplated therapeutic strategies adhere to the theranostic-like principle to avoid the past failed

treatments that indiscriminately targeted heterogenous patients (with sepsis as an example). Consensus-based “Master Protocols” for data reporting and clinical trials constitute the basis for uniform contingency protocols, rapid and coordinated implementation of emergency measures, and reliable evaluation of therapeutics and vaccines. Advanced data analysis techniques can help in the interpretation of different clinical COVID-19 presentations, rapid risk stratification, and prediction of outcomes. In the absence of approved drugs to prevent and/or treat COVID-19, the magnitude of the current pandemic may justify extraordinary measures to save patient lives but these have to be balanced against ethical and scientific safeguards. Any review of an ongoing pandemic is highly fluid and the dynamic nature of the research on the disease, its progression and our understanding of its epidemiology and pathogenesis may already be partly outdated on the day of publication. Thus, the complete, hopefully inspiring, story of the SARS-CoV-2/COVID-19 pandemic will be written in years from now.

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