Report and Opinion

Websites:
http://www.sciencepub.net
http://www.sciencepub.net/report

Emails:
editor@sciencepub.net
reportopinion@gmail.com

MARSLAND PRESS
Multidisciplinary Academic Journal Publisher

COVID-19 Research Literatures

Mark Herbert

World Development Institute
39-06 Main Street, Flushing, Queens, New York 1354, USA, ma708090@gmail.com

Abstract: Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The virus is mainly spread during close contact and via respiratory droplets that are produced when a person talks, coughs, or sneezes. Respiratory droplets may be produced during breathing, however, current research indicates that the virus is not considered airborne. People may also contract COVID-19 by touching a contaminated surface (Fomite) and then inadvertently transfer the pathogen to a mucous membrane (such as the eyes, nose, or mouth). It is most contagious when people are symptomatic, although spread may be possible before symptoms appear. The virus can live on surfaces up to 72 hours. Time from exposure to onset of symptoms is generally between two and fourteen days, with an average of five days. The standard method of diagnosis is by reverse transcription polymerase chain reaction (rRT-PCR) from a nasopharyngeal swab. The infection can also be diagnosed from a combination of symptoms, risk factors and a chest CT scan showing features of pneumonia. This article introduces recent research reports as references in the related studies.

[Mark Herbert. **COVID-19 Research Literatures.** *Rep Opinion* 2020;12(3):5-73]. ISSN 1553-9873 (print); ISSN 2375-7205 (online). http://www.sciencepub.net/report. 2. doi:10.7537/marsroj120320.02.

Key words: Coronavirus disease 2019 (COVID-19); life; research; literature

Introduction

Coronavirus disease 2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The virus is mainly spread during close contact and via respiratory droplets that are produced when a person talks, coughs, or sneezes. Respiratory droplets may be produced during breathing, however, current research indicates that the virus is not considered airborne. People may also contract COVID-19 by touching a contaminated surface (Fomite) and then inadvertently transfer the pathogen to a mucous membrane (such as the eyes, nose, or mouth). It is most contagious when people are symptomatic, although spread may be possible before symptoms appear. The virus can live on surfaces up to 72 hours. Time from exposure to onset of symptoms is generally between two and fourteen days, with an average of five days. The standard method of diagnosis is by reverse transcription polymerase chain reaction (rRT-PCR) from a nasopharyngeal swab. The infection can also be diagnosed from a combination of symptoms, risk factors and a chest CT scan showing features of pneumonia. This article introduces recent research reports as references in the related studies.

The following introduces recent reports as references in the related studies.

Adhikari, S. P., et al. (2020). "Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease (COVID-19) during the early outbreak period: a scoping review." Infect Dis Poverty **9**(1): 29.

BACKGROUND: The coronavirus disease (COVID-19) has been identified as the cause of an outbreak of respiratory illness in Wuhan, Hubei Province, China beginning in December 2019. As of 31 January 2020, this epidemic had spread to 19 countries with 11 791 confirmed cases, including 213 deaths. The World Health Organization has declared it a Public Health Emergency of International Concern. METHODS: A scoping review was conducted following the methodological framework suggested by Arksey and O'Malley. In this scoping review, 65 research articles published before 31 January 2020 were analyzed and discussed to better understand the epidemiology, causes, clinical diagnosis, prevention and control of this virus. The research domains, dates of publication, journal language, authors' affiliations, and methodological characteristics were included in the analysis. All the findings and statements in this review regarding the outbreak are based on published information as listed in the references. RESULTS: Most of the publications were written using the English language (89.2%). The largest proportion of published articles were related to causes (38.5%) and a majority (67.7%) were published by Chinese scholars.

Research articles initially focused on causes, but over time there was an increase of the articles related to prevention and control. Studies thus far have shown that the virus' origination is in connection to a seafood market in Wuhan, but specific animal associations have not been confirmed. Reported symptoms include fever, cough, fatigue, pneumonia, headache, diarrhea, hemoptysis, and dyspnea. Preventive measures such as masks, hand hygiene practices, avoidance of public contact, case detection, contact tracing, and quarantines have been discussed as ways to reduce transmission. To date, no specific antiviral treatment has proven effective; hence, infected people primarily rely on symptomatic treatment and supportive care. CONCLUSIONS: There has been a rapid surge in research in response to the outbreak of COVID-19. During this early period, published research primarily explored the epidemiology, causes, clinical manifestation and diagnosis, as well as prevention and control of the novel coronavirus. Although these studies are relevant to control the current public emergency, more high-quality research is needed to provide valid and reliable ways to manage this kind of public health emergency in both the short- and long-term.

Agarwal, A., et al. (2020). "Guidance for building a dedicated health facility to contain the spread of the 2019 novel coronavirus outbreak." Indian J Med Res.

Preparedness for the ongoing coronavirus disease 2019 (COVID-19) and its spread in India calls for setting up of adequately equipped and dedicated health facilities to manage sick patients while protecting healthcare workers and the environment. In the wake of other emerging dangerous pathogens in recent times, such as Ebola, Nipah and Zika, it is important that such facilities are kept ready during the inter-epidemic period for training of health professionals and for managing cases of multi-drug resistant and difficult-to-treat pathogens. While endemic potential of such critically ill patients is not yet known, the health system should have surge capacity for such critical care units and preferably each tertiary government hospital should have at least one such facility. This article describes elements of design of such unit (e.g., space, infection control, waste disposal, safety of healthcare workers, partners to be involved in design and plan) which can be adapted to the context of either a new construction or makeshift construction on top of an existing structure. In view of a potential epidemic of COVID-19, specific requirements to handle it are also given.

Ahmed, S. F., et al. (2020). "Preliminary Identification of Potential Vaccine Targets for the COVID-19 Coronavirus (SARS-CoV-2) Based on SARS-CoV Immunological Studies." Viruses **12**(3).

The beginning of 2020 has seen the emergence of COVID-19 outbreak caused by a novel coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2). There is an imminent need to better understand this new virus and to develop ways to control its spread. In this study, we sought to gain insights for vaccine design against SARS-CoV-2 by considering the high genetic similarity between SARS-CoV-2 and SARS-CoV, which caused the outbreak in 2003, and leveraging existing immunological studies of SARS-CoV. By screening the experimentally-determined SARS-CoV-derived B cell and T cell epitopes in the immunogenic structural proteins of SARS-CoV, we identified a set of B cell and T cell epitopes derived from the spike (S) and nucleocapsid (N) proteins that map identically to SARS-CoV-2 proteins. As no mutation has been observed in these identified epitopes among the 120 available SARS-CoV-2 sequences (as of 21 February 2020), immune targeting of these epitopes may potentially offer protection against this novel virus. For the T cell epitopes, we performed a population coverage analysis of the associated MHC alleles and proposed a set of epitopes that is estimated to provide broad coverage globally, as well as in China. Our findings provide a screened set of epitopes that can help guide experimental efforts towards the development of vaccines against SARS-CoV-2.

Ai, T., et al. (2020). "Correlation of Chest CT and RT-PCR Testing in Coronavirus Disease 2019 (COVID-19) in China: A Report of 1014 Cases." Radiology: 200642.

Background Chest CT is used for diagnosis of 2019 novel coronavirus disease (COVID-19), as an important complement to the reverse-transcription polymerase chain reaction (RT-PCR) tests. Purpose To investigate the diagnostic value and consistency of chest CT as compared with comparison to RT-PCR assay in COVID-19. Methods From January 6 to February 6, 2020, 1014 patients in Wuhan, China who underwent both chest CT and RT-PCR tests were included. With RT-PCR as reference standard, the performance of chest CT in diagnosing COVID-19 was assessed. Besides, for patients with multiple RT-PCR assays, the dynamic conversion of RT-PCR results (negative to positive, positive to negative, respectively) was analyzed as compared with serial chest CT scans for those with time-interval of 4 days or more. Results Of 1014 patients, 59% (601/1014) had positive RT-PCR results, and 88% (888/1014) had positive chest CT scans. The sensitivity of chest CT in suggesting COVID-19 was 97% (95%CI, 95-98%, 580/601 patients) based on positive RT-PCR results.

In patients with negative RT-PCR results, 75% (308/413) had positive chest CT findings; of 308, 48% were considered as highly likely cases, with 33% as probable cases. By analysis of serial RT-PCR assays and CT scans, the mean interval time between the initial negative to positive RT-PCR results was 5.1 +/- 1.5 days; the initial positive to subsequent negative RT-PCR result was 6.9 +/- 2.3 days). 60% to 93% of cases had initial positive CT consistent with COVID-19 prior (or parallel) to the initial positive RT-PCR results. 42% (24/57) cases showed improvement in follow-up chest CT scans before the RT-PCR results turning negative. Conclusion Chest CT has a high sensitivity for diagnosis of COVID-19. Chest CT may be considered as a primary tool for the current COVID-19 detection in epidemic areas.

Al-Ahmadi, K., et al. (2020). "Spatial association between primary Middle East respiratory syndrome coronavirus infection and exposure to dromedary camels in Saudi Arabia." Zoonoses Public Health.

Middle East respiratory syndrome coronavirus (MERS-CoV) is an emerging zoonotic disease. Exposure to dromedary camels (Camelus dromedaries) has been consistently considered the main source of primary human infection. Although Saudi Arabia reports the highest rate of human MERS-CoV infection and has one of the largest populations of dromedary camels worldwide, their spatial association has not yet been investigated. Thus, this study aimed to examine the correlation between the spatial distribution of primary MERS-CoV cases with or without a history of camel exposure reported between 2012 and 2019 and dromedary camels at the provincial level in Saudi Arabia. In most provinces, a high proportion of older men develop infections after exposure to camels. Primary human infections during spring and winter were highest in provinces characterized by seasonal breeding and calving, increased camel mobilization and camel-human interactions. A strong and significant association was found between the total number of dromedary camels and the numbers of primary camel-exposed and non-exposed MERS-CoV cases. Furthermore, spatial correlations between MERS-CoV cases and camel sex, age and dairy status were significant. Via a cluster analysis, we identified Riyadh, Makkah and Eastern provinces as having the most primary MERS-CoV cases and the highest number of camels. Transmission of MERS-CoV from camels to humans occurs in most primary cases, but there is still a high proportion of primary infections with an ambiguous link to camels. The results from this study include significant correlations between primary MERS-CoV cases and camel populations in all provinces, regardless of camel exposure history. This supports the hypothesis of the role of an asymptomatic human carrier or, less likely, an unknown animal host that has direct contact with both infected camels and humans. In this study, we performed a preliminary risk assessment of prioritization measures to control the transmission of infection from camels to humans.

Albarello, F., et al. (2020). "2019-novel Coronavirus severe adult respiratory distress syndrome in two cases in Italy: An uncommon radiological presentation." Int J Infect Dis **93**: 192-197.

INTRODUCTION: Several recent case reports have described common early chest imaging findings of lung pathology caused by 2019 novel Coronavirus (SARS-COV2) which appear to be similar to those seen previously in SARS-CoV and MERS-CoV infected patients. OBJECTIVE: We present some remarkable imaging findings of the first two patients identified in Italy with COVID-19 infection travelling from Wuhan, China. The follow-up with chest X-Rays and CT scans was also included, showing a progressive adult respiratory distress syndrome (ARDS). RESULTS: Moderate to severe progression of the lung infiltrates, with increasing percentage of high-density infiltrates sustained by a bilateral and multi-segmental extension of lung opacities, were seen. During the follow-up, apart from pleural effusions, a tubular and enlarged appearance of pulmonary vessels with a sudden caliber reduction was seen, mainly found in the dichotomic tracts, where the center of a new insurgent pulmonary lesion was seen. It could be an early alert radiological sign to predict initial lung deterioration. Another uncommon element was the presence of mediastinal lymphadenopathy with short-axis oval nodes. CONCLUSIONS: Although only two patients have been studied, these findings are consistent with the radiological pattern described in literature. Finally, the pulmonary vessels enlargement in areas where new lung infiltrates develop in the follow-up CT scan, could describe an early predictor radiological sign of lung impairment.

Alderman, C. (2020). "Pharmacy Services and the Novel Coronavirus." Sr Care Pharm **35**(4): 146-147.

Pharmacists around the world can expect to be affected by the coronavirus, especially those who provide care for older people who are at a much higher risk for grave consequences from the virus. It is critical that pharmacists maintain awareness of the evolving pandemic and access reliable information to remain familiar with developments.

Alfano, F., et al. (2020). "Circulation of pantropic canine coronavirus in autochthonous and imported dogs, Italy." Transbound Emerg Dis.

Canine coronavirus (CCoV) strains with the ability to spread to internal organs, also known as pantropic CCoVs (pCCoVs), have been detected in domestic dogs and wild carnivores. Our study focused on the detection and molecular characterization of pCCoV strains circulating in Italy during the period 2014-2017 in autochthonous dogs, in dogs imported from eastern Europe or illegally imported from an unknown country. Samples from the gut and internal organs of 352 dogs were screened for CCoV; putative pCCoV strains, belonging to subtype CCoV-IIa, were identified in the internal organs of 35 of the examined dogs. Fifteen pCCoV strains were subjected to sequence and phylogenetic analyses, showing that three strains (98960-1/2016, 98960-3/2016, 98960-4/2016) did not cluster either with Italian or European CCoVs, being more closely related to alphacoronaviruses circulating in Asia with which they displayed a 94-96% nucleotide identity in partial spike protein gene sequences. The pCCoV positive samples were also tested for other canine viruses, showing coinfections mainly with canine parvovirus.

Algaissi, A., et al. (2020). "Quantification of the Middle East Respiratory Syndrome-Coronavirus RNA in Tissues by Quantitative Real-Time RT-PCR." Methods Mol Biol **2099**: 99-106.

Since the emergence of the Middle East respiratory syndrome-coronavirus (MERS-CoV) in 2012, more than 2280 confirmed human infections and 800 associated deaths had been reported to the World Health Organization. MERS-CoV is a single-stranded RNA virus that belongs to the Coronaviridae family. MERS-CoV infection leads to a variety of clinical outcomes in humans ranging from asymptomatic and mild infection to severe acute lung injury and multi-organ failure and death. To study the pathogenesis of MERS-CoV infection and development of medical countermeasures (MCMs) for MERS, a number of genetically modified mouse models have been developed, including various versions of transgenic mice expressing the human DPP4 viral receptor. Tracking and quantifying viral infection, among others, in permissive hosts is a key endpoint for studying MERS pathogenesis and evaluating the efficacy of selected MCMs developed for MERS. In addition to quantifying infectious progeny virus which requires high-containment biosafety level (BSL)-3 laboratory, here we outlined an established real-time quantitative RT-PCR (RT-qPCR)-based procedure to unequivocally quantify MERS-CoV-specific RNAs within the lungs of infected human DPP4 (hDPP4, transgenic (hDPP4 Tg) mice under a standard BSL-2 laboratory.

Allam, Z. and D. S. Jones (2020). "On the Coronavirus (COVID-19) Outbreak and the Smart City Network: Universal Data Sharing Standards Coupled with Artificial Intelligence (AI) to Benefit Urban Health Monitoring and Management." Healthcare (Basel) **8**(1).

As the Coronavirus (COVID-19) expands its impact from China, expanding its catchment into surrounding regions and other countries, increased national and international measures are being taken to contain the outbreak. The placing of entire cities in 'lockdown' directly affects urban economies on a multi-lateral level, including from social and economic standpoints. This is being emphasised as the outbreak gains ground in other countries, leading towards a global health emergency, and as global collaboration is sought in numerous quarters. However, while effective protocols in regard to the sharing of health data is emphasised, urban data, on the other hand, specifically relating to urban health and safe city concepts, is still viewed from a nationalist perspective as solely benefiting a nation's economy and its economic and political influence. This perspective paper, written one month after detection and during the outbreak, surveys the virus outbreak from an urban standpoint and advances how smart city networks should work towards enhancing standardization protocols for increased data sharing in the event of outbreaks or disasters, leading to better global understanding and management of the same.

Al-Mandhari, A., et al. (2020). "Coronavirus Disease 2019 outbreak: preparedness and readiness of countries in the Eastern Mediterranean Region." East Mediterr Health J **26**(2): 136-137.

On 31 December 2019, a cluster of acute respiratory illness was reported from China and later confirmed as novel coronavirus on 7 January 2020. This virus is the same member of the coronavirus family that caused the severe acute respiratory syndrome (SARS-CoV) reported in China 2003, and Middle East respiratory syndrome (MERS-CoV) reported in Saudi Arabia in 2012. The initial cases have been linked to a live seafood market in Wuhan, China, and the specific animal source is yet to be determined. The detection of this new virus in humans without knowing the source of the infection has raised greatly heightened concerns not only in China, but also internationally. To date, the outbreak has spread to most provinces in China and 25 other countries within a relatively short period. Consequent to its spread, Dr Tedros Ghebreyesus, Director General of the World Health Organization (WHO), declared the outbreak a Public Health Emergency of International Concern (PHEIC) on 30 January 2020.

An, P., et al. (2020). "CT Manifestations of Novel Coronavirus Pneumonia: A Case Report." Balkan Med J.

Background: Since December 2019, the outbreak of the novel coronavirus has impacted nearly >90,000 people in more than 75 countries. In this case report, we aim to define the chest computed tomography findings of 2019-novel coronavirus associated with pneumonia and its successful resolution after treatment. Case Report: A fifty-year-old female patient, who is a businesswoman, presented with chief complaints of "fever for one week, diarrhea, anorexia, and asthenia." Initially, she was given Tamiflu. The influenza A virus serology was negative. Three days later, levofloxacin was started because the patient's symptoms did not improve. The novel coronavirus nucleic acid test was negative. It was noted that before the onset of the disease, the patient went to Wuhan on a business trip. Despite the given treatment, her body temperature rose to 39.2 degrees C and she was referred to our clinic for further evaluation. Then, chest computed tomography was performed and showed bilateral multifocal ground glass opacities with consolidation which suggested viral pneumonia as a differential diagnosis, and the subsequent 2019-novel coronavirus pneumonia nucleic acid test was positive. Conclusion: Chest computed tomography offers fast and convenient evaluation of patients with suspected 2019-novel coronavirus pneumonia.

Andrea, G., et al. (2020). "Coronavirus Disease 2019 and Transplantation: a view from the inside." Am J Transplant.

Since December 2019, world healthcare community faced with Coronavirus Disease 2019 (COVID-19) outbreak caused by SARS-CoV-2. Due to the high viral contagiousness and the possible transmission during the pre-symptomatic phase, COVID-19 progressively spread to several countries. Currently, Italy is the third Country for number of confirmed cases after mainland China and South Chorea, and the first western nation with a well-established deceased transplant program to tackle a COVID-19 outbreak (1).

Anzai, A., et al. (2020). "Assessing the Impact of Reduced Travel on Exportation Dynamics of Novel Coronavirus Infection (COVID-19)." J Clin Med **9**(2).

The impact of the drastic reduction in travel volume within mainland China in January and February 2020 was quantified with respect to reports of novel coronavirus (COVID-19) infections outside China. Data on confirmed cases diagnosed outside China were analyzed using statistical models to estimate the impact of travel reduction on three epidemiological outcome measures: (i) the number of exported cases, (ii) the probability of a major epidemic, and (iii) the time delay to a major epidemic. From 28 January to 7 February 2020, we estimated that 226 exported cases (95% confidence interval: 86,449) were prevented, corresponding to a 70.4% reduction in incidence compared to the counterfactual scenario. The reduced probability of a major epidemic ranged from 7% to 20% in Japan, which resulted in a median time delay to a major epidemic of two days. Depending on the scenario, the estimated delay may be less than one day. As the delay is small, the decision to control travel volume through restrictions on freedom of movement should be balanced between the resulting estimated epidemiological impact and predicted economic fallout.

Arshad Ali, S., et al. (2020). "The outbreak of Coronavirus Disease 2019 (COVID-19)-An emerging global health threat." J Infect Public Health.

The outbreak of Coronavirus Disease 2019 (COVID-19) causing novel coronavirus-infected pneumonia (NCIP), has affected the lives of 71,429 people globally. Originating in China, the disease has a rapid progression to other countries. Research suggests remarkable genomic resemblance of 2019-nCoV with Severe Acute Respiratory Syndrome (SARS) which has a history of a pandemic in 2002. With evidence of nosocomial spread, a number of diligent measures are being employed to constrain its propagation. Hence, the Public Health Emergency of International Concern (PHEIC) has been established by the World Health Organization (WHO) with strategic objectives for public health to curtail its impact on global health and economy.

Ashour, H. M., et al. (2020). "Insights into the Recent 2019 Novel Coronavirus (SARS-CoV-2) in Light of Past Human Coronavirus Outbreaks." Pathogens **9**(3).

Coronaviruses (CoVs) are RNA viruses that have become a major public health concern since the Severe Acute Respiratory Syndrome-CoV (SARS-CoV) outbreak in 2002. The continuous evolution of coronaviruses was further highlighted with the emergence of the Middle East Respiratory Syndrome-CoV (MERS-CoV) outbreak in 2012. Currently, the world is concerned about the 2019 novel CoV (SARS-CoV-2) that was initially identified in the city of Wuhan, China in December 2019. Patients presented with severe viral pneumonia and respiratory illness. The number of cases has been mounting since then. As of late February 2020, tens of thousands of cases and several thousand deaths have been reported in China alone, in addition to thousands of cases in other countries. Although the fatality rate of SARS-CoV-2 is currently lower than SARS-CoV, the virus seems to be highly contagious based on the number of infected cases to date. In this review, we discuss structure, genome organization, entry of CoVs into target cells, and provide insights into past and present outbreaks. The future of human CoV outbreaks will not only depend on how the viruses will evolve, but will also depend on how we develop efficient prevention and treatment strategies to deal with this continuous threat.

Baglivo, M., et al. (2020). "Natural small molecules as inhibitors of coronavirus lipid-dependent attachment to host cells: a possible strategy for reducing SARS-COV-2 infectivity?" Acta Biomed **91**(1): 161-164.

BACKGROUND: Viral infectivity depends on interactions between components of the host cell plasma membrane and the virus envelope. Here we review strategies that could help stem the advance of the SARS-COV-2 epidemic. METHODS AND RESULTS: We focus on the role of lipid structures, such as lipid rafts and cholesterol, involved in the process, mediated by endocytosis, by which viruses attach to and infect cells. Previous studies have shown that many naturally derived substances, such as cyclodextrin and sterols, could reduce the infectivity of many types of viruses, including the coronavirus family, through interference with lipid-dependent attachment to human host cells. CONCLUSIONS: Certain molecules prove able to reduce the infectivity of some coronaviruses, possibly by inhibiting viral lipid-dependent attachment to host cells. More research into these molecules and methods would be worthwhile as it could provide insights the mechanism of transmission of SARS-COV-2 and, into how they could become a basis for new antiviral strategies.

Bai, S. L., et al. (2020). "[Analysis of the first cluster of cases in a family of novel coronavirus pneumonia in Gansu Province]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E005.

The epidemiological history and clinical characteristics of 7 cases of COVID-19 and 1 case of close contact in the first family aggregation epidemic of COVID-19 in Gansu Province were analyzed. The first patient A developed on January 22, 2020, with a history of residence in Wuhan, and confirmed severe cases of NCP on January 24, 2020; patient B, on January 23, 2020, diagnosed on January 31, severe cases; patient C, asymptomatic, diagnosed on January 27; patient D, asymptomatic, diagnosed on January 27; patient E, on January 24, diagnosed on January 28; patient F, asymptomatic, diagnosed on January 31; Patient G was asymptomatic and was diagnosed on January 31. In close contact, H was asymptomatic, PCR test was negative and asymptomatic, and he was discharged early. Among the 7 patients, 1 case died of (B) aggravation, and the other patients' condition was effectively controlled after active treatment. Except for the discharged cases, 5 cases were positive for COVID-19 specific IgM antibody and 1 case was negative. In this clustering outbreak, 4 patients remained asymptomatic, but PCR and IgM antibodies were positive, indicating that asymptomatic patients may be the key point to control the epidemic. Specific IgM antibody screening for patients whose pharyngeal swab nucleic acid test is negative but with ground glass-like lung lesions is very important for early detection and early isolation.

Bajema, K. L., et al. (2020). "Persons Evaluated for 2019 Novel Coronavirus - United States, January 2020." MMWR Morb Mortal Wkly Rep **69**(6): 166-170.

In December 2019, a cluster of cases of pneumonia emerged in Wuhan City in central China's Hubei Province. Genetic sequencing of isolates obtained from patients with pneumonia identified a novel coronavirus (2019-nCoV) as the etiology (1). As of February 4, 2020, approximately 20,000 confirmed cases had been identified in China and an additional 159 confirmed cases in 23 other countries, including 11 in the United States (2,3). On January 17, CDC and the U.S. Department of Homeland Security's Customs and Border Protection began health screenings at U.S. airports to identify ill travelers returning from Wuhan City (4). CDC activated its Emergency Operations Center on January 21 and formalized a process for inquiries regarding persons suspected of having 2019-nCoV infection (2). As of January 31, 2020, CDC had responded to clinical inquiries from public health officials and health care providers to assist in evaluating approximately 650 persons thought to be at risk for 2019-nCoV infection. Guided by CDC criteria for the evaluation of persons under investigation (PUIs) (5), 210 symptomatic persons were tested for 2019-nCoV; among these persons, 148 (70%) had travel-related risk only, 42 (20%) had close contact with an ill laboratory-confirmed 2019-nCoV patient or PUI, and 18 (9%) had both travel- and contact-related risks. Eleven of these persons had laboratory-confirmed 2019-nCoV infection. Recognizing persons at risk for 2019-nCoV is critical to identifying cases and preventing further transmission. Health care providers should remain vigilant and adhere to recommended infection prevention and control practices when evaluating patients for possible 2019-nCoV infection (6). Providers should consult with their local and state health departments when assessing not only ill travelers from 2019-nCoV-affected countries but also ill persons who have been in close contact with patients with laboratory-confirmed 2019-nCoV infection in the United States.

Benvenuto, D., et al. (2020). "The 2019-new coronavirus epidemic: Evidence for virus evolution." J Med Virol **92**(4): 455-459.

There is a worldwide concern about the new coronavirus 2019-nCoV as a global public health threat. In this article, we provide a preliminary evolutionary and molecular epidemiological analysis of this new virus. A phylogenetic tree has been built using the 15 available whole genome sequences of 2019-nCoV, 12 whole genome sequences of 2019-nCoV, and 12 highly similar whole genome sequences available in gene bank (five from the severe acute respiratory syndrome, two from Middle East respiratory syndrome, and five from bat SARS-like coronavirus). Fast unconstrained Bayesian approximation analysis shows that the nucleocapsid and the spike glycoprotein have some sites under positive pressure, whereas homology modeling revealed some molecular and structural differences between the viruses. The phylogenetic tree showed that 2019-nCoV significantly clustered with bat SARS-like coronavirus sequence isolated in 2015, whereas structural analysis revealed mutation in Spike Glycoprotein and nucleocapsid protein. From these results, the new 2019-nCoV is distinct from SARS virus, probably trasmitted from bats after mutation conferring ability to infect humans.

Bernard Stoecklin, S., et al. (2020). "First cases of coronavirus disease 2019 (COVID-19) in France: surveillance, investigations and control measures, January 2020." Euro Surveill **25**(6).

A novel coronavirus (severe acute respiratory syndrome coronavirus 2, SARS-CoV-2) causing a cluster of respiratory infections (coronavirus disease 2019, COVID-19) in Wuhan, China, was identified on 7 January 2020. The epidemic quickly disseminated from Wuhan and as at 12 February 2020, 45,179 cases have been confirmed in 25 countries, including 1,116 deaths. Strengthened surveillance was implemented in France on 10 January 2020 in order to identify imported cases early and prevent secondary transmission. Three categories of risk exposure and follow-up procedure were defined for contacts. Three cases of COVID-19 were confirmed on 24 January, the first cases in Europe. Contact tracing was immediately initiated. Five contacts were evaluated as at low risk of exposure and 18 at moderate/high risk. As at 12 February 2020, two cases have been discharged and the third one remains symptomatic with a persistent cough, and no secondary transmission has been identified. Effective collaboration between all parties involved in the surveillance and response to emerging threats is required to detect imported cases early and to implement adequate control measures.

Bernheim, A., et al. (2020). "Chest CT Findings in Coronavirus Disease-19 (COVID-19): Relationship to Duration of Infection." Radiology: 200463.

In this retrospective study, chest CTs of 121 symptomatic patients infected with coronavirus disease-19 (COVID-19) from four centers in China from January 18, 2020 to February 2, 2020 were reviewed for common CT findings in relationship to the time between symptom onset and the initial CT scan (i.e. early, 0-2 days (36 patients), intermediate 3-5 days (33 patients), late 6-12 days (25 patients)). The hallmarks of COVID-19 infection on imaging were bilateral and peripheral ground-glass and consolidative pulmonary opacities. Notably, 20/36 (56%) of early patients had a normal CT. With a longer time after the onset of symptoms, CT findings were more frequent, including consolidation, bilateral and peripheral disease, greater total lung involvement, linear opacities, "crazy-paving" pattern and the "reverse halo" sign. Bilateral lung involvement was observed in 10/36 early patients (28%), 25/33 intermediate patients (76%), and 22/25 late patients (88%).

Bhatnagar, T., et al. (2020). "Lopinavir/ritonavir combination therapy amongst symptomatic coronavirus disease 2019 patients in India: Protocol for restricted public health emergency use." Indian J Med Res.

As of February 29, 2020, more than 85,000 cases of coronavirus disease 2019 (COVID-19) have been reported from China and 53 other countries with 2,924 deaths. On January 30, 2020, the first laboratory-confirmed case of COVID was reported from Kerala, India. In view of the earlier evidence about effectiveness of repurposed lopinavir/ritonavir against severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) coronavirus (CoV), as well as preliminary docking studies conducted by the ICMR-National Institute of Virology, Pune, the Central Drugs Standard Control Organization approved the restricted public health use of lopinavir/ritonavir combination amongst symptomatic COVID-19 patients detected in the country. Hospitalized adult patients with laboratory-confirmed SARS-CoV-2 infection with any one of the following criteria will be eligible to receive lopinavir/ritonavir for 14 days after obtaining written informed consent: (i) respiratory distress with respiratory rate >/=22/min or SpO2 of <94 per cent; (ii) lung parenchymal infiltrates on chest X-ray; (iii) hypotension defined as systolic blood pressure <90 mmHg or need for vasopressor/inotropic medication; (iv) new-onset organ dysfunction; and (v) high-risk groups - age >60 yr, diabetes mellitus, renal failure, chronic lung disease and immunocompromised persons. Patients will be monitored to document clinical (hospital length of stay and mortality at 14, 28 and 90 days), laboratory (presence of viral RNA in serial throat swab samples) and safety (adverse events and serious adverse events) outcomes. Treatment outcomes amongst initial cases would be useful in providing guidance about the clinical management of patients with COVID-19. If found useful in managing initial SARS-CoV-2-infected patients, further evaluation using a randomized control trial design is warranted to guide future therapeutic use of this combination.

Bhattacharya, M., et al. (2020). "Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach." J Med Virol.

Recently, a novel coronavirus (SARS-COV-2) emerged which is responsible for the recent outbreak in Wuhan, China. Genetically, it is closely related to SARS-CoV and MERS-CoV. The situation is getting worse and worse, therefore, there is an urgent need for designing a suitable peptide vaccine component against the SARS-COV-2. Here, we characterized spike glycoprotein to obtain immunogenic epitopes. Next, we chose 13 Major Histocompatibility Complex-(MHC) I and 3 MHC-II epitopes, having antigenic properties. These epitopes are usually linked to specific linkers to build vaccine components and molecularly dock on toll-like receptor-5 to get binding affinity. Therefore, to provide a fast immunogenic profile of these epitopes, we performed immunoinformatics analysis so that the rapid development of the vaccine might bring this disastrous situation to the end earlier.

Boldog, P., et al. (2020). "Risk Assessment of Novel Coronavirus COVID-19 Outbreaks Outside China." J Clin Med **9**(2).

We developed a computational tool to assess the risks of novel coronavirus outbreaks outside of China. We estimate the dependence of the risk of a major outbreak in a country from imported cases on key parameters such as: (i) the evolution of the cumulative number of cases in mainland China outside the closed areas; (ii) the connectivity of the destination country with China, including baseline travel frequencies, the effect of travel restrictions, and the efficacy of entry screening at destination; and (iii) the efficacy of control measures in the destination country (expressed by the local reproduction number R loc). We found that in countries with low connectivity to China but with relatively high R loc, the most beneficial control measure to reduce the risk of outbreaks is a further reduction in their importation number either by entry screening or travel restrictions. Countries with high connectivity but low R loc benefit the most from policies that further reduce R loc. Countries in the middle should consider a combination of such policies. Risk assessments were illustrated for selected groups of countries from America, Asia, and Europe. We investigated how their risks depend on those parameters, and how the risk is increasing in time as the number of cases in China is growing.

Bonilla-Aldana, D. K., et al. (2020). "Coronavirus infections reported by ProMED, February 2000-January 2020." Travel Med Infect Dis: 101575.

INTRODUCTION: Sources describing the global burden of emerging diseases accurately are still limited. We reviewed coronavirus infections reported by ProMED and assessed the reliability of the data retrieved compared to published reports. We evaluated the effectiveness of ProMED as a source of epidemiological data on coronavirus. METHODS: Using the keyword "coronavirus" in the ProMED search engine, we reviewed all the information from the reports and collected data using a structured form, including year, country, gender, occupation, the number of infected individuals, and the number of fatal cases. RESULTS: We identified 109 entries reported between February 29, 2000 and January 22, 2020. A total of 966 cases were reported, with death reported in 188 cases, suggesting an overall case fatality rate (CFR) of 19.5%. Of 70 cases for which the gender was reported, 47 (67.1%) were male. Most of the cases were reported from China, the United Arab Emirates, and Saudi Arabia, with reports from other countries, including imported cases in Europe and North America. CONCLUSIONS: Internet-based reporting systems such as ProMED are useful to gather information and synthesize knowledge on emerging infections. Although certain areas need to be improved, ProMED provided useful information about coronaviruses especially during outbreaks.

Bordi, L., et al. (2020). "Differential diagnosis of illness in patients under investigation for the novel coronavirus (SARS-CoV-2), Italy, February 2020." Euro Surveill **25**(8).

A novel coronavirus (SARS-CoV-2) has been identified as the causative pathogen of an ongoing outbreak of respiratory disease, now named COVID-19. Most cases and sustained transmission occurred in China, but travel-associated cases have been reported in other countries, including Europe and Italy. Since the symptoms are similar to other respiratory infections, differential diagnosis in travellers arriving from countries with wide-spread COVID-19 must include other more common infections such as influenza and other respiratory tract diseases.

Bouwman, K. M., et al. (2020). "Three Amino Acid Changes in Avian Coronavirus Spike Protein Allow Binding to Kidney Tissue." J Virol **94**(2).

Infectious bronchitis virus (IBV) infects ciliated epithelial cells in the chicken respiratory tract. While some IBV strains replicate locally, others can disseminate to various organs, including the kidney. Here, we elucidate the determinants for kidney tropism by studying interactions between the receptor-binding domain (RBD) of the viral attachment protein spike from two IBV strains with different tropisms. Recombinantly produced RBDs from the nephropathogenic IBV strain QX and from the nonnephropathogenic strain M41 bound to the epithelial cells of the trachea. In contrast, only QX-RBD binds more extensively to cells of the digestive tract, urogenital tract, and kidneys. While removal of sialic acids from tissues prevented binding of all proteins to all tissues, binding of QX-RBD to trachea and kidney could not be blocked by preincubation with synthetic alpha-2,3-linked sialic acids. The lack of binding of QX-RBD to a previously identified IBV-M41 receptor was confirmed by enzyme-linked immunosorbent assay (ELISA), demonstrating that tissue binding of QX-RBD is dependent on a different sialylated glycan receptor. Using chimeric RBD proteins, we discovered that the region encompassing amino acids 99 to 159 of QX-RBD was required to establish kidney binding. In particular, QX-RBD amino acids 110 to 112 (KIP) were sufficient to render IBV-M41 with the ability to bind to kidney, while the reciprocal mutations in IBV-QX abolished kidney binding completely. Structural analysis of both RBDs suggests that the receptor-binding site for QX is located at a different location on the spike than that of M41.IMPORTANCE Infectious bronchitis virus is the causative agent of infectious bronchitis in chickens. Upon infection of chicken flocks, the poultry industry faces substantial economic losses by diminished egg quality and increased morbidity and mortality of infected animals. While all IBV strains infect the chicken respiratory tract via the ciliated epithelial layer of the trachea, some strains can also replicate in the kidneys, dividing IBV into the following two pathotypes: nonnephropathogenic (example, IBV-M41) and nephropathogenic viruses (including IBV-QX). Here, we set out to identify the determinants for the extended nephropathogenic tropism of IBV-QX. Our data reveal that each pathotype makes use of a different sialylated glycan ligand, with binding sites on opposite sides of the attachment protein. This knowledge should facilitate the design of antivirals to prevent coronavirus infections in the field.

Cardenas-Conejo, Y., et al. (2020). "An exclusive 42 amino acid signature in pp1ab protein provides insights into the evolutive history of the 2019 novel human-pathogenic coronavirus (SARS-CoV-2)." J Med Virol.

The city of Wuhan, Hubei province, China, was the origin of a severe pneumonia outbreak in December 2019, attributed to a novel coronavirus (severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2]), causing a total of 2761 deaths and 81109 cases (25 February 2020). SARS-CoV-2 belongs to genus Betacoronavirus, subgenus Sarbecovirus. The polyprotein 1ab (pp1ab) remains unstudied thoroughly since it is similar to other sarbecoviruses. In this short communication, we performed phylogenetic-structural sequence analysis of pp1ab protein of SARS-CoV-2. The analysis showed that the viral pp1ab has not changed in most isolates throughout the outbreak time, but interestingly a deletion of 8 aa in the virulence factor nonstructural protein 1 was found in a virus isolated from a Japanese patient that did not display critical symptoms. While comparing pp1ab protein with other betacoronaviruses, we found a 42 amino acid signature that is only present in SARS-CoV-2 (AS-SCoV2). Members from clade 2 of sarbecoviruses have traces of this signature. The AS-SCoV2 located in the acidic-domain of papain-like protein of SARS-CoV-2 and bat-SL-CoV-RatG13 guided us to suggest that the novel 2019 coronavirus probably emerged by genetic drift from bat-SL-CoV-RaTG13. The implication of this amino acid signature in papain-like protein structure arrangement and function is something worth to be explored.

Ceraolo, C. and F. M. Giorgi (2020). "Genomic variance of the 2019-nCoV coronavirus." J Med Virol **92**(5): 522-528.

There is a rising global concern for the recently emerged novel coronavirus (2019-nCoV). Full genomic sequences have been released by the worldwide scientific community in the last few weeks to understand the evolutionary origin and molecular characteristics of this virus. Taking advantage of all the genomic information currently available, we constructed a phylogenetic tree including also representatives of other coronaviridae, such as Bat coronavirus (BCoV) and severe acute respiratory syndrome. We confirm high sequence similarity (>99%) between all sequenced 2019-nCoVs genomes available, with the closest BCoV sequence sharing 96.2% sequence identity, confirming the notion of a zoonotic origin of 2019-nCoV. Despite the low heterogeneity of the 2019-nCoV genomes, we could identify at least two hypervariable genomic hotspots, one of which is responsible for a Serine/Leucine variation in the viral ORF8-encoded protein. Finally, we perform a full proteomic comparison with other coronaviridae, identifying key aminoacidic differences to be considered for antiviral strategies deriving from previous anti-coronavirus approaches.

Chan, J. F., et al. (2020). "Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan." Emerg Microbes Infect **9**(1): 221-236.

A mysterious outbreak of atypical pneumonia in late 2019 was traced to a seafood wholesale market in Wuhan of China. Within a few weeks, a novel coronavirus tentatively named as 2019 novel coronavirus (2019-nCoV) was announced by the World Health Organization. We performed bioinformatics analysis on a virus genome from a patient with 2019-nCoV infection and compared it with other related coronavirus genomes. Overall, the genome of 2019-nCoV has 89% nucleotide identity with bat SARS-like-CoVZXC21 and 82% with that of human SARS-CoV. The phylogenetic trees of their orf1a/b, Spike, Envelope, Membrane and Nucleoprotein also clustered closely with those of the bat, civet and human SARS coronaviruses. However, the external subdomain of Spike's receptor binding domain of 2019-nCoV shares only 40% amino acid identity with other SARS-related coronaviruses. Remarkably, its orf3b encodes a completely novel short protein. Furthermore, its new orf8 likely encodes a secreted protein with an alpha-helix, following with a beta-sheet (s) containing six strands. Learning from the roles of civet in SARS and camel in MERS, hunting for the animal source of 2019-nCoV and its more ancestral virus would be important for understanding the origin and evolution of this novel lineage B betacoronavirus. These findings provide the basis for starting further studies on the pathogenesis, and optimizing the design of diagnostic, antiviral and vaccination strategies for this emerging infection.

Chan, J. F., et al. (2020). "A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster." Lancet **395**(10223): 514-523.

BACKGROUND: An ongoing outbreak of pneumonia associated with a novel coronavirus was reported in Wuhan city, Hubei province, China. Affected patients were geographically linked with a local wet market as a potential source. No data on person-to-person or nosocomial transmission have been published to date. METHODS: In this study, we report the epidemiological, clinical, laboratory, radiological, and microbiological findings of five patients in a family cluster who presented with unexplained pneumonia after returning to Shenzhen, Guangdong province, China, after a visit to Wuhan, and an additional family member who did not travel to Wuhan. Phylogenetic analysis of genetic sequences from these patients were done. FINDINGS: From Jan 10, 2020, we enrolled a family of six patients who travelled to Wuhan from Shenzhen between Dec 29, 2019 and Jan 4, 2020. Of six family members who travelled to Wuhan, five were identified as infected with the novel coronavirus. Additionally, one family member, who did not travel to Wuhan, became infected with the virus after several days of contact with four of the family members. None of the family members had contacts with Wuhan markets or animals, although two had visited a Wuhan hospital. Five family members (aged 36-66 years) presented with fever, upper or lower respiratory tract symptoms, or diarrhoea, or a combination of these 3-6 days after exposure. They presented to our hospital (The University of Hong Kong-Shenzhen Hospital, Shenzhen) 6-10 days after symptom onset. They and one asymptomatic child (aged 10 years) had radiological ground-glass lung opacities. Older patients (aged >60 years) had more systemic symptoms, extensive radiological ground-glass lung changes, lymphopenia, thrombocytopenia, and increased C-reactive protein and lactate dehydrogenase levels. The nasopharyngeal or throat swabs of these six patients were negative for known respiratory microbes by point-of-care multiplex RT-PCR, but five patients (four adults and the child) were RT-PCR positive for genes encoding the internal RNA-dependent RNA polymerase and surface Spike protein of this novel coronavirus, which were confirmed by Sanger sequencing. Phylogenetic analysis of these five patients' RT-PCR amplicons and two full genomes by next-generation sequencing showed that this is a novel coronavirus, which is closest to the bat severe acute respiatory syndrome (SARS)-related coronaviruses found in Chinese horseshoe bats. INTERPRETATION: Our findings are consistent with person-to-person transmission of this novel coronavirus in hospital and family settings, and the reports of infected travellers in other geographical regions. FUNDING: The Shaw Foundation Hong Kong, Michael Seak-Kan Tong, Respiratory Viral Research Foundation Limited, Hui Ming, Hui Hoy and Chow Sin Lan Charity Fund Limited, Marina Man-Wai Lee, the Hong Kong Hainan Commercial Association South China Microbiology Research Fund, Sanming Project of Medicine (Shenzhen), and High Level-Hospital Program (Guangdong Health Commission).

Chen, L., et al. (2020). "[Analysis of clinical features of 29 patients with 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 203-208.

Objective: To analyze the clinical characteristics of 2019 novel coronavirus (2019-nCoV) pneumonia and to investigate the correlation between serum inflammatory cytokines and severity of the disease. Methods: 29 patients with 2019-ncov admitted to the isolation ward of Tongji hospital affiliated to Tongji medical college of Huazhong University of Science and Technology in January 2020 were selected as the study subjects. Clinical data were collected and the general information, clinical symptoms, blood test and CT imaging characteristics were analyzed. According to the relevant diagnostic criteria, the patients were divided into three groups: mild (15 cases), severe (9 cases) and critical (5 cases). The expression levels of inflammatory cytokines and other markers in the serum of each group were detected, and the changes of these indicators of the three groups were compared and analyzed, as well as their relationship with the clinical classification of the disease. Results: (1) The main symptoms of 2019-nCoV pneumonia was fever (28/29) with or without respiratory and other systemic symptoms. Two patients died with underlying disease and co-bacterial infection, respectively. (2) The blood test of the patients showed normal or decreased white blood cell count (23/29), decreased lymphocyte count (20/29), increased hypersensitive C reactive protein (hs-CRP) (27/29), and normal procalcitonin. In most patients, serum lactate dehydrogenase (LDH) was significantly increased (20/29), while albumin was decreased (15/29). Alanine aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin (Tbil), serum creatinine (Scr) and other items showed no significant changes. (3) CT findings of typical cases were single or multiple patchy ground glass shadows accompanied by septal thickening. When the disease progresses, the lesion increases and the scope expands, and the ground glass shadow coexists with the solid shadow or the stripe shadow. (4) There were statistically significant differences in the expression levels of interleukin-2 receptor (IL-2R) and IL-6 in the serum of the three groups ($P<0.05$), among which the critical group was higher than the severe group and the severe group was higher than the mild group. However, there were no statistically significant differences in serum levels of tumor necrosis factor-alpha (TNF-alpha), IL-1, IL-8, IL-10, hs-CRP, lymphocyte count and LDH among the three groups ($P>0.05$). Conclusion: The clinical characteristics of 2019-nCoV pneumonia are similar to those of common viral pneumonia. High resolution CT is of great value in the differential diagnosis of this disease. The increased expression of IL-2R and IL-6 in serum is expected to predict the severity of the 2019-nCoV pneumonia and the prognosis of patients.

Chen, L., et al. (2020). "[Analysis of clinical features of 29 patients with 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E005.

Objective: To analyze the clinical characteristics of 2019 novel coronavirus (2019-nCoV) pneumonia and to investigate the correlation between serum inflammatory cytokines and severity of the disease. Methods: 29 patients with 2019-ncov admitted to the isolation ward of Tongji hospital affiliated to Tongji medical college of Huazhong University of Science and Technology in January 2020 were selected as the study subjects. Clinical data were collected and the general information, clinical symptoms, blood test and CT imaging characteristics were analyzed. According to the relevant diagnostic criteria, the patients were divided into three groups: mild (15 cases), severe (9 cases) and critical (5 cases). The expression levels of inflammatory cytokines and other markers in the serum of each group were detected, and the changes of these indicators of the three groups were compared and analyzed, as well as their relationship with the clinical classification of the disease. Results: (1) The main symptoms of 2019-nCoV pneumonia was fever (28/29) with or without respiratory and other systemic symptoms. Two patients died with underlying disease and co-bacterial infection, respectively. (2) The blood test of the patients showed normal or decreased white blood cell count (23/29), decreased lymphocyte count (20/29), increased hypersensitive C reactive protein (hs-CRP) (27/29), and normal procalcitonin. In most patients,serum lactate dehydrogenase (LDH) was significantly increased (20/29), while albumin was decreased (15/29). Alanine aminotransferase (ALT), aspartate aminotransferase (AST), total bilirubin (Tbil), serum creatinine (Scr) and other items showed no significant changes. (3) CT findings of typical cases were single or multiple patchy ground glass shadows accompanied by septal thickening. When the disease progresses, the lesion increases and the scope expands, and the ground glass shadow coexists with the solid shadow or the stripe shadow. (4) There were statistically significant differences in the expression levels of interleukin-2 receptor (IL-2R) and IL-6 in the serum of the three groups ($P<0.05$), among which the critical group was higher than the severe group and the severe group was higher than the mildgroup. However, there were no statistically significant differences in serum levels of tumor necrosis factor-alpha (TNF-alpha), IL-1, IL-8, IL-10, hs-CRP, lymphocyte count and LDH among the three groups ($P>0.05$). Conclusion: The clinical characteristics of 2019-nCoV pneumonia are similar to those of common viral pneumonia. High resolution CT is of great value in the differential diagnosis of this disease. The increased expression of IL-2R and IL-6 in serum is expected to

predict the severity of the 2019-nCoV pneumonia and the prognosis of patients.

Chen, L., et al. (2020). "RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak." Emerg Microbes Infect **9**(1): 313-319.

From December 2019, an outbreak of unusual pneumonia was reported in Wuhan with many cases linked to Huanan Seafood Market that sells seafood as well as live exotic animals. We investigated two patients who developed acute respiratory syndromes after independent contact history with this market. The two patients shared common clinical features including fever, cough, and multiple ground-glass opacities in the bilateral lung field with patchy infiltration. Here, we highlight the use of a low-input metagenomic next-generation sequencing (mNGS) approach on RNA extracted from bronchoalveolar lavage fluid (BALF). It rapidly identified a novel coronavirus (named 2019-nCoV according to World Health Organization announcement) which was the sole pathogens in the sample with very high abundance level (1.5% and 0.62% of total RNA sequenced). The entire viral genome is 29,881 nt in length (GenBank MN988668 and MN988669, Sequence Read Archive database Bioproject accession PRJNA601736) and is classified into beta-coronavirus genus. Phylogenetic analysis indicates that 2019-nCoV is close to coronaviruses (CoVs) circulating in Rhinolophus (Horseshoe bats), such as 98.7% nucleotide identity to partial RdRp gene of bat coronavirus strain BtCoV/4991 (GenBank KP876546, 370 nt sequence of RdRp and lack of other genome sequence) and 87.9% nucleotide identity to bat coronavirus strain bat-SL-CoVZC45 and bat-SL-CoVZXC21. Evolutionary analysis based on ORF1a/1b, S, and N genes also suggests 2019-nCoV is more likely a novel CoV independently introduced from animals to humans.

Chen, N., et al. (2020). "Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study." Lancet **395**(10223): 507-513.

BACKGROUND: In December, 2019, a pneumonia associated with the 2019 novel coronavirus (2019-nCoV) emerged in Wuhan, China. We aimed to further clarify the epidemiological and clinical characteristics of 2019-nCoV pneumonia. METHODS: In this retrospective, single-centre study, we included all confirmed cases of 2019-nCoV in Wuhan Jinyintan Hospital from Jan 1 to Jan 20, 2020. Cases were confirmed by real-time RT-PCR and were analysed for epidemiological, demographic, clinical, and radiological features and laboratory data. Outcomes were followed up until Jan 25, 2020. FINDINGS: Of the 99 patients with 2019-nCoV pneumonia, 49 (49%) had a history of exposure to the Huanan seafood market. The average age of the patients was 55.5 years (SD 13.1), including 67 men and 32 women. 2019-nCoV was detected in all patients by real-time RT-PCR. 50 (51%) patients had chronic diseases. Patients had clinical manifestations of fever (82 [83%] patients), cough (81 [82%] patients), shortness of breath (31 [31%] patients), muscle ache (11 [11%] patients), confusion (nine [9%] patients), headache (eight [8%] patients), sore throat (five [5%] patients), rhinorrhoea (four [4%] patients), chest pain (two [2%] patients), diarrhoea (two [2%] patients), and nausea and vomiting (one [1%] patient). According to imaging examination, 74 (75%) patients showed bilateral pneumonia, 14 (14%) patients showed multiple mottling and ground-glass opacity, and one (1%) patient had pneumothorax. 17 (17%) patients developed acute respiratory distress syndrome and, among them, 11 (11%) patients worsened in a short period of time and died of multiple organ failure. INTERPRETATION: The 2019-nCoV infection was of clustering onset, is more likely to affect older males with comorbidities, and can result in severe and even fatal respiratory diseases such as acute respiratory distress syndrome. In general, characteristics of patients who died were in line with the MuLBSTA score, an early warning model for predicting mortality in viral pneumonia. Further investigation is needed to explore the applicability of the MuLBSTA score in predicting the risk of mortality in 2019-nCoV infection. FUNDING: National Key R & D Program of China.

Chen, X., et al. (2020). "Application of a Risk Analysis Tool to Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Outbreak in Saudi Arabia." Risk Anal.

The Grunow-Finke assessment tool (GFT) is an accepted scoring system for determining likelihood of an outbreak being unnatural in origin. Considering its high specificity but low sensitivity, a modified Grunow-Finke tool (mGFT) has been developed with improved sensitivity. The mGFT has been validated against some past disease outbreaks, but it has not been applied to ongoing outbreaks. This study is aimed to score the outbreak of Middle East respiratory syndrome coronavirus (MERS-CoV) in Saudi Arabia using both the original GFT and mGFT. The publicly available data on human cases of MERS-CoV infections reported in Saudi Arabia (2012-2018) were sourced from the FluTrackers, World Health Organization, Saudi Ministry of Health, and published literature associated with MERS outbreaks investigations. The risk assessment of MERS-CoV in Saudi Arabia was analyzed using the original GFT and mGFT criteria, algorithms, and thresholds. The scoring points for each criterion were determined by three researchers to minimize the subjectivity. The results showed 40 points of total possible 54 points using the original GFT (likelihood: 74%), and 40 points of a total possible 60 points (likelihood: 67%) using the mGFT, both tools indicating a high likelihood that human MERS-CoV in Saudi Arabia is unnatural in origin. The findings simply flag unusual patterns in this outbreak, but do not prove unnatural etiology. Proof of bioattacks can only be obtained by law enforcement and intelligence agencies. This study demonstrated the value and flexibility of the mGFT in assessing and predicting the risk for an ongoing outbreak with simple criteria.

Chen, X., et al. (2020). "Perioperative Management of Patients Infected with the Novel Coronavirus: Recommendation from the Joint Task Force of the Chinese Society of Anesthesiology and the Chinese Association of Anesthesiologists." Anesthesiology.

The outbreak of the new Coronavirus disease, COVID-19, has been involved in 77,262 cases in China as well as in 27 other countries as of February 24, 2020. Because the virus is novel to human beings, and there is no vaccine yet available, every individual is susceptible and can become infected. Healthcare workers are at high risk, and unfortunately, more than 3,000 healthcare workers in China have been infected. Anesthesiologists are among healthcare workers who are at an even higher risk of becoming infected because of their close contact with infected patients and high potential of exposure to respiratory droplets or aerosol from their patients' airways. In order to provide healthcare workers with updated recommendations on the management of patients in the perioperative setting as well as for emergency airway management outside of the operating room, the two largest anesthesia societies, the Chinese Society of Anesthesiology (CSA) and the Chinese Association of Anesthesiologists (CAA) have formed a task force to produce the recommendations. The task force hopes to help healthcare workers, particularly anesthesiologists, optimize the care of their patients and protect patients, healthcare workers, and the public from becoming infected. The recommendations were created mainly based on the practice and experience of anesthesiologists who provide care to patients in China. Therefore, adoption of these recommendations outside of China must be done with caution, and the local environment, culture, uniqueness of the healthcare system, and patients' needs should be considered. The task force will continuously update the recommendations and incorporate new information in future versions.

Chen, X. and B. Yu (2020). "First two months of the 2019 Coronavirus Disease (COVID-19) epidemic in China: real-time surveillance and evaluation with a second derivative model." Glob Health Res Policy **5**: 7.

Background: Similar to outbreaks of many other infectious diseases, success in controlling the novel 2019 coronavirus infection requires a timely and accurate monitoring of the epidemic, particularly during its early period with rather limited data while the need for information increases explosively. Methods: In this study, we used a second derivative model to characterize the coronavirus epidemic in China with cumulatively diagnosed cases during the first 2 months. The analysis was further enhanced by an exponential model with a close-population assumption. This model was built with the data and used to assess the detection rate during the study period, considering the differences between the true infections, detectable and detected cases. Results: Results from the second derivative modeling suggest the coronavirus epidemic as nonlinear and chaotic in nature. Although it emerged gradually, the epidemic was highly responsive to massive interventions initiated on January 21, 2020, as indicated by results from both second derivative and exponential modeling analyses. The epidemic started to decelerate immediately after the massive actions. The results derived from our analysis signaled the decline of the epidemic 14 days before it eventually occurred on February 4, 2020. Study findings further signaled an accelerated decline in the epidemic starting in 14 days on February 18, 2020. Conclusions: The coronavirus epidemic appeared to be nonlinear and chaotic, and was responsive to effective interventions. The methods used in this study can be applied in surveillance to inform and encourage the general public, public health professionals, clinicians and decision-makers to take coordinative and collaborative efforts to control the epidemic.

Cheng, V. C. C., et al. (2020). "Escalating infection control response to the rapidly evolving epidemiology of the Coronavirus disease 2019 (COVID-19) due to SARS-CoV-2 in Hong Kong." Infect Control Hosp Epidemiol: 1-24.

BACKGROUND: To describe the infection control preparedness for Coronavirus Disease (COVID-19) due to SARS-CoV-2 [previously known as 2019-novel coronavirus] in the first 42 days after announcement of a cluster of pneumonia in China, on 31 December 2019 (day 1) in Hong Kong. METHODS: A bundle approach of active and enhanced laboratory surveillance, early airborne infection isolation, rapid molecular diagnostic testing, and contact tracing for healthcare workers (HCWs) with unprotected exposure

in the hospitals was implemented. Epidemiological characteristics of confirmed cases, environmental and air samples were collected and analyzed. RESULTS: From day 1 to day 42, forty-two (3.3%) of 1275 patients fulfilling active (n=29) and enhanced laboratory surveillance (n=13) confirmed to have SARS-CoV-2 infection. The number of locally acquired case significantly increased from 1 (7.7%) of 13 [day 22 to day 32] to 27 (93.1%) of 29 confirmed case [day 33 to day 42] (p<0.001). Twenty-eight patients (66.6%) came from 8 family clusters. Eleven (2.7%) of 413 HCWs caring these confirmed cases were found to have unprotected exposure requiring quarantine for 14 days. None of them was infected and nosocomial transmission of SARS-CoV-2 was not observed. Environmental surveillance performed in a patient with viral load of 3.3x106 copies/ml (pooled nasopharyngeal/ throat swab) and 5.9x106 copies/ml (saliva) respectively. SARS-CoV-2 revealed in 1 (7.7%) of 13 environmental samples, but not in 8 air samples collected at a distance of 10 cm from patient's chin with or without wearing a surgical mask. CONCLUSION: Appropriate hospital infection control measures could prevent nosocomial transmission of SARS-CoV-2.

Chronic obstructive pulmonary disease group of Chinese Thoracic, S. and P. Chronic obstructive pulmonary disease committee of Chinese Association of Chest (2020). "[Medical management and prevention instruction of chronic obstructive pulmonary disease during the coronavirus disease 2019 epidemic]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E034.

Currently, coronavirus disease 2019 (COVID-19) was of clustering onset in China and challenging to the Chinese healthcare system. Epidemiological data showed that the older patients with chronic commodities were at high risk of the involvement of the severe and critical type of COVID-19, especially patients with chronic obstructive pulmonary disease (COPD) resulting in high mortalities. There were nearly 100 million COPD patients in China, and most of them were the elderly. Once infected with COVID-19, it would be life-threatening for the COPD patients. Therefore, during the epidemic, it was of vital significance for us to attach great importance to optimize the management of COPD patients. Based on these considerations, the COPD Group of the Chinese Thoracic Society (CTS) and the COPD working Committee of the Chinese Association of Chest Physicians (CACP) altogether drafted the instruction for medical management and prevention of COPD during the COVID-19 epidemic period for the healthcare practitioner and patients.

Chu, D. K. W., et al. (2020). "Molecular Diagnosis of a Novel Coronavirus (2019-nCoV) Causing an Outbreak of Pneumonia." Clin Chem.

BACKGROUND: A novel coronavirus of zoonotic origin (2019-nCoV) has recently been identified in patients with acute respiratory disease. This virus is genetically similar to SARS coronavirus and bat SARS-like coronaviruses. The outbreak was initially detected in Wuhan, a major city of China, but has subsequently been detected in other provinces of China. Travel-associated cases have also been reported in a few other countries. Outbreaks in health care workers indicate human-to-human transmission. Molecular tests for rapid detection of this virus are urgently needed for early identification of infected patients. METHODS: We developed two 1-step quantitative real-time reverse-transcription PCR assays to detect two different regions (ORF1b and N) of the viral genome. The primer and probe sets were designed to react with this novel coronavirus and its closely related viruses, such as SARS coronavirus. These assays were evaluated using a panel of positive and negative controls. In addition, respiratory specimens from two 2019-nCoV-infected patients were tested. RESULTS: Using RNA extracted from cells infected by SARS coronavirus as a positive control, these assays were shown to have a dynamic range of at least seven orders of magnitude (2x10-4-2000 TCID50/reaction). Using DNA plasmids as positive standards, the detection limits of these assays were found to be below 10 copies per reaction. All negative control samples were negative in the assays. Samples from two 2019-nCoV-infected patients were positive in the tests. CONCLUSIONS: The established assays can achieve a rapid detection of 2019n-CoV in human samples, thereby allowing early identification of patients.

Deng, S. Q. and H. J. Peng (2020). "Characteristics of and Public Health Responses to the Coronavirus Disease 2019 Outbreak in China." J Clin Med **9**(2).

In December 2019, cases of unidentified pneumonia with a history of exposure in the Huanan Seafood Market were reported in Wuhan, Hubei Province. A novel coronavirus, SARS-CoV-2, was identified to be accountable for this disease. Human-to-human transmission is confirmed, and this disease (named COVID-19 by World Health Organization (WHO)) spread rapidly around the country and the world. As of 18 February 2020, the number of confirmed cases had reached 75,199 with 2009 fatalities. The COVID-19 resulted in a much lower case-fatality rate (about 2.67%) among the confirmed cases, compared with Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory

Syndrome (MERS). Among the symptom composition of the 45 fatality cases collected from the released official reports, the top four are fever, cough, short of breath, and chest tightness/pain. The major comorbidities of the fatality cases include hypertension, diabetes, coronary heart disease, cerebral infarction, and chronic bronchitis. The source of the virus and the pathogenesis of this disease are still unconfirmed. No specific therapeutic drug has been found. The Chinese Government has initiated a level-1 public health response to prevent the spread of the disease. Meanwhile, it is also crucial to speed up the development of vaccines and drugs for treatment, which will enable us to defeat COVID-19 as soon as possible.

Deng, X., et al. (2020). "Structure-Guided Mutagenesis Alters Deubiquitinating Activity and Attenuates Pathogenesis of a Murine Coronavirus." J Virol.

Coronaviruses express a multifunctional papain-like protease, termed PLP2. PLP2 acts as a protease that cleaves the viral replicase polyprotein, and a deubiquitinating (DUB) enzyme which removes ubiquitin moieties from ubiquitin-conjugated proteins. Previous in vitro studies implicated PLP2 DUB activity as a negative regulator of the host interferon (IFN) response, but the role of DUB activity during virus infection was unknown. Here, we used X-ray structure-guided mutagenesis and functional studies to identify amino acid substitutions within the ubiquitin-binding surface of PLP2 that reduced DUB activity without affecting polyprotein processing activity. We engineered a DUB mutation (Asp1772 to Ala) into a murine coronavirus and evaluated the replication and pathogenesis of the DUB mutant virus (DUBmut) in cultured macrophages and in mice. We found that the DUBmut virus replicates similarly as the wild-type virus in cultured cells, but the DUBmut virus activates an IFN response at earlier times compared to the wild-type virus infection in macrophages, consistent with DUB activity negatively regulating the IFN response. We compared the pathogenesis of the DUBmut virus to the wild-type virus and found that the DUBmut-infected mice had a statistically significant reduction ($p<0.05$) in viral titer in livers and spleens at day 5 post-infection, albeit both wild-type and DUBmut virus infections resulted in similar liver pathology. Overall, this study demonstrates that structure-guided mutagenesis aids the identification of critical determinants of PLP2-ubiquitin complex, and that PLP2 DUB activity plays a role as an interferon antagonist in coronavirus pathogenesis.IMPORTANCE Coronaviruses employ a genetic economy by encoding multifunctional proteins that function in viral replication and also modify the host environment to disarm the innate immune response. The coronavirus papain-like protease 2 (PLP2) domain possesses protease activity, which cleaves the viral replicase polyprotein, and also DUB activity (de-conjugating ubiquitin/ubiquitin-like molecules from modified substrates) using identical catalytic residues. To separate the DUB activity from the protease activity, we employed a structure-guided mutagenesis approach and identified residues that are important for ubiquitin-binding. We found that mutating the ubiquitin-binding residues results in a PLP2 that has reduced DUB activity but retains protease activity. We engineered a recombinant murine coronavirus to express the DUB mutant and showed that the DUB mutant virus activated an earlier type I interferon response in macrophages and exhibited reduced replication in mice. The results of this study demonstrate that PLP2/DUB is an interferon antagonist and a virulence trait of coronaviruses.

Devaux, C. A., et al. (2020). "New insights on the antiviral effects of chloroquine against coronavirus: what to expect for COVID-19?" Int J Antimicrob Agents: 105938.

Recently, a novel coronavirus (2019-nCoV), officially known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), emerged in China. Despite drastic containment measures, the spread of this virus is ongoing. SARS-CoV-2 is the aetiological agent of coronavirus disease 2019 (COVID-19) characterised by pulmonary infection in humans. The efforts of international health authorities have since focused on rapid diagnosis and isolation of patients as well as the search for therapies able to counter the most severe effects of the disease. In the absence of a known efficient therapy and because of the situation of a public-health emergency, it made sense to investigate the possible effect of chloroquine/hydroxychloroquine against SARS-CoV-2 since this molecule was previously described as a potent inhibitor of most coronaviruses, including SARS-CoV-1. Preliminary trials of chloroquine repurposing in the treatment of COVID-19 in China have been encouraging, leading to several new trials. Here we discuss the possible mechanisms of chloroquine interference with the SARS-CoV-2 replication cycle.

Dhama, K., et al. (2020). "COVID-19, an emerging coronavirus infection: advances and prospects in designing and developing vaccines, immunotherapeutics, and therapeutics." Hum Vaccin Immunother: 1-7.

The novel coronavirus infection (COVID-19 or Coronavirus disease 2019) that emerged from Wuhan, Hubei province of China has spread to many countries worldwide. Efforts have been made to develop vaccines against human coronavirus (CoV) infections such as MERS and SARS in the past decades. However, to date, no licensed antiviral treatment or vaccine exists for MERS and SARS. Most of the efforts for developing CoV vaccines and drugs target the spike glycoprotein or S protein, the major inducer of neutralizing antibodies. Although a few candidates have shown efficacy in in vitro studies, not many have progressed to randomized animal or human trials, hence may have limited use to counter COVID-19 infection. This article highlights ongoing advances in designing vaccines and therapeutics to counter COVID-19 while also focusing on such experiences and advances as made with earlier SARS- and MERS-CoVs, which together could enable efforts to halt this emerging virus infection.

Ding, Q., et al. (2020). "The clinical characteristics of pneumonia patients co-infected with 2019 novel coronavirus and influenza virus in Wuhan, China." J Med Virol.

The outbreak of 2019 novel coronavirus (COVID-19) infection emerged in Wuhan, China on December 2019. Since then the novel coronavirus pneumonia disease has been spreading quickly and many countries and territories have been affected, with major outbreaks in China, South Korea, Italy and Iran. Influenza virus has been known as a common pathogen in winter and it can cause pneumonia. It was found clinically that very few patients were diagnosed with both COVID-19 and influenza virus. 5 out of the 115 patients confirmed with COVID-19 were also diagnosed with influenza virus infection, with three cases being influenza A and two cases being influenza B. In this study, we describe the clinical characteristics of those patients who got infected with COVID-19 as well as influenza virus. Common symptoms at onset of illness included fever (5 [100%] patients), Cough (5 [100%] patients), shortness of breath (5 [100%] patients), nasal tampon (3 [60%] patients), pharyngalgia (3 [60%] patients), myalgia (2 [40%] patients), fatigue (2 [40%] patients), headache (2 [40%] patients), and expectoration (2 [40%] patients). The laboratory results showed that compared to the normal values, the patients' lymphocytes were reduced (4 [80%] patients), and liver function ALT and AST (2 [40%] patients, 2 [40%] patients) and C-reactive protein (4 [80%] patients) were increased when admitted to hospital. They stayed in hospital for 14, 30, 17, 12, and 19 days (28.4+/-7.02), respectively. The main complications for the patients were acute respiratory distress syndrome (ARDS) (1 [20%] patients), acute liver injury (3 [60%] patients), and diarrhea (2 [40%] patients). All patients were given antiviral therapy (including oseltamivir), oxygen inhalation, and antibiotics. Three patients were treated with glucocorticoids including two treated with oral glucocorticoids. One of the five patients had transient hemostatic medication for hemoptysis. Fortunately, all patients did not need ICU care and were discharged from hospital without death. In conclusion, those patients with both COVID-19 and influenza virus infection did not appear to show a more severe condition because based on the laboratory findings, imaging studies, and patient prognosis, they showed similar clinical characteristics as those patients with COVID-19 infection only. However, it is worth noting that the symptoms of nasal tampon and pharyngalgia may be more prone to appear for those co-infection patients. This article is protected by copyright. All rights reserved.

Driggin, E., et al. (2020). "Cardiovascular Considerations for Patients, Health Care Workers, and Health Systems During the Coronavirus Disease 2019 (COVID-19) Pandemic." J Am Coll Cardiol.

The coronavirus disease-2019 (COVID-19) is an infectious disease caused by severe acute respiratory syndrome coronavirus 2 that has significant implications for the cardiovascular care of patients. First, those with COVID-19 and preexisting cardiovascular disease (CVD) have an increased risk of severe disease and death. Second, infection has been associated with multiple direct and indirect cardiovascular complications including acute myocardial injury, myocarditis, arrhythmias and venous thromboembolism. Third, therapies under investigation for COVID-19 may have cardiovascular side effects. Fourth, the response to COVID-19 can compromise the rapid triage of non-COVID-19 patients with cardiovascular conditions. Finally, the provision of cardiovascular care may place health care workers in a position of vulnerability as they become host or vectors of virus transmission. We hereby review the peer-reviewed and preprint literature pertaining to cardiovascular considerations related to COVID-19 and highlight gaps in knowledge that require further study pertinent to patients, health care workers, and health systems.

Du, B., et al. (2020). "[Pharmacotherapeutics for the new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 173-176.

The new coronavirus pneumonia (NCP), also named as COVID-19 by WHO on Feb 11 2020, is now causing a severe public health emergency in China since. The number of diagnosed cases is more than 40,000 until the submission of this manuscript. Coronavirus has caused several epidemic situations world widely, but the present contagious disease caused by 2019 new coronavirus is unprecedentedly fulminating. The published cohorts of 2019 new coronavirus (n-Cov) are single-center studies, or retrospective studies. We here share the therapeutic experiences of NCP treatment with literature review. Combination of Ribavirin and interferon-alpha is recommended by the 5(th) edition National Health Commission's Regimen (Revised Edition) because of the effect on Middle East respiratory syndrome (MERS), and the effectiveness of Lopinavir/Ritonavir and Remdisivir needs to be confirmed by randomized controlled trial (RCT), given the situation of no specific antivirus drug on NCP is unavailable. Systemic glucocorticosteroid is recommended as a short term use (1~2 mg.kg (-1).d (-1), 3~5 d) by the 5(th) edition National Health Commission's Regimen (Revised Edition) yet RCTs are expected to confirm the effectiveness. Inappropriate application of antibiotics should be avoided, especially the combination of broad-spectrum antibiotics, for the NCP is not often complicated with bacterial infection.

Du, B., et al. (2020). "[Pharmacotherapeutics for the New Coronavirus Pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E012.

The New Coronavirus Pneumonia (NCP, also named as COVID-19 by WHO on Feb 11 2020, is now causing a severe public health emergency in China since. The number of diagnosed cases is more than 40,000 until the submission of this manuscript. Coronavirus has caused several epidemic situations world widely, but the present contagious disease caused by 2019 new Coronavirus is unprecedentedly fulminating. The published cohorts of 2019 new Coronavirus (n-Cov) are single-center studies, or retrospective studies. We here share the therapeutic experiences of NCP treatment with literature review. Combination of Ribavirin and Interferon-alpha is recommended by the 5(th) edition National Health Commission's Regimen (Revised Edition) because of the effect on MERS (Middle East Respiratory Syndrome), and the effectiveness of Lopinavir/Ritonavir and Remdisivir needs to be confirmed by randomized controlled trial (RCT), given the situation of no specific antivirus drug on NCP is unavailable. Systemic glucocorticosteroid is recommended as a short term use (1~2 mg.kg (-1).d (-1), 3~5d) by the 5(th) edition National Health Commission's Regimen (Revised Edition) yet RCTs are expected to confirm the effectiveness. Inappropriate application of antibiotics should be avoided, especially the combination of broad-spectrum antibiotics, for the NCP is not often complicated with bacterial infection.

Fan, C., et al. (2020). "Prediction of Epidemic Spread of the 2019 Novel Coronavirus Driven by Spring Festival Transportation in China: A Population-Based Study." Int J Environ Res Public Health **17**(5).

After the 2019 novel coronavirus (2019-nCoV) outbreak, we estimated the distribution and scale of more than 5 million migrants residing in Wuhan after they returned to their hometown communities in Hubei Province or other provinces at the end of 2019 by using the data from the 2013-2018 China Migrants Dynamic Survey (CMDS). We found that the distribution of Wuhan's migrants is centred in Hubei Province (approximately 75%) at a provincial level, gradually decreasing in the surrounding provinces in layers, with obvious spatial characteristics of circle layers and echelons. The scale of Wuhan's migrants, whose origins in Hubei Province give rise to a gradient reduction from east to west within the province, and account for 66% of Wuhan's total migrants, are from the surrounding prefectural-level cities of Wuhan. The distribution comprises 94 districts and counties in Hubei Province, and the cumulative percentage of the top 30 districts and counties exceeds 80%. Wuhan's migrants have a large proportion of middle-aged and high-risk individuals. Their social characteristics include nuclear family migration (84%), migration with families of 3-4 members (71%), a rural household registration (85%), and working or doing business (84%) as the main reason for migration. Using a quasi-experimental analysis framework, we found that the size of Wuhan's migrants was highly correlated with the daily number of confirmed cases. Furthermore, we compared the epidemic situation in different regions and found that the number of confirmed cases in some provinces and cities in Hubei Province may be underestimated, while the epidemic situation in some regions has increased rapidly. The results are conducive to monitoring the epidemic prevention and control in various regions.

Fan, H. H., et al. (2020). "Repurposing of clinically approved drugs for treatment of coronavirus disease 2019 in a 2019-novel coronavirus (2019-nCoV) related coronavirus model." Chin Med J (Engl).

BACKGROUND: Medicines for the treatment of 2019-novel coronavirus (2019-nCoV) infections are urgently needed. However, drug screening using live 2019-nCoV requires high-level biosafety facilities, which imposes an obstacle for those without such facilities or 2019-novel coronavirus (2019-nCoV). This study aims to repurpose the clinically approved drugs for the treatment of coronavirus disease 2019 (COVID-19) in a 2019-nCoV related coronavirus model. METHODS: A 2019-nCoV related pangolin coronavirus GX_P2V/pangolin/2017/ Guangxi was described. Whether GX_P2X uses angiotensin-converting enzyme 2 (ACE2) as the cell receptor was investigated by using small interfering RNA (siRNA) -

mediated silencing of ACE2. The pangolin coronavirus model was used to identify drug candidates for treating 2019-nCoV infection. Two libraries of 2406 clinically approved drugs were screened for their ability to inhibit cytopathic effects on Vero E6 cells by GX_P2X infection. The antiviral activities and antiviral mechanisms of potential drugs were further investigated. Viral yields of RNAs and infectious particles were quantified by quantitative real-time polymerase chain reaction (qRT-PCR) and plaque assay, respectively. RESULTS: The spike protein of coronavirus GX_P2V shares 92.2% amino acid identity with that of 2019-nCoV isolate Wuhan-hu-1, and uses ACE2 as the receptor for infection just like 2019-nCoV. Three drugs-cepharanthine (CEP), selamectin and mefloquine hydrochloride exhibited complete inhibition of cytopathic effects in cell culture at 10 mumol/L. CEP demonstrated the most potent inhibition of GX_P2V infection, with a concentration for 50% of maximal effect [EC50] of 0.98 mumol/L. The viral RNA yield in cells treated with 10 mumol/L CEP was 15,393-fold lower than in cells without CEP treatment ([6.48 +/- 0.02] x 10vs. 1.00 +/- 0.12, t = 150.38, P < 0.001) at 72 h post-infection (p.i.). Plaque assays found no production of live viruses in media containing 10 mumol/L CEP at 48 h p.i. Furthermore, we found CEP has potent antiviral activities against both viral entry (1.00 +/- 0.37 vs. 0.46 +/- 0.12, t = 2.42, P < 0.05) and viral replication (1.00 +/- 0.43 vs. [6.18 +/- 0.95] x 10, t = 3.98, P < 0.05). CONCLUSIONS: Our pangolin coronavirus GX_P2V is a workable model for 2019-nCoV research. CEP, selamectin and mefloquine hydrochloride are potential drugs for treating 2019-nCoV infection. Our results strongly suggest that CEP is a wide-spectrum inhibitor of pan-betacoronavirus, and clinical trial of CEP for treatment of 2019-nCoV infection is warranted.

Frieden, T. R. and C. T. Lee (2020). "Identifying and Interrupting Superspreading Events-Implications for Control of Severe Acute Respiratory Syndrome Coronavirus 2." Emerg Infect Dis **26**(6).

It appears inevitable that severe acute respiratory syndrome coronavirus 2 will continue to spread. Although we still have limited information on the epidemiology of this virus, there have been multiple reports of superspreading events (SSEs), which are associated with both explosive growth early in an outbreak and sustained transmission in later stages. Although SSEs appear to be difficult to predict and therefore difficult to prevent, core public health actions can prevent and reduce the number and impact of SSEs. To prevent and control of SSEs, speed is essential. Prevention and mitigation of SSEs depends, first and foremost, on quickly recognizing and understanding these events, particularly within healthcare settings. Better understanding transmission dynamics associated with SSEs, identifying and mitigating high-risk settings, strict adherence to healthcare infection prevention and control measures, and timely implementation of nonpharmaceutical interventions can help prevent and control severe acute respiratory syndrome coronavirus 2, as well as future infectious disease outbreaks.

Fung, J., et al. (2020). "Antigen Capture Enzyme-Linked Immunosorbent Assay for Detecting Middle East Respiratory Syndrome Coronavirus in Humans." Methods Mol Biol **2099**: 89-97.

The Middle East respiratory syndrome (MERS) is the second novel zoonotic disease infecting humans caused by coronavirus (CoV) in this century. To date, more than 2200 laboratory-confirmed human cases have been identified in 27 countries, and more than 800 MERS-CoV associated deaths have been reported since its outbreak in 2012. Rapid laboratory diagnosis of MERS-CoV is the key to successful containment and prevention of the spread of infection. Though the gold standard for diagnosing MERS-CoV infection in humans is still nucleic acid amplification test (NAAT) of the up-E region, an antigen capture enzyme-linked immunosorbent assay (ELISA) could also be of use for early diagnosis in less developed locations. In the present method, a step-by-step guide to perform a MERS-CoV nucleocapsid protein (NP) capture ELISA using two NP-specific monoclonal antibodies is provided for readers to develop their in-house workflow or diagnostic kit for clinical use and for mass-screening project of animals (e.g., dromedaries and bats) to better understand the spread and evolution of the virus.

Gordon, C. J., et al. (2020). "The antiviral compound remdesivir potently inhibits RNA-dependent RNA polymerase from Middle East respiratory syndrome coronavirus." J Biol Chem.

Antiviral drugs for managing infections with human coronaviruses are not yet approved, posing a serious challenge to current global efforts aimed at containing the outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Remdesivir (RDV) is an investigational compound with a broad spectrum of antiviral activities against RNA viruses, including SARS-CoV and Middle East respiratory syndrome (MERS-CoV). RDV is a nucleotide analog inhibitor of RNA-dependent RNA polymerases (RdRps). Here, we co-expressed the MERS-CoV nonstructural proteins nsp5, nsp7, nsp8, and nsp12 (RdRp) in insect cells as a part a polyprotein to study the mechanism of inhibition of MERS-CoV RdRp by RDV. We initially demonstrated that nsp8 and nsp12 form an active complex. The triphosphate form of the inhibitor (RDV-TP) competes with its natural counterpart ATP. Of note, the selectivity value for RDV-TP obtained here with a steady-state approach suggests that it is more efficiently incorporated than ATP and two other nucleotide analogues. Once incorporated at position i, the inhibitor caused RNA synthesis arrest at position i+3. Hence, the likely mechanism of action is delayed RNA chain termination. The additional three nucleotides may protect the inhibitor from excision by the viral 3'-5' exonuclease activity. Together, these results help to explain the high potency of RDV against RNA viruses in cell-based assays.

Gorse, G. J., et al. (2020). "Antibodies to coronaviruses are higher in older compared with younger adults and binding antibodies are more sensitive than neutralizing antibodies in identifying coronavirus-associated illnesses." J Med Virol **92**(5): 512-517.

Human coronaviruses (HCoV) are common causes of respiratory illnesses (RI) despite preexisting humoral immunity. Sera were obtained near the onset of RI and 3 to 4 weeks later as part of a prospective study of 200 subjects evaluated for RI from 2009 to 2013. Antibodies against common HCoV strains were measured by enzyme-linked immunosorbent assay and neutralization assay comparing older adults with cardiopulmonary diseases (99 subjects) to younger, healthy adults (101 subjects). Virus shedding was detected in respiratory secretions by polymerase chain reaction. Of 43 HCoV-associated illnesses, 15 (35%) occurred in 14 older adults (aged >/=60 years) and 28 (65%) in 28 younger adults (aged 21-40 years). Binding and neutralizing antibodies were higher in older adults. Only 16 (35.7%) of RI with increases in binding antibodies also had increases in neutralizing antibodies to HCoV. Increases in binding antibodies with RI were more frequent than increased neutralizing antibodies and virus shedding, and more frequent in younger compared to older adults. Functional neutralizing antibodies were not stimulated as often as binding antibodies, explaining in part a susceptibility to reinfection with HCoV. Monitoring binding antibodies may be more sensitive for the serologic detection of HCoV infections.

Group of Interventional Respiratory Medicine, C. T. S. (2020). "[Expert consensus for bronchoscopy during the epidemic of 2019 novel coronavirus infection (Trial version)]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 199-202.

Infection with 2019 Novel Coronavirus (2019-nCoV) is mainly transmitted by respiratory droplets, airborne transmission and direct contact. However, conducting bronchoscopy on patients with 2019-nCoV is a high-risk procedure in which health care workers are directly exposed to the virus, and the protection and operation procedures need to be strictly regulated. According to the characteristics of bronchoscopy, it is necessary to formulate the procedure, requirements and precautions when conducting bronchoscopy in the current epidemic situation. Relevant standards for preventing from infections should be strictly implemented in the operation of bronchoscopy. It needs to emphasize that bronchoscopy should not be used as a routine means for the diagnosis of 2019-nCoV infection sampling. The indications for bronchoscopy for other diseases should be strictly mastered, and it is suggested that bronchoscopy should be postponed for those patients who is not in urgent situation.

Group of Interventional Respiratory Medicine, C. T. S. (2020). "[Expert consensus for bronchoscopy during the epidemic of 2019 Novel Coronavirus infection (Trial version)]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E006.

Infection with 2019 Novel Coronavirus (2019-nCoV) is mainly transmitted by respiratory droplets, airborne transmission and direct contact. However, conducting bronchoscopy on patients with 2019-nCoV is a high-risk procedure in which health care workers are directly exposed to the virus, and the protection and operation procedures need to be strictly regulated. According to the characteristics of bronchoscopy, it is necessary to formulate the procedure, requirements and precautions when conducting bronchoscopy in the current epidemic situation. Relevant standards for preventing from infections should be strictly implemented in the operation of bronchoscopy. It needs to emphasize that bronchoscopy should not be used as a routine means for the diagnosis of 2019-nCoV infection sampling. The indications for bronchoscopy for other diseases should be strictly mastered, and it is suggested that bronchoscopy should be postponed for those patients who is not in urgent situation.

Grunewald, M. E., et al. (2020). "Murine Coronavirus Infection Activates the Aryl Hydrocarbon Receptor in an Indoleamine 2,3-Dioxygenase-Independent Manner, Contributing to Cytokine Modulation and Proviral TCDD-Inducible-PARP Expression." J Virol **94**(3).

The aryl hydrocarbon receptor (AhR) is a cytoplasmic receptor/transcription factor that modulates several cellular and immunological processes following activation by pathogen-associated stimuli, though its role during virus infection is largely unknown. Here, we show that AhR is activated in cells infected with mouse hepatitis virus (MHV), a coronavirus (CoV), and contributes to the upregulation of downstream effector TCDD-inducible poly (ADP-ribose) polymerase (TiPARP) during infection. Knockdown of TiPARP reduced viral replication and increased interferon expression, suggesting that TiPARP functions in a proviral manner during MHV infection. We also show that MHV replication induced the expression of other genes known to be downstream of AhR in macrophages and dendritic cells and in livers of infected mice. Further, we found that chemically inhibiting or activating AhR reciprocally modulated the expression levels of cytokines induced by infection, specifically, interleukin 1beta (IL-1beta), IL-10, and tumor necrosis factor alpha (TNF-alpha), consistent with a role for AhR activation in the host response to MHV infection. Furthermore, while indoleamine 2,3-dioxygenase (IDO1) drives AhR activation in other settings, MHV infection induced equal expression of downstream genes in wild-type (WT) and IDO1(-/-) macrophages, suggesting an alternative pathway of AhR activation. In summary, we show that coronaviruses elicit AhR activation by an IDO1-independent pathway, contributing to upregulation of downstream effectors, including the proviral factor TiPARP, and to modulation of cytokine gene expression, and we identify a previously unappreciated role for AhR signaling in CoV pathogenesis.IMPORTANCE Coronaviruses are a family of positive-sense RNA viruses with human and agricultural significance. Characterizing the mechanisms by which coronavirus infection dictates pathogenesis or counters the host immune response would provide targets for the development of therapeutics. Here, we show that the aryl hydrocarbon receptor (AhR) is activated in cells infected with a prototypic coronavirus, mouse hepatitis virus (MHV), resulting in the expression of several effector genes. AhR is important for modulation of the host immune response to MHV and plays a role in the expression of TiPARP, which we show is required for maximal viral replication. Taken together, our findings highlight a previously unidentified role for AhR in regulating coronavirus replication and the immune response to the virus.

Guan, C. S., et al. (2020). "Imaging Features of Coronavirus disease 2019 (COVID-19): Evaluation on Thin-Section CT." Acad Radiol.

RATIONALE AND OBJECTIVES: To retrospectively analyze the chest imaging findings in patients with coronavirus disease 2019 (COVID-19) on thin-section CT. MATERIALS AND METHODS: Fifty-three patients with confirmed COVID-19 infection underwent thin-section CT examination. Two chest radiologists independently evaluated the imaging in terms of distribution, ground-glass opacity (GGO), consolidation, air bronchogram, stripe, enlarged mediastinal lymph node, and pleural effusion. RESULTS: Fourty-seven cases (88.7%) had findings of COVID-19 infection, and the other six (11.3%) were normal. Among the 47 cases, 78.7% involved both lungs, and 93.6% had peripheral infiltrates distributed along the subpleural area. All cases showed GGO, 59.6% of which were round and 40.4% patchy. Other imaging features included "crazy-paving pattern" (89.4%), consolidation (63.8%), and air bronchogram (76.6%). Air bronchograms were observed within GGO (61.7%) and consolidation (70.3%). Neither enlarged mediastinal lymph nodes nor pleural effusion were present. Thirty-three patients (62.3%) were followed an average interval of 6.2 +/- 2.9 days. The lesions increased in 75.8% and resorbed in 24.2% of patients. CONCLUSION: COVID-19 showed the pulmonary lesions in patients infected with COVID-19 were predominantly distributed peripherally in the subpleural area.

Guan, G. W., et al. (2020). "[Exploring the mechanism of liver enzyme abnormalities in patients with novel coronavirus-infected pneumonia]." Zhonghua Gan Zang Bing Za Zhi **28**(2): E002.

Objective: To explore and analyze the possible mechanism of liver injury in patients with coronavirus disease 2019 (novel coronavirus pneumonia, NCP). Methods: The correlation between ALT, AST and other liver enzyme changes condition and NCP patients' disease status reported in the literature was comprehensively analyzed. ACE2 expression in liver tissue for novel coronavirus was analyzed based on single cell sequencing (GSE115469) data. RNA-Seq method was used to analyze Ace2 expression and transcription factors related to its expression in liver tissues at various time-points after hepatectomy in mouse model of acute liver injury with partial hepatectomy. t-test or Spearman rank correlation analysis was used for statistical analysis. Results: ALT and AST were abnormally elevated in some patients with novel coronavirus infection, and the rate and extent of ALT and AST elevation in severe NCP patients were higher than those in non-severe patients. Liver tissue results of single cell sequencing and immunohistochemistry showed that ACE2 was only expressed in bile duct epithelial cells of normal liver tissues, and very low in hepatocytes. In a mouse model of acute liver injury with partial hepatectomy, Ace2 expression was down-regulated on the first day, but it was elevated up to twice of the normal level on the third day, and returned to normal level on seventh day when the liver recovered and hepatocyte proliferation stopped. Whether this phenomenon suggests that the bile duct epithelial cells with positive expression of Ace2 participate in the process of liver regeneration after partial hepatectomy deserves further study. In RNA-Seq data, 77 transcription factors were positively correlated with the expression of ACE2 (r > 0.2, FDR < 0.05), which were mainly enriched in the development, differentiation, morphogenesis and cell proliferation of glandular epithelial cells. Conclusion: We assumed that in addition to the over activated inflammatory response in patients with NCP, the up-regulation of ACE2 expression in liver tissue caused by compensatory proliferation of hepatocytes derived from bile duct epithelial cells may also be the possible mechanism of liver tissue injury caused by 2019 novel coronavirus infection.

Han, R., et al. (2020). "Early Clinical and CT Manifestations of Coronavirus Disease 2019 (COVID-19) Pneumonia." AJR Am J Roentgenol: 1-6.

OBJECTIVE. The purpose of this study was to investigate early clinical and CT manifestations of coronavirus disease (COVID-19) pneumonia. MATERIALS AND METHODS. Patients with COVID-19 pneumonia confirmed by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) nucleic acid test (reverse transcription-polymerase chain reaction) were enrolled in this retrospective study. The clinical manifestations, laboratory results, and CT findings were evaluated. RESULTS. One hundred eight patients (38 men, 70 women; age range, 21-90 years) were included in the study. The clinical manifestations were fever in 94 of 108 (87%) patients, dry cough in 65 (60%), and fatigue in 42 (39%). The laboratory results were normal WBC count in 97 (90%) patients and normal or reduced lymphocyte count in 65 (60%). High-sensitivity C-reactive protein level was elevated in 107 (99%) patients. The distribution of involved lobes was one lobe in 38 (35%) patients, two or three lobes in 24 (22%), and four or five lobes in 46 (43%). The major involvement was peripheral (97 patients [90%]), and the common lesion shape was patchy (93 patients [86%]). Sixty-five (60%) patients had ground-glass opacity (GGO), and 44 (41%) had GGO with consolidation. The size of lesions varied from smaller than 1 cm (10 patients [9%]) to larger than 3 cm (56 patients [52%]). Vascular thickening (86 patients [80%]), crazy paving pattern (43 patients [40%]), air bronchogram sign (52 patients [48%]), and halo sign (69 [64%]) were also observed in this study. CONCLUSION. The early clinical and laboratory findings of COVID-19 pneumonia are low to midgrade fever, dry cough, and fatigue with normal WBC count, reduced lymphocyte count, and elevated high-sensitivity C-reactive protein level. The early CT findings are patchy GGO with or without consolidation involving multiple lobes, mainly in the peripheral zone, accompanied by halo sign, vascular thickening, crazy paving pattern, or air bronchogram sign.

Hu, X. H., et al. (2020). "[Thinking of treatment strategies for colorectal cancer patients in tumor hospitals under the background of coronavirus pneumonia]." Zhonghua Wei Chang Wai Ke Za Zhi **23**(3): E002.

In December 2019, a new outbreak of coronavirus pneumonia began to occur. Its pathogen is 2019-nCoV, which has the characteristics of strong infectivity and general susceptibility. The current situation of prevention and control of new coronavirus pneumonia is severe. In this context, as front-line medical workers bearing important responsibilities and pressure, while through strict management strategy, we can minimize the risk of infection exposure. By summarizing the research progress and guidelines in recent years in the fields of colorectal cancer disease screening, treatment strategies (including early colorectal cancer, locally advanced colorectal cancer, obstructive colorectal cancer, metastatic colorectal cancer and the treatment of patients after neoadjuvant therapy), the choice of medication and time limit for adjuvant therapy, the protective measures for patients undergoing emergency surgery, the re-examination of postoperative patients and the protection of medical staff, etc., authors improve treatment strategies in order to provide more choices for patients to obtain the best treatment under the severe epidemic situation of new coronavirus pneumonia. Meanwhile we hope that it can also provide more timely treatment modeling schemes for colleagues.

Huan, C., et al. (2020). "Characterization and evolution of the coronavirus porcine epidemic diarrhoea virus HLJBY isolated in China." Transbound Emerg Dis **67**(1): 65-79.

A strain of porcine epidemic diarrhoea virus (PEDV), namely HLJBY, was isolated in Heilongjiang province, China. To provide insight into the understanding of the phylogenetic and the current epidemiological status of PEDV, PEDV HLJBY was compared with CV777 and other PEDV strains deposited in the GenBank. The homology between the entire genomic nucleotide sequences of PEDV HLJBY and CV777 was 97.7%. The homology of M gene was the highest (99.0%). However, the homology of ORF3 gene was 97.7%, and protein of ORF3 was 90.1%. In addition, HLJBY showed the highest nucleotide identity (99.9%) with PEDV-SX/China/2017 strain and lowest similarity (91.2%) to PEDV/Belgorod/dom/2008 strain. We analysed the changes in S gene and its protein of PEDV HLJBY with 65 historic PEDV strains. The highest nucleotide identity was 99.9% compared with PEDV-

SX/China/2017 strain, and the lowest nucleotide identity was 60.0% compared with PEDV/Belgorod/dom/2008 strain. The length of deduced amino acid sequences of S proteins varied from 1,372 to 1,390 amino acids (aa). Compared with most aa sequences of S proteins, HLJBY exhibited 5 aa deletions (position 55, 59-61, 144). Analysis and comparison of open reading frame 3 (ORF3) proteins between HLJBY strain and other PEDV strains were also focused in this study. We revealed that the length of deduced amino acid sequences of ORF3 proteins was 80-224 aa among tested strains and the identity of HLJBY ORF3 amino acids with other PEDV strains was 71.4%-98.9%. ORF3 protein of both HLJBY strain and PEDV-SX/China/2017 strain consists of 91 aa, with 133 aa deletions at their C' end in relation to the other tested PEDV strains. The phylogenetic tree based on different proteins or genes resulted in different phylogenetic groups. For pathogenicity evaluation of PEDV HLJBY strain, colostrum deprivation piglets were challenged with PEDV HLJBY, and PEDV reference strain CV777 as a control, the results showed that animals challenged with either of these PEDV strains developed diarrhoea, and histopathological examination of small intestines of challenged animals showed acute viral enteritis with villous atrophy in either PEDV HLJBY-P10 or PEDV CV777-P8 inoculated piglets.

Huang, C., et al. (2020). "Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China." Lancet **395**(10223): 497-506.

BACKGROUND: A recent cluster of pneumonia cases in Wuhan, China, was caused by a novel betacoronavirus, the 2019 novel coronavirus (2019-nCoV). We report the epidemiological, clinical, laboratory, and radiological characteristics and treatment and clinical outcomes of these patients. METHODS: All patients with suspected 2019-nCoV were admitted to a designated hospital in Wuhan. We prospectively collected and analysed data on patients with laboratory-confirmed 2019-nCoV infection by real-time RT-PCR and next-generation sequencing. Data were obtained with standardised data collection forms shared by WHO and the International Severe Acute Respiratory and Emerging Infection Consortium from electronic medical records. Researchers also directly communicated with patients or their families to ascertain epidemiological and symptom data. Outcomes were also compared between patients who had been admitted to the intensive care unit (ICU) and those who had not. FINDINGS: By Jan 2, 2020, 41 admitted hospital patients had been identified as having laboratory-confirmed 2019-nCoV infection. Most of the infected patients were men (30 [73%] of 41); less than half had underlying diseases (13 [32%]), including diabetes (eight [20%]), hypertension (six [15%]), and cardiovascular disease (six [15%]). Median age was 49.0 years (IQR 41.0-58.0). 27 (66%) of 41 patients had been exposed to Huanan seafood market. One family cluster was found. Common symptoms at onset of illness were fever (40 [98%] of 41 patients), cough (31 [76%]), and myalgia or fatigue (18 [44%]); less common symptoms were sputum production (11 [28%] of 39), headache (three [8%] of 38), haemoptysis (two [5%] of 39), and diarrhoea (one [3%] of 38). Dyspnoea developed in 22 (55%) of 40 patients (median time from illness onset to dyspnoea 8.0 days [IQR 5.0-13.0]). 26 (63%) of 41 patients had lymphopenia. All 41 patients had pneumonia with abnormal findings on chest CT. Complications included acute respiratory distress syndrome (12 [29%]), RNAaemia (six [15%]), acute cardiac injury (five [12%]) and secondary infection (four [10%]). 13 (32%) patients were admitted to an ICU and six (15%) died. Compared with non-ICU patients, ICU patients had higher plasma levels of IL2, IL7, IL10, GSCF, IP10, MCP1, MIP1A, and TNFalpha. INTERPRETATION: The 2019-nCoV infection caused clusters of severe respiratory illness similar to severe acute respiratory syndrome coronavirus and was associated with ICU admission and high mortality. Major gaps in our knowledge of the origin, epidemiology, duration of human transmission, and clinical spectrum of disease need fulfilment by future studies. FUNDING: Ministry of Science and Technology, Chinese Academy of Medical Sciences, National Natural Science Foundation of China, and Beijing Municipal Science and Technology Commission.

Jang, K. J., et al. (2020). "A high ATP concentration enhances the cooperative translocation of the SARS coronavirus helicase nsP13 in the unwinding of duplex RNA." Sci Rep **10**(1): 4481.

Severe acute respiratory syndrome coronavirus nonstructural protein 13 (SCV nsP13), a superfamily 1 helicase, plays a central role in viral RNA replication through the unwinding of duplex RNA and DNA with a 5' single-stranded tail in a 5' to 3' direction. Despite its putative role in viral RNA replication, nsP13 readily unwinds duplex DNA by cooperative translocation. Herein, nsP13 exhibited different characteristics in duplex RNA unwinding than that in duplex DNA. nsP13 showed very poor processivity on duplex RNA compared with that on duplex DNA. More importantly, nsP13 inefficiently unwinds duplex RNA by increasing the 5'-ss tail length. As the concentration of nsP13 increased, the amount of unwound duplex DNA increased and that of unwound duplex RNA decreased. The accumulation of duplex RNA/nsP13 complexes increased as the concentration of nsP13 increased. An increased ATP concentration in the unwinding of duplex RNA relieved the decrease in duplex RNA unwinding. Thus, nsP13 has a strong affinity for duplex RNA as a substrate for the unwinding reaction, which requires increased ATPs to processively unwind duplex RNA. Our results suggest that duplex RNA is a preferred substrate for the helicase activity of nsP13 than duplex DNA at high ATP concentrations.

Jang, W. M., et al. (2020). "Influence of trust on two different risk perceptions as an affective and cognitive dimension during Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak in South Korea: serial cross-sectional surveys." BMJ Open **10**(3): e033026.

OBJECTIVES: This study aimed to assess the affective and cognitive risk perceptions in the general population of Middle East respiratory syndrome (MERS) during the 2015 MERS coronavirus (MERS-CoV) outbreak in South Korea and the influencing factors. DESIGN: Serial cross-sectional design with four consecutive surveys. SETTING: Nationwide general population in South Korea. PARTICIPANTS: Overall 4010 respondents (aged 19 years and over) from the general population during the MERS-CoV epidemic were included. PRIMARY AND SECONDARY OUTCOME MEASURES: The main outcome measures were (1) affective risk perception, (2) cognitive risk perception, and (3) trust in the government. Multivariate logistic regression models were used to identify factors (demographic, socioeconomic, area and political orientation) associated with risk perceptions. RESULTS: Both affective and cognitive risk perceptions decreased as the MERS-CoV epidemic progressed. Proportions of affective risk perception were higher in all surveys and slowly decreased compared with cognitive risk perception over time. Females (adjusted OR (aOR) 1.72-2.00; 95% CI 1.14 to 2.86) and lower self-reported household economic status respondents were more likely to perceive the affective risk. The older the adults, the higher the affective risk perception, but the lower the cognitive risk perception compared with younger adults. The respondents who had low trust in the government had higher affective (aOR 2.19-3.11; 95 CI 1.44 to 4.67) and cognitive (aOR 3.55-5.41; 95 CI 1.44 to 9.01) risk perceptions. CONCLUSIONS: This study suggests that even if cognitive risk perception is dissolved, affective risk perception can continue during MERS-CoV epidemic. Risk perception associating factors (ie, gender, age and self-reported household economic status) appear to be noticeably different between affective and cognitive dimensions. It also indicates that trust in the government influences affective risk perception and cognitive risk perception. There is a need for further efforts to understand the mechanism regarding the general public's risk perception for effective risk communication.

Jazieh, A. R., et al. (2020). "Outcome of Oncology Patients Infected With Coronavirus." JCO Glob Oncol **6**: 471-475.

PURPOSE: This study investigated the features of oncology patients with confirmed Middle East respiratory syndrome (MERS) at the Ministry of National Guard Health Affairs-Riyadh during the outbreak of June 2015 to determine the clinical course and outcome of affected patients. METHODS: The patients' demographic information, cancer history, treatment pattern, information about MERS-coronavirus (CoV) infection, history of travel, clinical symptoms, test results, and outcome were collected and analyzed as part of a quality improvement project to improve the care and safety of our patients. Only patients with confirmed infection were included. RESULTS: A total of 19 patients were identified, with a median age of 66 years (range, 16-88 years), and 12 patients (63%) were males. The most common underlying disease was hematologic malignancies (47.4%), followed by colorectal cancer (21%) and lung cancer (15.8%). Hypertension and diabetes mellitus were the most common comorbidities (57.9% and 52.6%, respectively). Infection was diagnosed by nasopharyngeal swab in all patients. All patients contracted the infection during their hospitalization for other reasons. Sixteen patients (80%) were admitted to the intensive care unit; 13 patients (81%) had acute respiratory distress syndrome, 11 were intubated (68.75%), 9 had acute renal injury (56.25%), and 3 required dialysis (18.75%). Only 3 patients (15.8%) with early-stage cancers survived. Patients with hematologic malignancies and advanced solid tumors had a 100% case fatality rate. The majority of the causes of death were due to multi-organ failure and septic shock. CONCLUSION: MERS-CoV infection resulted in a high case fatality rate in patients with malignancy. Therefore, it is critical to implement effective primary preventive measures to avoid exposure of patients with cancer to the virus.

Jernigan, D. B. and C. C.-R. Team (2020). "Update: Public Health Response to the Coronavirus Disease 2019 Outbreak - United States, February 24, 2020." MMWR Morb Mortal Wkly Rep **69**(8): 216-219.

An outbreak of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) began in Wuhan, Hubei Province, China in December 2019, and has spread throughout China and to 31 other countries and territories, including the United States (1). As of February 23, 2020, there were 76,936 reported cases in mainland China and 1,875 cases in locations outside mainland China (1). There have been 2,462 associated deaths worldwide; no deaths have been reported in the United States. Fourteen cases have been diagnosed in the United States, and an additional 39 cases have occurred among repatriated persons from high-risk settings, for a current total of 53 cases within the United States. This report summarizes the aggressive measures (2,3) that CDC, state and local health departments, multiple other federal agencies, and other partners are implementing to slow and try to contain transmission of COVID-19 in the United States. These measures require the identification of cases and contacts of persons with COVID-19 in the United States and the recommended assessment, monitoring, and care of travelers arriving from areas with substantial COVID-19 transmission. Although these measures might not prevent widespread transmission of the virus in the United States, they are being implemented to 1) slow the spread of illness; 2) provide time to better prepare state and local health departments, health care systems, businesses, educational organizations, and the general public in the event that widespread transmission occurs; and 3) better characterize COVID-19 to guide public health recommendations and the development and deployment of medical countermeasures, including diagnostics, therapeutics, and vaccines. U.S. public health authorities are monitoring the situation closely, and CDC is coordinating efforts with the World Health Organization (WHO) and other global partners. Interim guidance is available at https://www.cdc.gov/coronavirus/index.html. As more is learned about this novel virus and this outbreak, CDC will rapidly incorporate new knowledge into guidance for action by CDC, state and local health departments, health care providers, and communities.

Ji, W., et al. (2020). "Cross-species transmission of the newly identified coronavirus 2019-nCoV." J Med Virol **92**(4): 433-440.

The current outbreak of viral pneumonia in the city of Wuhan, China, was caused by a novel coronavirus designated 2019-nCoV by the World Health Organization, as determined by sequencing the viral RNA genome. Many initial patients were exposed to wildlife animals at the Huanan seafood wholesale market, where poultry, snake, bats, and other farm animals were also sold. To investigate possible virus reservoir, we have carried out comprehensive sequence analysis and comparison in conjunction with relative synonymous codon usage (RSCU) bias among different animal species based on the 2019-nCoV sequence. Results obtained from our analyses suggest that the 2019-nCoV may appear to be a recombinant virus between the bat coronavirus and an origin-unknown coronavirus. The recombination may occurred within the viral spike glycoprotein, which recognizes a cell surface receptor. Additionally, our findings suggest that 2019-nCoV has most similar genetic information with bat coronovirus and most similar codon usage bias with snake. Taken together, our results suggest that homologous recombination may occur and contribute to the 2019-nCoV cross-species transmission.

Kang, X., et al. (2020). "[Anesthesia management in cesarean section for a patient with coronavirus disease 2019]." Zhejiang Da Xue Xue Bao Yi Xue Ban **49**(1): 0.

Since the corona virus disease 2019 (COVID-19) affects the cardio-pulmonary function of pregnant women, the anesthetic management in the cesarean section for the patients, as well as the protection for medical staff is significantly different from that in ordinary surgical operation. This paper reports a pregnant woman with COVID-19, for whom a cesarean section was successfully performed in our hospital on February 8, 2020. Anesthetic management, protection of medical staff and psychological intervention for the patients during the operation are discussed. Importance should be attached to the preoperative evaluation of pregnant women with COVID-19 and the implementation of anesthesia plan. For ordinary COVID-19 patients intraspinal anesthesia is preferred in cesarean section, and the influence on respiration and circulation in both maternal and infant should be reduced; while for severe or critically ill patients general anesthesia with endotracheal intubation should be adopted. The safety of medical environment should be ensured, and level- standard protection should be taken for anesthetists. Special attention and support should be given to maternal psychology. It is important to give full explanation before operation to reduce anxiety; to relieve the discomfort during operation to reduce tension; to avoid the bad mood of patients due to pain after operation.

Kannan, S., et al. (2020). "COVID-19 (Novel Coronavirus 2019) - recent trends." Eur Rev Med Pharmacol Sci **24**(4): 2006-2011.

The World Health Organization (WHO) has issued a warning that, although the 2019 novel coronavirus (COVID-19) from Wuhan City (China), is not pandemic, it should be contained to prevent the global spread. The COVID-19 virus was known earlier as 2019-nCoV. As of 12 February 2020, WHO reported 45,171 cases and 1115 deaths related to COVID-19. COVID-19 is similar to Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) virus

in its pathogenicity, clinical spectrum, and epidemiology. Comparison of the genome sequences of COVID-19, SARS-CoV, and Middle East Respiratory Syndrome coronavirus (MERS-CoV) showed that COVID-19 has a better sequence identity with SARS-CoV compared to MERS CoV. However, the amino acid sequence of COVID-19 differs from other coronaviruses specifically in the regions of 1ab polyprotein and surface glycoprotein or S-protein. Although several animals have been speculated to be a reservoir for COVID-19, no animal reservoir has been already confirmed. COVID-19 causes COVID-19 disease that has similar symptoms as SARS-CoV. Studies suggest that the human receptor for COVID-19 may be angiotensin-converting enzyme 2 (ACE2) receptor similar to that of SARS-CoV. The nucleocapsid (N) protein of COVID-19 has nearly 90% amino acid sequence identity with SARS-CoV. The N protein antibodies of SARS-CoV may cross react with COVID-19 but may not provide cross-immunity. In a similar fashion to SARS-CoV, the N protein of COVID-19 may play an important role in suppressing the RNA interference (RNAi) to overcome the host defense. This mini-review aims at investigating the most recent trend of COVID-19.

Killerby, M. E., et al. (2020). "Middle East Respiratory Syndrome Coronavirus Transmission." Emerg Infect Dis **26**(2): 191-198.

Middle East respiratory syndrome coronavirus (MERS-CoV) infection causes a spectrum of respiratory illness, from asymptomatic to mild to fatal. MERS-CoV is transmitted sporadically from dromedary camels to humans and occasionally through human-to-human contact. Current epidemiologic evidence supports a major role in transmission for direct contact with live camels or humans with symptomatic MERS, but little evidence suggests the possibility of transmission from camel products or asymptomatic MERS cases. Because a proportion of case-patients do not report direct contact with camels or with persons who have symptomatic MERS, further research is needed to conclusively determine additional mechanisms of transmission, to inform public health practice, and to refine current precautionary recommendations.

Kim, J. M., et al. (2020). "Identification of Coronavirus Isolated from a Patient in Korea with COVID-19." Osong Public Health Res Perspect **11**(1): 3-7.

Objectives: Following reports of patients with unexplained pneumonia at the end of December 2019 in Wuhan, China, the causative agent was identified as coronavirus (SARS-CoV-2), and the 2019 novel coronavirus disease was named COVID-19 by the World Health Organization. Putative patients with COVID-19 have been identified in South Korea, and attempts have been made to isolate the pathogen from these patients. Methods: Upper and lower respiratory tract secretion samples from putative patients with COVID-19 were inoculated onto cells to isolate the virus. Full genome sequencing and electron microscopy were used to identify the virus. Results: The virus replicated in Vero cells and cytopathic effects were observed. Full genome sequencing showed that the virus genome exhibited sequence homology of more than 99.9% with SARS-CoV-2 which was isolated from patients from other countries, for instance China. Sequence homology of SARS-CoV-2 with SARS-CoV, and MERS-CoV was 77.5% and 50%, respectively. Coronavirus-specific morphology was observed by electron microscopy in virus-infected Vero cells. Conclusion: SARS-CoV-2 was isolated from putative patients with unexplained pneumonia and intermittent coughing and fever. The isolated virus was named BetaCoV/Korea/KCDC03/2020.

Kim, J. Y., et al. (2020). "The First Case of 2019 Novel Coronavirus Pneumonia Imported into Korea from Wuhan, China: Implication for Infection Prevention and Control Measures." J Korean Med Sci **35**(5): e61.

In December 2019, a viral pneumonia outbreak caused by a novel betacoronavirus, the 2019 novel coronavirus (2019-nCoV), began in Wuhan, China. We report the epidemiological and clinical features of the first patient with 2019-nCoV pneumonia imported into Korea from Wuhan. This report suggests that in the early phase of 2019-nCoV pneumonia, chest radiography would miss patients with pneumonia and highlights taking travel history is of paramount importance for early detection and isolation of 2019-nCoV cases.

Kinross, P., et al. (2020). "Rapidly increasing cumulative incidence of coronavirus disease (COVID-19) in the European Union/European Economic Area and the United Kingdom, 1 January to 15 March 2020." Euro Surveill **25**(11).

The cumulative incidence of coronavirus disease (COVID-19) cases is showing similar trends in European Union/European Economic Area countries and the United Kingdom confirming that, while at a different stage depending on the country, the COVID-19 pandemic is progressing rapidly in all countries. Based on the experience from Italy, countries, hospitals and intensive care units should increase their preparedness for a surge of patients with COVID-19 who will require healthcare, and in particular intensive care.

Koonin, L. M. (2020). "Novel coronavirus disease (COVID-19) outbreak: Now is the time to refresh pandemic plans." J Bus Contin Emer Plan **13**(4): 1-15.

This article outlines practical steps that businesses can take now to prepare for a pandemic. Given the current growing spread of coronavirus disease 2019 (COVID-19) around the world, it is imperative that businesses review their pandemic plans and be prepared in case this epidemic expands and affects more people and communities. Preparing for a potential infectious disease pandemic from influenza or a novel corona virus is an essential component of a business continuity plan, especially for businesses that provide critical healthcare and infrastructure services. Although many businesses and organisations have a pandemic plan or address pandemic preparedness in their business continuity plans, few have recently tested and updated their plans. Pandemics can not only interrupt an organisation's operations and compromise long-term viability of an enterprise, but also disrupt the provision of critical functions. Businesses that regularly test and update their pandemic plan can significantly reduce harmful impacts to the business, play a key role in protecting employees' and customers' health and safety, and limit the negative impact of a pandemic on the community and economy.

Kooraki, S., et al. (2020). "Coronavirus (COVID-19) Outbreak: What the Department of Radiology Should Know." J Am Coll Radiol.

In December 2019, a novel coronavirus (COVID-19) pneumonia emerged in Wuhan, China. Since then, this highly contagious COVID-19 has been spreading worldwide, with a rapid rise in the number of deaths. Novel COVID-19-infected pneumonia (NCIP) is characterized by fever, fatigue, dry cough, and dyspnea. A variety of chest imaging features have been reported, similar to those found in other types of coronavirus syndromes. The purpose of the present review is to briefly discuss the known epidemiology and the imaging findings of coronavirus syndromes, with a focus on the reported imaging findings of NCIP. Moreover, the authors review precautions and safety measures for radiology department personnel to manage patients with known or suspected NCIP. Implementation of a robust plan in the radiology department is required to prevent further transmission of the virus to patients and department staff members.

Korean Society of Infectious, D., et al. (2020). "Report on the Epidemiological Features of Coronavirus Disease 2019 (COVID-19) Outbreak in the Republic of Korea from January 19 to March 2, 2020." J Korean Med Sci **35**(10): e112.

Since the first case of coronavirus disease19 (COVID-19) was reported in Wuhan, China, as of March 2, 2020, the total number of confirmed cases of COVID-19 was 89,069 cases in 67 countries and regions. As of 0 am, March 2, 2020, the Republic of Korea had the second-largest number of confirmed cases (n = 4,212) after China (n = 80,026). This report summarizes the epidemiologic features and the snapshots of the outbreak in the Republic of Korea from January 19 and March 2, 2020.

Kritas, S. K., et al. (2020). "Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy." J Biol Regul Homeost Agents **34**(1).

Coronavirus can cause respiratory syndrome which to date has affected about twelve thousand individuals, especially in China. Coronavirus is interspecies and can also be transmitted from man to man, with an incubation ranging from 1 to 14 days. Human coronavirus infections can induce not only mild to severe respiratory diseases, but also inflammation, high fever, cough, acute respiratory tract infection and dysfunction of internal organs that may lead to death. Coronavirus infection (regardless of the various types of corona virus) is primarily attacked by immune cells including mast cells (MCs), which are located in the submucosa of the respiratory tract and in the nasal cavity and represent a barrier of protection against microorganisms. Viral activate MCs release early inflammatory chemical copounds including histamine and protease; while late activation provoke the generation of pro-inflammatory IL-1 family members including IL-1, IL-6 and IL-33. Here, we propose for the first time that inflammation by coronavirus maybe inhibited by anti-inflammatory cytokines belonging to the IL-1 family members.

Kruse, R. L. (2020). "Therapeutic strategies in an outbreak scenario to treat the novel coronavirus originating in Wuhan, China." F1000Res **9**: 72.

A novel coronavirus (2019-nCoV) originating in Wuhan, China presents a potential respiratory viral pandemic to the world population. Current efforts are focused on containment and quarantine of infected individuals. Ultimately, the outbreak could be controlled with a protective vaccine to prevent 2019-nCoV infection. While vaccine research should be pursued intensely, there exists today no therapy to treat 2019-nCoV upon infection, despite an urgent need to find options to help these patients and preclude potential death. Herein, I review the potential options to treat 2019-nCoV in patients, with an emphasis on the necessity for speed and timeliness in developing new and effective therapies in this outbreak. I consider the options of drug repurposing, developing neutralizing monoclonal antibody therapy, and an oligonucleotide strategy targeting the viral RNA genome, emphasizing the promise and pitfalls of these approaches. Finally, I advocate for the fastest strategy to develop a treatment now, which could be resistant to any mutations the virus may have in the future. The proposal is a biologic that blocks 2019-nCoV entry using a soluble version of the viral receptor, angiotensin-converting enzyme 2 (ACE2), fused to an immunoglobulin Fc domain, providing a neutralizing antibody with maximal breath to avoid any viral escape, while also helping to recruit the immune system to build lasting immunity. The sequence of the ACE2-Fc protein is provided to investigators, allowing its possible use in recombinant protein expression systems to start producing drug today to treat patients under compassionate use, while formal clinical trials are later undertaken. Such a treatment could help infected patients before a protective vaccine is developed and widely available in the coming months to year (s).

Kumar, S., et al. (2020). "Structural, glycosylation and antigenic variation between 2019 novel coronavirus (2019-nCoV) and SARS coronavirus (SARS-CoV)." Virusdisease **31**(1): 13-21.

The emergence of 2019 novel coronavirus (2019-nCoV) is of global concern and might have emerged from RNA recombination among existing coronaviruses. CoV spike (S) protein which is crucial for receptor binding, membrane fusion via conformational changes, internalization of the virus, host tissue tropism and comprises crucial targets for vaccine development, remain largely uncharacterized. Therefore, the present study has been planned to determine the sequence variation, structural and antigenic divergence of S glycoprotein which may be helpful for the management of 2019-nCoV infection. The sequences of spike glycoprotein of 2019-nCoV and SARS coronavirus (SARS-CoV) were used for the comparison. The sequence variations were determined using EMBOSS Needle pairwise sequence alignment tools. The variation in glycosylation sites was predicted by NetNGlyc 1.0 and validated by N-GlyDE server. Antigenicity was predicted by NetCTL 1.2 and validated by IEDB Analysis Resource server. The structural divergence was determined by using SuperPose Version 1.0 based on cryo-EM structure of the SARS coronavirus spike glycoprotein. Our data suggests that 2019-nCoV is newly spilled coronavirus into humans in China is closely related to SARS-CoV, which has only 12.8% of difference with SARS-CoV in S protein and has 83.9% similarity in minimal receptor-binding domain with SARS-CoV. Addition of a novel glycosylation sites were observed in 2019-nCoV. In addition, antigenic analysis proposes that great antigenic differences exist between both the viral strains, but some of the epitopes were found to be similar between both the S proteins. In spite of the variation in S protein amino acid composition, we found no significant difference in their structures. Collectively, for the first time our results exhibit the emergence of human 2019-nCoV is closely related to predecessor SARS-CoV and provide the evidence that 2019-nCoV uses various novel glycosylation sites as SARS-CoV and may have a potential to become pandemic owing its antigenic discrepancy. Further, demonstration of novel Cytotoxic T lymphocyte epitopes may impart opportunities for the development of peptide based vaccine for the prevention of 2019-nCoV.

Lai, C. C., et al. (2020). "Asymptomatic carrier state, acute respiratory disease, and pneumonia due to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): Facts and myths." J Microbiol Immunol Infect.

Since the emergence of coronavirus disease 2019 (COVID-19) (formerly known as the 2019 novel coronavirus [2019-nCoV]) in Wuhan, China in December 2019, which is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), more than 75,000 cases have been reported in 32 countries/regions, resulting in more than 2000 deaths worldwide. Despite the fact that most COVID-19 cases and mortalities were reported in China, the WHO has declared this outbreak as the sixth public health emergency of international concern. The COVID-19 can present as an asymptomatic carrier state, acute respiratory disease, and pneumonia. Adults represent the population with the highest infection rate; however, neonates, children, and elderly patients can also be infected by SARS-CoV-2. In addition, nosocomial infection of hospitalized patients and healthcare workers, and viral transmission from asymptomatic carriers are possible. The most common finding on chest imaging among patients with pneumonia was ground-glass opacity with bilateral involvement. Severe cases are more likely to be older patients with underlying comorbidities compared to mild cases. Indeed, age and disease severity may be correlated with the outcomes of COVID-19. To date, effective treatment is lacking; however, clinical trials investigating the efficacy of several agents, including remdesivir and chloroquine, are underway in China. Currently, effective infection control intervention is the only way to prevent the spread of SARS-CoV-2.

Lai, C. C., et al. (2020). "Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): The epidemic and the challenges." Int J Antimicrob Agents **55**(3): 105924.

The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2; previously provisionally named 2019 novel coronavirus or 2019-nCoV) disease (COVID-19) in China at the end of 2019 has caused a large global outbreak and is a major public health issue. As of 11 February 2020, data from the World Health Organization (WHO) have shown that more than 43 000 confirmed cases have been identified in 28 countries/regions, with >99% of cases being detected in China. On 30 January 2020, the WHO declared COVID-19 as the sixth public health emergency of international concern. SARS-CoV-2 is closely related to two bat-derived severe acute respiratory syndrome-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21. It is spread by human-to-human transmission via droplets or direct contact, and infection has been estimated to have mean incubation period of 6.4 days and a basic reproduction number of 2.24-3.58. Among patients with pneumonia caused by SARS-CoV-2 (novel coronavirus pneumonia or Wuhan pneumonia), fever was the most common symptom, followed by cough. Bilateral lung involvement with ground-glass opacity was the most common finding from computed tomography images of the chest. The one case of SARS-CoV-2 pneumonia in the USA is responding well to remdesivir, which is now undergoing a clinical trial in China. Currently, controlling infection to prevent the spread of SARS-CoV-2 is the primary intervention being used. However, public health authorities should keep monitoring the situation closely, as the more we can learn about this novel virus and its associated outbreak, the better we can respond.

Lai, C. C., et al. (2020). "Global epidemiology of coronavirus disease 2019: disease incidence, daily cumulative index, mortality, and their association with country healthcare resources and economic status." Int J Antimicrob Agents: 105946.

It has been 2 months since the first case of coronavirus disease 2019 (COVID-19) was reported in Wuhan. So far, COVID-19 has affected 84,503 patients in 57 countries/territories and caused 2,924 deaths in nine countries. However, the epidemiology data differ across countries. Although China had higher morbidity and mortality than other sites, the number of new cases per day in China is lesser than that outside of China since February 26, 2020. The incidence ranged from 61.4 per 1,000,000 people in Republic of Korea to 0.0002 per 1,000,000 people in India. The daily cumulative index (DCI) of COVID-19 (cumulative cases/no. of days between the first reported case and February 29, 2020) was greatest in China (1,320.85 per day), followed by Republic of Korea (78.78 per day), Iran (43.11 per day), and Italy (30.62 per day). However, the DCI in other countries/territories were less than 10 per day. Several effective measures including restricting travel from China, controlling the distribution of masks, extensive investigation of COVID-19 spread, and at once daily press conference by government to inform and educate people were aggressively conducted in Taiwan. This is probably the reason why there was only 39 cases (as of February 29, 2020) with a DCI of 1 case per day in Taiwan, which was much lower than that of nearby countries, such as Republic of Korea and Japan. Additionally, the incidence and mortality were correlated with DCI. However, further study and continued monitoring are needed to better understand the underlying mechanism of COVID-19.

Lai, J., et al. (2020). "Factors Associated With Mental Health Outcomes Among Health Care Workers Exposed to Coronavirus Disease 2019." JAMA Netw Open **3**(3): e203976.

Importance: Health care workers exposed to coronavirus disease 2019 (COVID-19) could be psychologically stressed. Objective: To assess the magnitude of mental health outcomes and associated factors among health care workers treating patients exposed to COVID-19 in China. Design, Settings, and Participants: This cross-sectional, survey-based, region-stratified study collected demographic data and mental health measurements from 1257 health care workers in 34 hospitals from January 29, 2020, to February 3, 2020, in China. Health care workers in hospitals equipped with fever clinics or wards for patients with COVID-19 were eligible. Main Outcomes and Measures: The degree of symptoms of depression, anxiety, insomnia, and distress was assessed by the Chinese versions of the 9-item Patient Health Questionnaire, the 7-item Generalized Anxiety Disorder scale, the 7-item Insomnia Severity Index, and the 22-item Impact of Event Scale-Revised, respectively. Multivariable logistic regression analysis was performed to identify factors associated with mental health outcomes. Results: A total of 1257 of 1830 contacted individuals completed the survey, with a participation rate of 68.7%. A total of 813 (64.7%) were aged 26 to 40 years, and 964 (76.7%) were women. Of all participants, 764 (60.8%) were nurses, and 493 (39.2%) were physicians; 760 (60.5%) worked in hospitals in Wuhan, and 522 (41.5%) were frontline health care workers. A considerable proportion of participants reported symptoms of depression (634 [50.4%]), anxiety (560 [44.6%]), insomnia (427 [34.0%]), and distress (899 [71.5%]). Nurses, women, frontline health care workers, and those working in Wuhan, China, reported more severe degrees of all measurements of mental health symptoms than other health care workers (eg, median [IQR] Patient Health Questionnaire scores among physicians vs nurses: 4.0 [1.0-7.0] vs 5.0 [2.0-8.0]; P =.007; median [interquartile range {IQR}] Generalized Anxiety Disorder scale scores among men vs women: 2.0 [0-6.0] vs 4.0 [1.0-7.0]; P <.001; median [IQR] Insomnia Severity Index scores among frontline vs second-line workers: 6.0 [2.0-11.0] vs 4.0 [1.0-8.0]; P <.001; median [IQR] Impact of Event Scale-Revised scores among those in Wuhan vs those in Hubei outside Wuhan and those outside Hubei: 21.0 [8.5-34.5] vs 18.0 [6.0-28.0] in Hubei outside Wuhan and 15.0 [4.0-26.0] outside Hubei; P <.001). Multivariable logistic regression analysis showed participants from outside Hubei province were associated with lower risk of experiencing symptoms of distress compared with those in Wuhan (odds ratio [OR], 0.62; 95% CI, 0.43-0.88; P =.008). Frontline health care workers engaged in direct diagnosis, treatment, and care of patients with COVID-19 were associated with a higher risk of symptoms of depression (OR, 1.52; 95% CI, 1.11-2.09; P =.01), anxiety (OR, 1.57; 95% CI, 1.22-2.02; P <.001), insomnia (OR, 2.97; 95% CI, 1.92-4.60; P <.001), and distress (OR, 1.60; 95% CI, 1.25-2.04; P <.001). Conclusions and Relevance: In this survey of heath care workers in hospitals equipped with fever clinics or wards for patients with COVID-19 in Wuhan and other regions in China, participants reported experiencing psychological burden, especially nurses, women, those in Wuhan, and frontline health care workers directly engaged in the diagnosis, treatment, and care for patients with COVID-19.

Lai, T. H. T., et al. (2020). "Stepping up infection control measures in ophthalmology during the novel coronavirus outbreak: an experience from Hong Kong." Graefes Arch Clin Exp Ophthalmol.

PURPOSE: Coronavirus disease (COVID-19) has rapidly emerged as a global health threat. The purpose of this article is to share our local experience of stepping up infection control measures in ophthalmology to minimise COVID-19 infection of both healthcare workers and patients. METHODS: Infection control measures implemented in our ophthalmology clinic are discussed. The measures are based on detailed risk assessment by both local ophthalmologists and infection control experts. RESULTS: A three-level hierarchy of control measures was adopted. First, for administrative control, in order to lower patient attendance, text messages with an enquiry phone number were sent to patients to reschedule appointments or arrange drug refill. In order to minimise cross-infection of COVID-19, a triage system was set up to identify patients with fever, respiratory symptoms, acute conjunctivitis or recent travel to outbreak areas and to encourage these individuals to postpone their appointments for at least 14 days. Micro-aerosol generating procedures, such as non-contact tonometry and operations under general anaesthesia were avoided. Nasal endoscopy was avoided as it may provoke sneezing and cause generation of droplets. All elective clinical services were suspended. Infection control training was provided to all clinical staff. Second, for environmental control, to reduce droplet transmission of COVID-19, installation of protective shields on slit lamps, frequent disinfection of equipment, and provision of eye protection to staff were implemented. All staff were advised to measure their own body temperatures before work and promptly report any symptoms of upper respiratory tract infection, vomiting or diarrhoea. Third, universal masking, hand hygiene, and appropriate use of personal protective equipment (PPE) were promoted. CONCLUSION: We hope our initial experience in stepping up infection control measures for COVID-19 infection in ophthalmology can help ophthalmologists globally to prepare for the potential community outbreak or pandemic. In order to minimise transmission of COVID-19, ophthalmologists should work closely with local infection control teams to implement infection control measures that are appropriate for their own clinical settings.

Leung, C. (2020). "Clinical features of deaths in the novel coronavirus epidemic in China." Rev Med Virol: e2103.

In response to the recent novel coronavirus outbreak originating in Wuhan, Hubei province, China, observations concerning novel coronavirus mortality are of urgent public health importance. The present work presents the first review of the fatal novel coronavirus cases in China. Clinical data of fatal cases published by the Chinese Government were studied. As of 2 February 2020, the clinical data of 46 fatal cases were identified. The case fatality rate was significantly higher in Hubei province than the rest of China. While 67% of all deceased patients were male, gender was unlikely to be associated with mortality. Diabetes was likely to be associated with mortality. There is, however, not yet sufficient evidence to support the association between hypertension and mortality as similar prevalence of hypertension was also observed in the Hubei population.

Li, G., et al. (2020). "Coronavirus infections and immune responses." J Med Virol **92**(4): 424-432.

Coronaviruses (CoVs) are by far the largest group of known positive-sense RNA viruses having an extensive range of natural hosts. In the past few decades, newly evolved Coronaviruses have posed a global threat to public health. The immune response is essential to control and eliminate CoV infections, however, maladjusted immune responses may result in immunopathology and impaired pulmonary gas exchange. Gaining a deeper understanding of the interaction between Coronaviruses and the innate immune systems of the hosts may shed light on the development and persistence of inflammation in the lungs and hopefully can reduce the risk of lung inflammation caused by CoVs. In this review, we provide an update on CoV infections and relevant diseases, particularly the host defense against CoV-induced inflammation of lung tissue, as well as the role of the innate immune system in the pathogenesis and clinical treatment.

Li, H., et al. (2020). "The novel coronavirus outbreak: what can be learned from China in public reporting?" Glob Health Res Policy **5**: 9.

The new coronavirus outbreak gets everyone's attention. China's national actions against the outbreak have contributed great contributions to the world. China has been learning from practice for better reporting and is fast to adapt itself. In this article we discuss China's practice in public reporting and its implications to global health. Confirmed cases, dynamic suspected cases, recovered cases, and deaths have been reported both in accumulative numbers and their daily updates. Some ratio indictors reporting (fatality rate, recovery rate, etc.), trend reporting, and global surveillance have been applied as well. Some improvements can still be made. It is necessary to further explore the influential factors behind the indicators for interventions. Recommendations are made to the World Health Organization and other countries for better public reporting and surveillance.

Li, H., et al. (2020). "[Potential antiviral therapeutics for 2019 Novel Coronavirus]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 170-172.

The recent outbreak of respiratory illness in Wuhan, China is caused by a novel coronavirus, named 2019-nCoV, which is genetically close to a bat-derived coronavirus. 2019-nCoV is categorized as beta genus coronavirus, same as the two other strains- severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV). Antiviral drugs commonly used in clinical practice, including neuraminidase inhibitors (oseltamivir, paramivir, zanamivir, etc.), ganciclovir, acyclovir and ribavirin, are invalid for 2019-nCoV and not recommended. Drugs are possibly effective for 2019-nCoV include: remdesivir, lopinavir/ritonavir, lopinavir/ritonavir combined with interferon-beta, convalescent plasma, and monoclonal antibodies. But the efficacy and safety of these drugs for 2019-nCoV pneumonia patients need to be assessed by further clinical trials.

Li, K. and P. B. McCray, Jr. (2020). "Development of a Mouse-Adapted MERS Coronavirus." Methods Mol Biol **2099**: 161-171.

First identified in 2012, Middle East respiratory syndrome coronavirus (MERS-CoV) is a novel virus that can cause acute respiratory distress syndrome (ARDS), multiorgan failure, and death, with a case fatality rate of ~35%. An animal model that supports MERS-CoV infection and causes severe lung disease is useful to study pathogenesis and evaluate therapies and vaccines. The murine dipeptidyl peptidase 4 (Dpp4) protein is not a functional receptor for MERS-CoV; thus, mice are resistant to MERS-CoV infection. We generated human DPP4 knock-in (hDPP4 KI) mice by replacing exons 10-12 at the mouse Dpp4 locus with exons 10-12 from the human DPP4 gene. The resultant human DPP4 KI mice are permissive to MERS-CoV (HCoV-EMC/2012 strain) infection but develop no disease. To generate a mouse model with associated morbidity and mortality from respiratory disease, we serially passaged HCoV-EMC/2012 strain in the lungs of young hDPP4 KI mice. After 30 in vivo passages, an adapted virus clone was isolated and designated MERSMA6.1.2. This virus clone produced significantly higher titers than the parental clone in the lungs of hDPP4 KI mice and caused diffuse lung injury and a fatal respiratory infection. In this chapter, we will describe in detail the procedures used to mouse adapt MERS-CoV by serial passage of the virus in lungs. We also describe the methods used to isolate virus clones and characterize virus infection.

Li, L. H., et al. (2020). "[Treatment strategies of Budd-Chiari syndrome during the epidemic period of 2019 coronavirus disease]." Zhonghua Wai Ke Za Zhi **58**(0): E007.

Prevention and control about the situation of 2019 coronavirus disease (COVID-19) are grim at present. In addition to supporting the frontline actively, medical workers in general surgery spare no efforts in making good diagnosis and treatment of specialized diseases by optimizing treatment process, providing medical advice online, mastering indications of delayed operation and emergency operation reasonably, etc. Budd-Chiari syndrome is a complex disorder, and severity of the disease varies, serious cases can be life threatening. While fighting the epidemic, medical workers should also ensure the medical needs of patients. However, instead of continuing the traditional treatment, a new management system should be developed. Based on the characteristics of Budd-Chiari syndrome patients in China and our experience, we divide the patients into ordinary and critical cases, and treatment strategies suitable for the epidemic period of COVID-19 are put forward for reference and discussion by physicians.

Li, L. Q., et al. (2020). "2019 novel coronavirus patients' clinical characteristics, discharge rate, and fatality rate of meta-analysis." J Med Virol.

The aim of this study was to analyze the clinical data, discharge rate, and fatality rate of COVID-19 patients for clinical help. The clinical data of COVID-19 patients from December 2019 to February 2020 were retrieved from four databases. We statistically analyzed the clinical symptoms and laboratory results of COVID-19 patients and explained the discharge rate and fatality rate with a single-arm meta-analysis. The available data of 1994 patients in 10 literatures were included in our study. The main clinical symptoms of COVID-19 patients were fever (88.5%), cough (68.6%), myalgia or fatigue (35.8%), expectoration (28.2%), and dyspnea (21.9%). Minor symptoms include headache or dizziness (12.1%), diarrhea (4.8%), nausea and vomiting (3.9%). The results of the laboratory showed that the lymphocytopenia (64.5%), increase of C-reactive protein (44.3%), increase of lactic dehydrogenase (28.3%), and leukocytopenia (29.4%) were more common. The results of single-arm meta-analysis showed that the male took a larger percentage in the gender distribution of COVID-19 patients 60% (95% CI [0.54, 0.65]), the discharge rate of COVID-19 patients was 42% (95% CI [0.29, 0.55]), and the fatality rate was 7% (95% CI [0.04,0.10]).

Li, X., et al. (2020). "[Preliminary Recommendations for Lung Surgery during 2019 Novel Coronavirus Disease (COVID-19) Epidemic Period]." Zhongguo Fei Ai Za Zhi **23**(3): 133-135.

In December 2019, China diagnosed the first patient with 2019 novel coronavirus disease (COVID-19), and the following development of the epidemic had a huge impact on China and the whole world. For patients with lung occupying lesions, the whole process of diagnosis and treatment can not be carried out as usual due to the epidemic. For thoracic surgeons, the timing of surgical intervention should be very carefully considered. All thoracic surgeons in China should work together to develop the proper procedures for the diagnosis and treatment in this special situation, and continuously update the recommendations based on epidemic changes and further understanding of COVID-19. Here, we only offer some preliminary suggestions based on our own knowledge for further reference and discussion.

Li, X. Y., et al. (2020). "[The keypoints in treatment of the critical coronavirus disease 2019 patient]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E026.

The treatment of critically ill patients with coronavirus disease 2019(COVID-19) faces compelling challenges. In this issue, we'd like to share our first-line treatment experience in treating COVID-19. Hemodynamics need be closely monitored and different types of shock should be distinguished. Vasoconstrictor drugs should be used rationally and alerting of complications is of the same importance. The risk of venous thromboembolism (VTE) needs to be assessed, and effective prevention should be carried out for high-risk patients. It is necessary to consider the possibility of pulmonary thromboembolism (PTE) in patients with sudden onset of oxygenation deterioration, respiratory distress, reduced blood pressure. However, comprehensive analysis of disease state should be taken into the interpretation of abnormally elevated D-Dimer. Nutritional support is the basis of treatment. It's important to establish individual therapy regimens and to evaluate, monitor and adjust dynamically. Under the current epidemic situation, convalescent plasma can only be used empirically, indications need to be strictly screened, the blood transfusion process should be closely monitored and the curative effect should be dynamically evaluated.

Li, Y. and L. Xia (2020). "Coronavirus Disease 2019 (COVID-19): Role of Chest CT in Diagnosis and Management." AJR Am J Roentgenol: 1-7.

OBJECTIVE. The objective of our study was to determine the misdiagnosis rate of radiologists for coronavirus disease 2019 (COVID-19) and evaluate the performance of chest CT in the diagnosis and management of COVID-19. The CT features of COVID-19 are reported and compared with the CT features of other viruses to familiarize radiologists with possible CT patterns. MATERIALS AND METHODS. This study included the first 51 patients with a diagnosis of COVID-19 infection confirmed by nucleic acid testing (23 women and 28 men; age range, 26-83 years) and two patients with adenovirus (one woman and one man; ages, 58 and 66 years). We reviewed the clinical information, CT images, and corresponding image reports of these 53 patients. The CT images included images from 99 chest CT examinations, including initial and follow-up CT studies. We compared the image reports of the initial CT study with the laboratory test results and identified CT patterns suggestive of viral infection. RESULTS. COVID-19 was misdiagnosed as a common infection at the initial CT study in two inpatients with underlying disease and COVID-19. Viral pneumonia was correctly diagnosed at the initial CT study in the remaining 49 patients with COVID-19 and two patients with adenovirus. These patients were isolated and obtained treatment. Ground-glass opacities (GGOs) and consolidation with or without vascular enlargement, interlobular septal thickening, and air bronchogram sign are common CT features of COVID-19. The The "reversed halo" sign and pulmonary nodules with a halo sign are uncommon CT features. The CT findings of COVID-19 overlap with the CT findings of adenovirus infection. There are differences as well as similarities in the CT features of COVID-19 compared with those of the severe acute respiratory syndrome. CONCLUSION. We found that chest CT had a low rate of missed diagnosis of COVID-19 (3.9%, 2/51) and may be useful as a standard method for the rapid diagnosis of COVID-19 to optimize the management of patients. However, CT is still limited for identifying specific viruses and distinguishing between viruses.

Li, Z. Y. and L. Y. Meng (2020). "[The prevention and control of a new coronavirus infection in department of stomatology]." Zhonghua Kou Qiang Yi Xue Za Zhi **55**(0): E001.

During a short period of time, the outbreak of pneumonia caused by a novel coronavirus, named Novel Coronavirus Pneumonia (NCP), was first reported in China, spreading to 24 countries and regions rapidly. The number of confirmed cases and deaths continued to rise. World Health Organization (WHO) announced that the outbreaks of the novel coronavirus have constituted a Public Health Emergency of International Concern. Efficient infection control can prevent the virus from further spreading, which makes the epidemic situation under control. Due to the specialty of oral healthcare settings, the risk of cross infection is severe among patients and oral healthcare practitioners. It's more urgent to implement strict and efficient infection control protocols. This paper, based on existing guidelines and published researches pertinent to dental infection-control principles and practices, mainly discusses epidemiological characteristics of NCP and the features of nosocomial infection in oral healthcare settings, and furthermore provides recommendations on patient's evaluation, and infection control protocols in department of stomatology under current circumstance..

Ling, Y., et al. (2020). "Persistence and clearance of viral RNA in 2019 novel coronavirus disease rehabilitation patients." Chin Med J (Engl).

BACKGROUND: A patient's infectivity is determined by the presence of the virus in different body fluids, secretions, and excreta. The persistence and clearance of viral RNA from different specimens of patients with 2019 novel coronavirus disease (COVID-19) remain unclear. This study analyzed the clearance time and factors influencing 2019 novel coronavirus (2019-nCoV) RNA in different samples from patients with COVID-19, providing further evidence to improve the management of patients during convalescence. METHODS: The clinical data and laboratory test results of convalescent patients with COVID-19 who were admitted to from January 20, 2020 to February 10, 2020 were collected retrospectively. The reverse transcription polymerase chain reaction (RT-PCR) results for patients' oropharyngeal swab, stool, urine, and serum samples were collected and analyzed. Convalescent patients refer to recovered non-febrile patients without respiratory symptoms who had two successive (minimum 24 h sampling interval) negative RT-PCR results for viral RNA from oropharyngeal swabs. The effects of cluster of differentiation 4 (CD4)+ T lymphocytes, inflammatory indicators, and glucocorticoid treatment on viral nucleic acid clearance were analyzed. RESULTS: In the 292 confirmed cases, 66 patients recovered after treatment and were included in our study. In total, 28 (42.4%) women and 38 men (57.6%) with a median age of 44.0 (34.0-62.0) years were analyzed. After in-hospital treatment, patients' inflammatory indicators decreased with improved clinical condition. The median time from the onset of symptoms to first negative RT-PCR results for oropharyngeal swabs in convalescent patients was 9.5 (6.0-11.0) days. By February 10, 2020, 11 convalescent patients (16.7%) still tested positive for viral RNA from stool specimens and the other 55 patients' stool specimens were negative for 2019-nCoV following a median duration of 11.0 (9.0-16.0) days after symptom onset. Among these 55 patients, 43 had a longer duration until stool specimens were negative for viral RNA than for throat swabs, with a median delay of 2.0 (1.0-4.0) days. Results for only four (6.9%) urine samples were positive for viral nucleic acid out of 58 cases; viral RNA was still present in three patients' urine specimens after throat swabs were negative. Using a multiple linear regression model ($F = 2.669$, $P = 0.044$, and adjusted $R = 0.122$), the analysis showed that the CD4+ T lymphocyte count may help predict the duration of viral RNA detection in patients' stools ($t = -2.699$, $P = 0.010$). The duration of viral RNA detection from oropharyngeal swabs and fecal samples in the glucocorticoid treatment group was longer than that in the non-glucocorticoid treatment group (15 days vs. 8.0 days, respectively; $t = 2.550$, $P = 0.013$) and the duration of viral RNA detection in fecal samples in the glucocorticoid treatment group was longer than that in the non-glucocorticoid treatment group (20 days vs. 11 days, respectively; $t = 4.631$, $P < 0.001$). There was no statistically significant difference in inflammatory indicators between patients with positive fecal viral RNA test results and those with negative results ($P > 0.05$). CONCLUSIONS: In brief, as the clearance of viral RNA in patients' stools was delayed compared to that in oropharyngeal swabs, it is important to identify viral RNA in feces during convalescence. Because of the delayed clearance of viral RNA in the glucocorticoid treatment group, glucocorticoids are not recommended in the treatment of COVID-19, especially for mild disease. The duration of RNA detection may relate to host cell immunity.

Linton, N. M., et al. (2020). "Incubation Period and Other Epidemiological Characteristics of 2019 Novel Coronavirus Infections with Right Truncation: A Statistical Analysis of Publicly Available Case Data." J Clin Med **9**(2).

The geographic spread of 2019 novel coronavirus (COVID-19) infections from the epicenter of Wuhan, China, has provided an opportunity to study the natural history of the recently emerged virus. Using publicly available event-date data from the ongoing epidemic, the present study investigated the incubation period and other time intervals that govern the epidemiological dynamics of COVID-19 infections. Our results show that the incubation period falls within the range of 2-14 days with 95% confidence and has a mean of around 5 days when approximated using the best-fit lognormal distribution. The mean time from illness onset to hospital admission (for treatment and/or isolation) was estimated at 3-4 days without truncation and at 5-9 days when right truncated. Based on the 95th percentile estimate of the incubation period, we recommend that the length of quarantine should be at least 14 days. The median time delay of 13 days from illness onset to death (17 days with right truncation) should be considered when estimating the COVID-19 case fatality risk.

Liu, C., et al. (2020). "[Preliminary study of the relationship between novel coronavirus pneumonia and liver function damage: a multicenter study]." Zhonghua Gan Zang Bing Za Zhi **28**(2): 148-152.

Objective: To analyze the clinical characteristics of cases of novel coronavirus pneumonia and a preliminary study to explore the relationship between different clinical classification and liver damage. Methods: Consecutively confirmed novel coronavirus infection cases admitted to seven designated hospitals during January 23, 2020 to February 8, 2020 were included. Clinical classification (mild, moderate, severe, and critical) was carried out according to the diagnosis and treatment program of novel coronavirus pneumonia (Trial Fifth Edition) issued by the National Health Commission. The research data were analyzed using SPSS19.0 statistical software. Quantitative data were expressed as median (interquartile range), and qualitative data were expressed as frequency and rate. Results: 32 confirmed cases that met the inclusion criteria were included. 28 cases were of mild or moderate type (87.50%), and four cases (12.50%) of severe or critical type. Four cases (12.5%) were combined with one underlying disease (bronchial asthma, coronary heart disease, malignant tumor, chronic kidney disease), and one case (3.13%) was simultaneously combined with high blood pressure and malignant tumor. The results of laboratory examination showed that the alanine aminotransferase (ALT), aspartate aminotransferase (AST), albumin (ALB), and total bilirubin (TBil) for entire cohort were 26.98 (16.88 ~ 46.09) U/L and 24.75 (18.71 ~ 31.79) U/L, 39.00 (36.20 ~ 44.20) g/L and 16.40 (11.34- ~ 21.15) mmol/L, respectively. ALT, AST, ALB and TBil of the mild or moderate subgroups were 22.75 (16.31- ~ 37.25) U/L, 23.63 (18.71 ~ 26.50) U/L, 39.70 (36.50 ~ 46.10) g/L, and 15.95 (11.34 ~ 20.83) mmol/L, respectively. ALT, AST, ALB and TBil of the severe or critical subgroups were 60.25 (40.88 ~ 68.90) U/L, 37.00 (20.88 ~ 64.45) U/L, 35.75 (28.68 ~ 42.00) g/L, and 20.50 (11.28 ~ 25.00) mmol/L, respectively. Conclusion: The results of this multicenter retrospective study suggests that novel coronavirus pneumonia combined with liver damage is more likely to be caused by adverse drug reactions and systemic inflammation in severe patients receiving medical treatment. Therefore, liver function monitoring and evaluation should be strengthened during the treatment of such patients.

Liu, D., et al. (2020). "Pregnancy and Perinatal Outcomes of Women With Coronavirus Disease (COVID-19) Pneumonia: A Preliminary Analysis." AJR Am J Roentgenol: 1-6.

OBJECTIVE. The purpose of this study was to describe the clinical manifestations and CT features of coronavirus disease (COVID-19) pneumonia in 15 pregnant women and to provide some initial evidence that can be used for guiding treatment of pregnant women with COVID-19 pneumonia. MATERIALS AND METHODS. We reviewed the clinical data and CT examinations of 15 consecutive pregnant women with COVID-19 pneumonia in our hospital from January 20, 2020, to February 10, 2020. A semiquantitative CT scoring system was used to estimate pulmonary involvement and the time course of changes on chest CT. Symptoms and laboratory results were analyzed, treatment experiences were summarized, and clinical outcomes were tracked. RESULTS. Eleven patients had successful delivery (10 cesarean deliveries and one vaginal delivery) during the study period, and four patients were still pregnant (three in the second trimester and one in the third trimester) at the end of the study period. No cases of neonatal asphyxia, neonatal death, stillbirth, or abortion were reported. The most common early finding on chest CT was ground-glass opacity (GGO). With disease progression, crazy paving pattern and consolidations were seen on CT. The abnormalities showed absorptive changes at the end of the study period for all patients. The most common onset symptoms of COVID-19 pneumonia in pregnant women were fever (13/15 patients) and cough (9/15 patients). The most common abnormal laboratory finding was lymphocytopenia (12/15 patients). CT images obtained before and after delivery showed no signs of pneumonia aggravation after delivery. The four patients who were still pregnant at the end of the study period were not treated with antiviral drugs but had achieved good recovery. CONCLUSION. Pregnancy and childbirth did not aggravate the course of symptoms or CT features of COVID-19 pneumonia. All the cases of COVID-19 pneumonia in the pregnant women in our study were the mild type. All the women in this study-some of whom did not receive antiviral drugs-achieved good recovery from COVID-19 pneumonia.

Liu, J., et al. (2020). "Community Transmission of Severe Acute Respiratory Syndrome Coronavirus 2, Shenzhen, China, 2020." Emerg Infect Dis **26**(6).

Since early January 2020, after the outbreak of 2019 novel coronavirus infection in Wuhan, China, approximately 365 confirmed cases have been reported in Shenzhen, China. The mode of community and intrafamily transmission is threatening residents in Shenzhen. Strategies to strengthen prevention and interruption of these transmissions should be urgently addressed.

Liu, J., et al. (2019). "Comprehensive Genomic Characterization Analysis of lncRNAs in Cells With Porcine Delta Coronavirus Infection." Front Microbiol **10**: 3036.

Porcine delta coronavirus (PDCoV) is a novel emerging enterocytetropic virus causing diarrhea, vomiting, dehydration, and mortality in suckling piglets. Long non-coding RNAs (lncRNAs) are known to be important regulators during virus infection. Here, we describe a comprehensive transcriptome profile of lncRNA in PDCoV-infected swine testicular (ST) cells. In total, 1,308 annotated and 1,190 novel lncRNA candidate sequences were identified. Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) analysis revealed that these lncRNAs might be involved in numerous biological processes. Clustering analysis of differentially expressed lncRNAs showed that 454 annotated and 376 novel lncRNAs were regulated after PDCoV infection. Furthermore, we constructed a lncRNA-protein-coding gene co-expression interaction network. The KEGG analysis of the co-expressed genes showed that these differentially expressed lncRNAs were enriched in pathways related to metabolism and TNF signaling. Our study provided comprehensive information about lncRNAs that would be a useful resource for studying the pathogenesis of and designing antiviral therapy for PDCoV infection.

Liu, M., et al. (2020). "[Clinical characteristics of 30 medical workers infected with new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 209-214.

Objective: To investigate the clinical characteristics of medical staff with novel coronavirus pneumonia (NCP). Methods: 30 patients infected with novel coronavirus referred to jianghan university hospital between January 11, 2020 and January 3, 2020 were studied. The data reviewed included those of clinical manifestations, laboratory investigation and Radiographic features. Results: The patients consisted of 10 men and 20 women, including 22 doctors and 8 nurses,aged 21~59 years (mean 35+/-8 years).They were divided to 26 common type and 4 severe cases, all of whom had close (within 1m) contact with patients infected of novel coronavirus pneumonia. The average contact times were 12 (7,16) and the average cumulative contact time was 2 (1.5,2.7) h.Clinical symptoms of these patients were fever in 23 patients (76.67%), headache in 16 petients (53.33%), fatigue or myalgia in 21patients (70%), nausea, vomiting or diarrhea in 9 petients (30%), cough in 25 petients (83.33%), and dyspnea in 14 petients (46.67%).Routine blood test revealed WBC<4.0x10(9)/L in 8 petients (26.67%), (4-10) x10(9)/L in 22 petients (73.33%), and WBC>4.0x10(9)/L in 4 petients (13.33%) during the disease.Lymphocyte count<1.0x10(9)/L occurred in 12 petients (40%),abnormal liver function in 7 petients (23.33%),myocardial damage in 5 petients (16.67%), elevated D-dimer (>0.5mg/l) in 5 patients (16.67%). Compared with normal patients, the average exposure times, cumulative exposure time, BMI, Fever time, white blood cell count, liver enzyme, LDH, myoenzyme and D-dimer were significantly increased in severe patients, while the lymphocyte count and albumin levels in peripheral blood were significantly decreased.Chest CT mainly showed patchy shadows and interstitial changes.According to imaging examination, 11 patients (36.67%) showed Unilateral pneumonia and 19 patients (63.33%) showed bilateral pneumonia,4 patients (13.33%) showed bilateral multiple mottling and ground-glass opacity.Compared with the patients infected in the protected period, the proportion of severe infection and bilateral pneumonia were both increased in the patients infected in unprotected period. Conclusion: Medical staffs are at higher risk of infection.Infection rates are associated with contact time, the amount of suction virus. Severe patients had BMI increased, heating time prolonged, white blood cell count, lymphocyte count, D-dimer and albumin level significantly changed and were prone to be complicated with liver damage and myocardial damage.Strict protection measures is important to prevent infection for medical workers.

Liu, M., et al. (2020). "[Clinical characteristics of 30 medical workers infected with new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E016.

Objective: To investigate the clinical characteristics of medical staff with novel coronavirus pneumonia (NCP). Methods: 30 patients infected with novel coronavirus referred to jianghan university hospital between January 11, 2020 and January 3, 2020 were studied. The data reviewed included those of clinical manifestations, laboratory investigation and Radiographic features. Results: The patients consisted of 10 men and 20 women, including 22 doctors and 8 nurses,aged 21~59 years (mean 35+/-8 years).They were divided to 26 common type and 4 severe cases, all of whom had close (within 1m) contact with patients infected of novel coronavirus pneumonia. The average contact times were 12 (7,16) and the average cumulative contact time was 2 (1.5,2.7) h.Clinical symptoms of these patients were fever in 23 patients (76.67%), headache in 16 petients (53.33%), fatigue or myalgia in 21patients (70%), nausea, vomiting or diarrhea in 9 petients (30%), cough in 25 petients (83.33%), and dyspnea in 14 petients (46.67%).Routine blood test revealed WBC <4.0x10(9)/L in 8 petients (26.67%), (4-10) x10(9)/L in 22 petients (73.33%), and WBC>4.0x10(9)/L in 4 petients (13.33%) during the disease.Lymphocyte count <1.0x10(9)/L occurred in 12 petients (40%),abnormal liver function in 7 petients (23.33%),myocardial damage in 5 petients (16.67%), elevated D-dimer (>0.5mg/l) in 5 patients (16.67%). Compared with normal patients, the average exposure times, cumulative exposure time, BMI, Fever time, white blood cell count, liver enzyme, LDH, myoenzyme and D-dimer were significantly increased in severe patients, while the lymphocyte count and albumin levels in peripheral blood were significantly decreased.Chest CT mainly showed patchy shadows and interstitial changes.According to imaging examination, 11 patients (36.67%) showed Unilateral pneumonia and 19 patients (63.33%) showed bilateral pneumonia,4 patients (13.33%) showed bilateral multiple mottling and ground-glass opacity.Compared with the patients infected in the protected period, the proportion of severe infection and bilateral pneumonia were both increased in the patients infected in unprotected period. Conclusion: Medical staffs are at higher risk of infection.Infection rates are associated with contact time, the amount of suction virus. Severe patients had BMI increased, heating time prolonged, white blood cell count, lymphocyte count, D-dimer and albumin level significantly changed and were prone to be complicated with liver damage and myocardial damage.Strict protection measures is important to prevent infection for medical workers.

Lu, R., et al. (2020). "Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding." Lancet **395**(10224): 565-574.

BACKGROUND: In late December, 2019, patients presenting with viral pneumonia due to an unidentified microbial agent were reported in Wuhan, China. A novel coronavirus was subsequently identified as the causative pathogen, provisionally named 2019 novel coronavirus (2019-nCoV). As of Jan 26, 2020, more than 2000 cases of 2019-nCoV infection have been confirmed, most of which involved people living in or visiting Wuhan, and human-to-human transmission has been confirmed. METHODS: We did next-generation sequencing of samples from bronchoalveolar lavage fluid and cultured isolates from nine inpatients, eight of whom had visited the Huanan seafood market in Wuhan. Complete and partial 2019-nCoV genome sequences were obtained from these individuals. Viral contigs were connected using Sanger sequencing to obtain the full-length genomes, with the terminal regions determined by rapid amplification of cDNA ends. Phylogenetic analysis of these 2019-nCoV genomes and those of other coronaviruses was used to determine the evolutionary history of the virus and help infer its likely origin. Homology modelling was done to explore the likely receptor-binding properties of the virus. FINDINGS: The ten genome sequences of 2019-nCoV obtained from the nine patients were extremely similar, exhibiting more than 99.98% sequence identity. Notably, 2019-nCoV was closely related (with 88% identity) to two bat-derived severe acute respiratory syndrome (SARS)-like coronaviruses, bat-SL-CoVZC45 and bat-SL-CoVZXC21, collected in 2018 in Zhoushan, eastern China, but were more distant from SARS-CoV (about 79%) and MERS-CoV (about 50%). Phylogenetic analysis revealed that 2019-nCoV fell within the subgenus Sarbecovirus of the genus Betacoronavirus, with a relatively long branch length to its closest relatives bat-SL-CoVZC45 and bat-SL-CoVZXC21, and was genetically distinct from SARS-CoV. Notably, homology modelling revealed that 2019-nCoV had a similar receptor-binding domain structure to that of SARS-CoV, despite amino acid variation at some key residues. INTERPRETATION: 2019-nCoV is sufficiently divergent from SARS-CoV to be considered a new human-infecting betacoronavirus. Although our phylogenetic analysis suggests that bats might be the original host of this virus, an animal sold at the seafood market in Wuhan might represent an intermediate host facilitating the emergence of the virus in humans. Importantly, structural analysis suggests that 2019-nCoV might be able to bind to the angiotensin-converting enzyme 2 receptor in humans. The future evolution, adaptation, and spread of this virus warrant urgent investigation. FUNDING: National Key Research and Development Program of China, National Major Project for Control and Prevention of Infectious Disease in China, Chinese Academy of Sciences, Shandong First Medical University.

Lu, S., et al. (2020). "Alert for non-respiratory symptoms of Coronavirus Disease 2019 (COVID-19) patients in epidemic period: A case report of familial cluster with three asymptomatic COVID-19 patients." J Med Virol.

At present, Coronavirus Disease 2019 (COVID-19) is rampaging around the world. However, asymptomatic carriers intensified the difficulty of prevention and management. Here we reported the screening, clinical feathers, and treatment process of a family cluster involving three COVID-19 patients. The discovery of the first asymptomatic carrier in this family cluster depends on the repeated and comprehensive epidemiological investigation by disease control experts. In addition, the combination of multiple detection methods can help clinicians find asymptomatic carriers as early as possible. In conclusion, the prevention and control experience of this family cluster showed that comprehensive rigorous epidemiological investigation and combination of multiple detection methods were of great value for the detection of hidden asymptomatic carriers. This article is protected by copyright. All rights reserved.

Lu, T. and H. Pu (2020). "Computed Tomography Manifestations of 5 Cases of the Novel Coronavirus Disease 2019 (COVID-19) Pneumonia From Patients Outside Wuhan." J Thorac Imaging.

Clinical, laboratory, and computed tomography (CT) findings of 5 cases of the novel Coronavirus Disease 2019 (COVID-19) pneumonia from patients outside of Wuhan were reviewed. The human-to-human transmission of the virus may explain the infection of the disease outside of Wuhan. CT examination is important in the early detection and follow-up of the disease. With a history of exposure or travelling, symptoms of fever and cough, and the typical CT manifestation such as ground-glass opacity with a peripheral distribution, we should also think of the possibility of the COVID-19 pneumonia in patients outside of Wuhan.

Mandal, S., et al. (2020). "Prudent public health intervention strategies to control the coronavirus disease 2019 transmission in India: A mathematical model-based approach." Indian J Med Res.

Background & objectives::Coronavirus disease 2019 (COVID-19) has raised urgent questions about containment and mitigation, particularly in countries where the virus has not yet established human-to-human transmission. The objectives of this study were to find out if it was possible to prevent, or delay, the local outbreaks of COVID-19 through restrictions on travel from abroad and if the virus has already established in-country transmission, to what extent would its impact be mitigated through quarantine of symptomatic patients?" Methods::These questions were addressed in the context of India, using simple mathematical models of infectious disease transmission. While there remained important uncertainties in the natural history of COVID-19, using hypothetical epidemic curves, some key findings were illustrated that appeared insensitive to model assumptions, as well as highlighting critical data gaps. Results::It was assumed that symptomatic quarantine would identify and quarantine 50 per cent of symptomatic individuals within three days of developing symptoms. In an optimistic scenario of the basic reproduction number (R00) being 1.5, and asymptomatic infections lacking any infectiousness, such measures would reduce the cumulative incidence by 62 per cent. In the pessimistic scenario of R0=4, and asymptomatic infections being half as infectious as symptomatic, this projected impact falls to two per cent. Interpretation & conclusions::Port-of-entry-based entry screening of travellers with suggestive clinical features and from COVID-19-affected countries, would achieve modest delays in the introduction of the virus into the community. Acting alone, however, such measures would be insufficient to delay the outbreak by weeks or longer. Once the virus establishes transmission within the community, quarantine of symptomatics may have a meaningful impact on disease burden. Model projections are subject to substantial uncertainty and can be further refined as more is understood about the natural history of infection of this novel virus. As a public health measure, health system and community preparedness would be critical to control any impending spread of COVID-19 in the country.

Martinez, M. A. (2020). "Compounds with therapeutic potential against novel respiratory 2019 coronavirus." Antimicrob Agents Chemother.

Currently, the expansion of the novel human respiratory coronavirus (known as: SARS-CoV-2, COVID-2019, or 2019-nCoV) has stressed the need for therapeutic alternatives to alleviate and stop this new epidemic. The previous epidemics of high-morbidity human coronaviruses, such as the acute respiratory syndrome coronavirus (SARS-CoV) in 2003, and the Middle East respiratory syndrome corona virus (MERS-CoV) in 2012, prompted the characterization of compounds that could be potentially active against the currently emerging novel coronavirus SARS-CoV-2. The most promising compound is remdesivir (GS-5734), a nucleotide analog prodrug currently in clinical trials for treating Ebola virus infections. Remdesivir inhibited the replication of SARS-CoV and MERS-CoV in tissue cultures, and it displayed efficacy in non-human animal models. In addition, a combination of the human immunodeficiency virus type 1 (HIV-1) protease inhibitors, lopinavir/ritonavir, and interferon beta (LPV/RTV-INFb) were shown to be effective in patients infected with SARS-CoV. LPV/RTV-INFb also improved clinical parameters in marmosets and mice infected with MERS-CoV. Remarkably, the therapeutic efficacy of remdesivir appeared to be superior to that of LPV/RTV-INFb against MERS-CoV in a transgenic humanized mice model. The relatively high mortality rates associated with these three novel human coronavirus infections, SARS-CoV, MERS-CoV, and SARS-CoV-2, has suggested that pro-inflammatory responses might play a role in the pathogenesis. It remains unknown whether the generated inflammatory state should be targeted. Therapeutics that target the coronavirus alone might not be able to reverse highly pathogenic infections. This minireview aimed to provide a summary of therapeutic compounds that showed potential in fighting SARS-CoV-2 infections.

Menachery, V. D., et al. (2020). "Trypsin Treatment Unlocks Barrier for Zoonotic Bat Coronavirus Infection." J Virol **94**(5).

Traditionally, the emergence of coronaviruses (CoVs) has been attributed to a gain in receptor binding in a new host. Our previous work with severe acute respiratory syndrome (SARS)-like viruses argued that bats already harbor CoVs with the ability to infect humans without adaptation. These results suggested that additional barriers limit the emergence of zoonotic CoV. In this work, we describe overcoming host restriction of two Middle East respiratory syndrome (MERS)-like bat CoVs using exogenous protease treatment. We found that the spike protein of PDF2180-CoV, a MERS-like virus found in a Ugandan bat, could mediate infection of Vero and human cells in the presence of exogenous trypsin. We subsequently show that the bat virus spike can mediate the infection of human gut cells but is unable to infect human lung cells. Using receptor-blocking antibodies, we show that infection with the PDF2180 spike does not require MERS-CoV receptor DPP4 and antibodies developed against the MERS spike receptor-binding domain and S2 portion are ineffective in neutralizing the PDF2180 chimera. Finally, we found that the addition of exogenous trypsin also rescues HKU5-CoV, a second bat group 2c CoV. Together, these results indicate that proteolytic cleavage of the spike, not receptor binding, is the primary infection barrier for these two group 2c CoVs. Coupled with receptor binding, proteolytic activation offers a new parameter to evaluate the emergence potential of bat CoVs and offers a means to recover previously unrecoverable zoonotic CoV strains.IMPORTANCE Overall, our studies demonstrate that proteolytic cleavage is the primary barrier to infection for a subset of zoonotic coronaviruses. Moving forward, the results argue that both receptor binding and proteolytic cleavage of the spike are critical factors that must be considered for evaluating the emergence potential and risk posed by zoonotic coronaviruses. In addition, the findings also offer a novel means to recover previously uncultivable zoonotic coronavirus strains and argue that other tissues, including the digestive tract, could be a site for future coronavirus emergence events in humans.

Meng, L., et al. (2020). "Coronavirus Disease 2019 (COVID-19): Emerging and Future Challenges for Dental and Oral Medicine." J Dent Res: 22034520914246.

The epidemic of coronavirus disease 2019 (COVID-19), originating in Wuhan, China, has become a major public health challenge for not only China but also countries around the world. The World Health Organization announced that the outbreaks of the novel coronavirus have constituted a public health emergency of international concern. As of February 26, 2020, COVID-19 has been recognized in 34 countries, with a total of 80,239 laboratory-confirmed cases and 2,700 deaths. Infection control measures are necessary to prevent the virus from further spreading and to help control the epidemic situation. Due to the characteristics of dental settings, the risk of cross infection can be high between patients and dental practitioners. For dental practices and hospitals in areas that are (potentially) affected with COVID-19, strict and effective infection control protocols are urgently needed. This article, based on our experience and relevant guidelines and research, introduces essential knowledge about COVID-19 and nosocomial

infection in dental settings and provides recommended management protocols for dental practitioners and students in (potentially) affected areas.

Meo, S. A., et al. (2020). "Novel coronavirus 2019-nCoV: prevalence, biological and clinical characteristics comparison with SARS-CoV and MERS-CoV." Eur Rev Med Pharmacol Sci **24**(4): 2012-2019.

OBJECTIVE: Human infections with zoonotic coronavirus contain emerging and reemerging pathogenic characteristics which have raised great public health concern. This study aimed at investigating the global prevalence, biological and clinical characteristics of novel coronavirus, Wuhan China (2019-nCoV), Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV), and Middle East Respiratory Syndrome Coronavirus (MERS-CoV) infection outbreaks. MATERIALS AND METHODS: The data on the global outbreak of "2019-nCoV, SARS-CoV, and MERS-CoV" were obtained from World Health Organization (WHO), Centers for Disease Control and Prevention (CDC), concerned ministries and research institutes. We also recorded the information from research documents published in global scientific journals indexed in ISI Web of Science and research centers on the prevalence, biological and clinical characteristics of 2019-nCoV, SARS-CoV, and MERS-CoV. RESULTS: Worldwide, SARS-CoV involved 32 countries, with 8422 confirmed cases and 916 (10.87%) casualties from November 2002 to August 2003. MERS-CoV spread over 27 states, causing 2496 cases and 868 (34.77%) fatalities during the period April 2012 to December 2019. However, the novel coronavirus 2019-nCoV spread swiftly the global borders of 27 countries. It infected 34799 people and resulted in 724 (2.08%) casualties during the period December 29, 2019 to February 7, 2020. The fatality rate of coronavirus MERS-CoV was (34.77%) higher than SARS-CoV (10.87%) and 2019-nCoV (2.08%); however, the 2019-nCoV transmitted rapidly in comparison to SARS-CoV and MERS-CoV. CONCLUSIONS: The novel coronavirus 2019-nCoV has diverse epidemiological and biological characteristics, making it more contagious than SARS-CoV and MERS-CoV. It has affected more people in a short time period compared to SARS-CoV and MERS-CoV, although the fatality rate of MERS-CoV was higher than SARS-CoV and 2019-nCoV. The major clinical manifestations in coronavirus infections 2019-nCoV, MERS-CoV, and SARS CoV are fever, chills, cough, shortness of breath, generalized myalgia, malaise, drowsy, diarrhea, confusion, dyspnea, and pneumonia. Global health authorities should take immediate measures to prevent the outbreaks of such emerging and reemerging pathogens across the globe to minimize the disease burden locally and globally.

Novel Coronavirus Pneumonia Emergency Response Epidemiology, T. (2020). "[The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (COVID-19) in China]." Zhonghua Liu Xing Bing Xue Za Zhi **41**(2): 145-151.

Objective: An outbreak of 2019 novel coronavirus diseases (COVID-19) in Wuhan, China has spread quickly nationwide. Here, we report results of a descriptive, exploratory analysis of all cases diagnosed as of February 11, 2020. Methods: All COVID-19 cases reported through February 11, 2020 were extracted from China's Infectious Disease Information System. Analyses included: 1) summary of patient characteristics; 2) examination of age distributions and sex ratios; 3) calculation of case fatality and mortality rates; 4) geo-temporal analysis of viral spread; 5) epidemiological curve construction; and 6) subgroup analysis. Results: A total of 72 314 patient records-44 672 (61.8%) confirmed cases, 16 186 (22.4%) suspected cases, 10567 (14.6%) clinical diagnosed cases (Hubei only), and 889 asymptomatic cases (1.2%)-contributed data for the analysis. Among confirmed cases, most were aged 30-79 years (86.6%), diagnosed in Hubei (74.7%), and considered mild (80.9%). A total of 1 023 deaths occurred among confirmed cases for an overall case-fatality rate of 2.3%. The COVID-19 spread outward from Hubei sometime after December 2019 and by February 11, 2020, 1 386 counties across all 31 provinces were affected. The epidemic curve of onset of symptoms peaked in January 23-26, then began to decline leading up to February 11. A total of 1 716 health workers have become infected and 5 have died (0.3%). Conclusions: The COVID-19 epidemic has spread very quickly. It only took 30 days to expand from Hubei to the rest of Mainland China. With many people returning from a long holiday, China needs to prepare for the possible rebound of the epidemic.

Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Health protection guideline of mobile cabin hospitals during Novel Coronavirus Pneumonia (NPC) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E006.

This guideline is applicable to the health protection requirements of large indoor stadiums which are reconstructed as treatment sites for the Novel Coronavirus Pneumonia (NPC) patients with mild symptoms during the outbreak. Focusing on the health emergency scenario of severe virus infectious diseases and atypical places where NPC patients with mild symptom gather, from perspectives of functional zones, hygiene facilities, personal protection, and

management system, health risk protection recommendations and countermeasures are comprehensively proposed to mainly protect staffs and surrounding environment. The implementation of this guideline will provide technique support for emergency requirements of indoor stadiums reconstructed as mobile cabin hospitals.

Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Health protection guideline of passenger transport stations and transportation facilities during novel coronavirus pneumonia (NCP) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E007.

During the coronavirus pneumonia (NCP) outbreak, the transportation industries are faced with the more burdensome tasks of outbreak prevention and control as well as ensuring smooth transportation. It is important to organize transportation in order to restore the order of production and life, ensure the normal economic and social operation, and control the outbreak in the whole society. From the perspective of health, this guideline puts forward technical requirements on the operation management, personnel requirements and health protection of passenger transportation places such as aviation, railway, subway, bus, taxi, ship, etc., which reduces the impact of the NCP outbreak on the transportation industry and personal health risks.

Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Technologies and requirements of protection and disinfection in key places during the novel coronavirus pneumonia (NCP) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E008.

Novel coronavirus pneumonia (NCP), a new respiratory infectious disease, has become an important public health problem. Inappropriate protection and disinfection measures are potential risk factors of transmission and outbreak of NCP in key places. This theme issue is concerned with the prevention and control of NCP. Comprehensive measures and suggestions for protection and disinfection are put forward from perspectives of functional areas in key places, such as hotels, mobile cabin hospitals, passenger transport stations and public transport facilities, environment and facilities, personal protection, operation management system, etc., so as to provide technical support for the prevention and control of new respiratory infectious diseases.

Patel, A., et al. (2020). "Initial Public Health Response and Interim Clinical Guidance for the 2019 Novel Coronavirus Outbreak - United States, December 31, 2019-February 4, 2020." MMWR Morb Mortal Wkly Rep **69**(5): 140-146.

On December 31, 2019, Chinese health officials reported a cluster of cases of acute respiratory illness in persons associated with the Hunan seafood and animal market in the city of Wuhan, Hubei Province, in central China. On January 7, 2020, Chinese health officials confirmed that a novel coronavirus (2019-nCoV) was associated with this initial cluster (1). As of February 4, 2020, a total of 20,471 confirmed cases, including 2,788 (13.6%) with severe illness,* and 425 deaths (2.1%) had been reported by the National Health Commission of China (2). Cases have also been reported in 26 locations outside of mainland China, including documentation of some person-to-person transmission and one death (2). As of February 4, 11 cases had been reported in the United States. On January 30, the World Health Organization (WHO) Director-General declared that the 2019-nCoV outbreak constitutes a Public Health Emergency of International Concern. (dagger) On January 31, the U.S. Department of Health and Human Services (HHS) Secretary declared a U.S. public health emergency to respond to 2019-nCoV. (section sign) Also on January 31, the president of the United States signed a "Proclamation on Suspension of Entry as Immigrants and Nonimmigrants of Persons who Pose a Risk of Transmitting 2019 Novel Coronavirus," which limits entry into the United States of persons who traveled to mainland China to U.S. citizens and lawful permanent residents and their families (3). CDC, multiple other federal agencies, state and local health departments, and other partners are implementing aggressive measures to slow transmission of 2019-nCoV in the United States (4,5). These measures require the identification of cases and their contacts in the United States and the appropriate assessment and care of travelers arriving from mainland China to the United States. These measures are being implemented in anticipation of additional 2019-nCoV cases in the United States. Although these measures might not prevent the eventual establishment of ongoing, widespread transmission of the virus in the United States, they are being implemented to 1) slow the spread of illness; 2) provide time to better prepare health care systems and the general public to be ready if widespread transmission with substantial associated illness occurs; and 3) better characterize 2019-nCoV infection to guide public health recommendations and the development of medical countermeasures including diagnostics, therapeutics, and vaccines. Public health authorities are monitoring the situation closely. As more is learned about this novel virus and this outbreak, CDC will rapidly incorporate new knowledge into guidance for action by CDC and state and local health departments.

Pullano, G., et al. (2020). "Novel coronavirus (2019-nCoV) early-stage importation risk to Europe, January 2020." Euro Surveill **25**(4).

As at 27 January 2020, 42 novel coronavirus (2019-nCoV) cases were confirmed outside China. We estimate the risk of case importation to Europe from affected areas in China via air travel. We consider travel restrictions in place, three reported cases in France, one in Germany. Estimated risk in Europe remains high. The United Kingdom, Germany and France are at highest risk. Importation from Beijing and Shanghai would lead to higher and widespread risk for Europe.

Ralph, R., et al. (2020). "2019-nCoV (Wuhan virus), a novel Coronavirus: human-to-human transmission, travel-related cases, and vaccine readiness." J Infect Dev Ctries **14**(1): 3-17.

On 31 December 2019 the Wuhan Health Commission reported a cluster of atypical pneumonia cases that was linked to a wet market in the city of Wuhan, China. The first patients began experiencing symptoms of illness in mid-December 2019. Clinical isolates were found to contain a novel coronavirus with similarity to bat coronaviruses. As of 28 January 2020, there are in excess of 4,500 laboratory-confirmed cases, with > 100 known deaths. As with the SARS-CoV, infections in children appear to be rare. Travel-related cases have been confirmed in multiple countries and regions outside mainland China including Germany, France, Thailand, Japan, South Korea, Vietnam, Canada, and the United States, as well as Hong Kong and Taiwan. Domestically in China, the virus has also been noted in several cities and provinces with cases in all but one province. While zoonotic transmission appears to be the original source of infections, the most alarming development is that human-to-human transmission is now prevelant. Of particular concern is that many healthcare workers have been infected in the current epidemic. There are several critical clinical questions that need to be resolved, including how efficient is human-to-human transmission? What is the animal reservoir? Is there an intermediate animal reservoir? Do the vaccines generated to the SARS-CoV or MERS-CoV or their proteins offer protection against 2019-nCoV? We offer a research perspective on the next steps for the generation of vaccines. We also present data on the use of in silico docking in gaining insight into 2019-nCoV Spike-receptor binding to aid in therapeutic development. Diagnostic PCR protocols can be found at https://www.who.int/health-topics/coronavirus/laboratory-diagnostics-for-novel-coronavirus.

Respiratory care committee of Chinese Thoracic, S. (2020). "[Expert consensus on preventing nosocomial transmission during respiratory care for critically ill patients infected by 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi **17**(0): E020.

Definite evidence has shown that the novel coronavirus (COVID-19) could be transmitted from person to person, so far more than 1,700 bedside clinicians have been infected. A lot of respiratory treatments for critically ill patients are deemed as high-risk factors for nosocomial transmission, such as intubation, manual ventilation by resuscitator, noninvasive ventilation, high-flow nasal cannula, bronchoscopy examination, suction and patient transportation, etc, due to its high possibility to cause or worsen the spread of the virus. As such, we developed this consensus recommendations on all those high-risk treatments, based on the current evidence as well as the resource limitation in some areas, with the aim to reduce the nosocomial transmission and optimize the treatment for the COVID-19 pneumonia patients. Those recommendations include: (1) Standard prevention and protection, and patient isolation; (2) Patient wearing mask during HFNC treatment; (3) Using dual limb ventilator with filters placed at the ventilator outlets, or using heat-moisture exchanger (HME) instead of heated humidification in single limb ventilator with HME placed between exhalation port and mask; avoid using mask with exhalation port on the mask; (4) Placing filter between resuscitator and mask or artificial airway; (5) For spontaneous breathing patients, placing mask for patients during bronchoscopy examination; for patients receiving noninvasive ventilation, using the special mask with bronchoscopy port to perform bronchoscopy; (6) Using sedation and paralytics during intubation, cuff pressure should be maintained between 25-30 cmH (2)O; (7) In-line suction catheter is recommended and it can be used for one week; (8) Dual-limb heated wire circuits are recommended and only changed with visible soiled; (9. For patients who need breathing support during transportation, placing an HME between ventilator and patient; (10) PSV is recommended for implementing spontaneous breathing trial (SBT), avoid using T-piece to do SBT. When tracheotomy patients are weaned from ventilator, HME should be used, avoid using T-piece or tracheostomy mask. (11) Avoid unnecessary bronchial hygiene therapy; (12) For patients who need aerosol therapy, dry powder inhaler metered dose inhaler with spacer is recommended for spontaneous breathing patients; while vibrating mesh nebulizer is recommended for ventilated patients and additional filter is recommended to be placed at the expiratory port of ventilation during nebulization.

Reusken, C., et al. (2020). "Laboratory readiness and response for novel coronavirus (2019-nCoV) in expert laboratories in 30 EU/EEA countries, January 2020." Euro Surveill **25**(6).

Timely detection of novel coronavirus (2019-nCoV) infection cases is crucial to interrupt the spread of this virus. We assessed the required expertise and capacity for molecular detection of 2019-nCoV in specialised laboratories in 30 European Union/European Economic Area (EU/EEA) countries. Thirty-eight laboratories in 24 EU/EEA countries had diagnostic tests available by 29 January 2020. A coverage of all EU/EEA countries was expected by mid-February. Availability of primers/probes, positive controls and personnel were main implementation barriers.

Runfeng, L., et al. (2020). "Lianhuaqingwen exerts anti-viral and anti-inflammatory activity against novel coronavirus (SARS-CoV-2)." Pharmacol Res: 104761.

PURPOSE: Lianhuaqingwen (LH) as traditional Chinese medicine (TCM) formula has been used to treat influenza and exerted broad-spectrum antiviral effects on a series of influenza viruses and immune regulatory effects [1]. The goal of this study is to demonstrate the antiviral activity of LH against the novel SARS-CoV-2 virus and its potential effect in regulating host immune response. METHODS: The antiviral activity of LH against SARS-CoV-2 was assessed in Vero E6 cells using CPE and plaque reduction assay. The effect of LH on virion morphology was visualized under transmission electron microscope. Pro-inflammatory cytokine expression levels upon SARS-CoV-2 infection in Huh-7 cells were measured by real-time quantitative PCR assays. RESULTS: LH significantly inhibited SARS-CoV-2 replication in Vero E6 cells and markedly reduced pro-inflammatory cytokines (TNF-alpha, IL-6, CCL-2/MCP-1 and CXCL-10/IP-10) production at the mRNA levels. Furthermore, LH treatment resulted in abnormal particle morphology of virion in cells. CONCLUSIONS: LH significantly inhibits the SARS-COV-2 replication, affects virus morphology and exerts anti-inflammatory activity in vitro. These findings indicate that LH protects against the virus attack, making its use a novel strategy for controlling the COVID-19 disease.

Ryu, S., et al. (2020). "An interim review of the epidemiological characteristics of 2019 novel coronavirus." Epidemiol Health **42**: e2020006.

OBJECTIVES: The 2019 novel coronavirus (2019-nCoV) from Wuhan, China is currently recognized as a public health emergency of global concern. METHODS: We reviewed the currently available literature to provide up-to-date guidance on control measures to be implemented by public health authorities. RESULTS: Some of the epidemiological characteristics of 2019-nCoV have been identified. However, there remain considerable uncertainties, which should be considered when providing guidance to public health authorities on control measures. CONCLUSIONS: Additional studies incorporating more detailed information from confirmed cases would be valuable.

Sekimukai, H., et al. (2020). "Gold nanoparticle-adjuvanted S protein induces a strong antigen-specific IgG response against severe acute respiratory syndrome-related coronavirus infection, but fails to induce protective antibodies and limit eosinophilic infiltration in lungs." Microbiol Immunol **64**(1): 33-51.

The spike (S) protein of coronavirus, which binds to cellular receptors and mediates membrane fusion for cell entry, is a candidate vaccine target for blocking coronavirus infection. However, some animal studies have suggested that inadequate immunization against severe acute respiratory syndrome coronavirus (SARS-CoV) induces a lung eosinophilic immunopathology upon infection. The present study evaluated two kinds of vaccine adjuvants for use with recombinant S protein: gold nanoparticles (AuNPs), which are expected to function as both an antigen carrier and an adjuvant in immunization; and Toll-like receptor (TLR) agonists, which have previously been shown to be an effective adjuvant in an ultraviolet-inactivated SARS-CoV vaccine. All the mice immunized with more than 0.5 microg S protein without adjuvant escaped from SARS after infection with mouse-adapted SARS-CoV; however, eosinophilic infiltrations were observed in the lungs of almost all the immunized mice. The AuNP-adjuvanted protein induced a strong IgG response but failed to improve vaccine efficacy or to reduce eosinophilic infiltration because of highly allergic inflammatory responses. Whereas similar virus titers were observed in the control animals and the animals immunized with S protein with or without AuNPs, Type 1 interferon and pro-inflammatory responses were moderate in the mice treated with S protein with and without AuNPs. On the other hand, the TLR agonist-adjuvanted vaccine induced highly protective antibodies without eosinophilic infiltrations, as well as Th1/17 cytokine responses. The findings of this study will support the development of vaccines against severe pneumonia-associated coronaviruses.

Shang, J., et al. (2020). "Structure of mouse coronavirus spike protein complexed with receptor reveals mechanism for viral entry." PLoS Pathog **16**(3): e1008392.

Coronaviruses recognize a variety of receptors using different domains of their envelope-anchored spike protein. How these diverse receptor recognition patterns affect viral entry is unknown. Mouse hepatitis coronavirus (MHV) is the only known coronavirus that uses the N-terminal domain (NTD) of its spike to recognize a protein receptor, CEACAM1a. Here we determined the cryo-EM structure of MHV spike complexed with mouse CEACAM1a. The trimeric spike contains three receptor-binding S1 heads sitting on top of a trimeric membrane-fusion S2 stalk. Three receptor molecules bind to the sides of the spike trimer, where three NTDs are located. Receptor binding induces structural changes in the spike, weakening the interactions between S1 and S2. Using protease sensitivity and negative-stain EM analyses, we further showed that after protease treatment of the spike, receptor binding facilitated the dissociation of S1 from S2, allowing S2 to transition from pre-fusion to post-fusion conformation. Together these results reveal a new role of receptor binding in MHV entry: in addition to its well-characterized role in viral attachment to host cells, receptor binding also induces the conformational change of the spike and hence the fusion of viral and host membranes. Our study provides new mechanistic insight into coronavirus entry and highlights the diverse entry mechanisms used by different viruses.

Shanmugaraj, B., et al. (2020). "Emergence of Novel Coronavirus 2019-nCoV: Need for Rapid Vaccine and Biologics Development." Pathogens **9**(2).

Novel Coronavirus (2019-nCoV) is an emerging pathogen that was first identified in Wuhan, China in late December 2019. This virus is responsible for the ongoing outbreak that causes severe respiratory illness and pneumonia-like infection in humans. Due to the increasing number of cases in China and outside China, the WHO declared coronavirus as a global health emergency. Nearly 35,000 cases were reported and at least 24 other countries or territories have reported coronavirus cases as early on as February. Inter-human transmission was reported in a few countries, including the United States. Neither an effective anti-viral nor a vaccine is currently available to treat this infection. As the virus is a newly emerging pathogen, many questions remain unanswered regarding the virus's reservoirs, pathogenesis, transmissibility, and much more is unknown. The collaborative efforts of researchers are needed to fill the knowledge gaps about this new virus, to develop the proper diagnostic tools, and effective treatment to combat this infection. Recent advancements in plant biotechnology proved that plants have the ability to produce vaccines or biopharmaceuticals rapidly in a short time. In this review, the outbreak of 2019-nCoV in China, the need for rapid vaccine development, and the potential of a plant system for biopharmaceutical development are discussed.

Shanmugaraj, B., et al. (2020). "Perspectives on monoclonal antibody therapy as potential therapeutic intervention for Coronavirus disease-19 (COVID-19)." Asian Pac J Allergy Immunol **38**(1): 10-18.

Last decade witnessed the outbreak of many life-threatening human pathogens including Nipah, Ebola, Chikungunya, Zika, Middle East respiratory syndrome coronavirus (MERS-CoV), Severe Acute respiratory syndrome coronavirus (SARS-CoV) and more recently novel coronavirus (2019-nCoV or SARS-CoV-2). The disease condition associated with novel coronavirus, referred to as Coronavirus disease (COVID-19). The emergence of novel coronavirus in 2019 in Wuhan, China marked the third highly pathogenic coronavirus infecting humans in the 21st century. The continuing emergence of coronaviruses at regular intervals poses a significant threat to human health and economy. Ironically, even after a decade of research on coronavirus, still there are no licensed vaccines or therapeutic agents to treat coronavirus infection which highlights an urgent need to develop effective vaccines or post-exposure prophylaxis to prevent future epidemics. Several clinical, genetic and epidemiological features of COVID-19 resemble SARS-CoV infection. Hence, the research advancements on SARS-CoV treatment might help scientific community in quick understanding of this virus pathogenesis and develop effective therapeutic/prophylactic agents to treat and prevent this infection. Monoclonal antibodies represent the major class of biotherapeutics for passive immunotherapy to fight against viral infection. The therapeutic potential of monoclonal antibodies has been well recognized in the treatment of many diseases. Here, we summarize the potential monoclonal antibody based therapeutic intervention for COVID-19 by considering the existing knowledge on the neutralizing monoclonal antibodies against similar coronaviruses SARS-CoV and MERS-CoV. Further research on COVID-19 pathogenesis could identify appropriate therapeutic targets to develop specific anti-virals against this newly emerging pathogen.

She, J., et al. (2020). "2019 novel coronavirus of pneumonia in Wuhan, China: emerging attack and management strategies." Clin Transl Med **9**(1): 19.

An ongoing outbreak of 2019-nCoV pneumonia was first identified in Wuhan, Hubei province, China at the end of 2019. With the spread of the new coronavirus accelerating, person-to-person transmission in family homes or hospitals, and intercity spread of 2019-nCoV occurred. At least 40,261 cases confirmed, 23,589 cases suspected, 909 cases death and 3444 cases cured in China and worldwide 24 countries confirmed 383 cases being diagnosed, 1 case death in February 10th, 2020. At present, the mortality of 2019-nCoV in China is 2.3%, compared with 9.6% of SARS and 34.4% of MERS reported by WHO. It seems the new virus is not as fatal as many people thought. Chinese authorities improved surveillance network, made the laboratory be able to recognize the outbreak within a few weeks and announced the virus genome that provide efficient epidemiological control. More comprehensive information is required to understand 2019-nCoV feature, the epidemiology of origin and spreading, and the clinical phenomina. According to the current status, blocking transmission, isolation, protection, and alternative medication are the urgent management strategies against 2019-nCoV.

Sheikh, A., et al. (2020). "Analysis of preferred codon usage in the coronavirus N genes and their implications for genome evolution and vaccine design." J Virol Methods **277**: 113806.

The nucleocapsid (N) protein of a coronavirus plays a crucial role in virus assembly and in its RNA transcription. It is important to characterize a virus at the nucleotide level to discover the virus's genomic sequence variations and similarities relative to other viruses that could have an impact on the functions of its genes and proteins. This entails a comprehensive and comparative analysis of the viral genomes of interest for preferred nucleotides, codon bias, nucleotide changes at the 3(rd) position (NT3s), synonymous codon usage and relative synonymous codon usage. In this study, the variations in the N proteins among 13 different coronaviruses (CoVs) were analysed at the nucleotide and amino acid levels in an attempt to reveal how these viruses adapt to their hosts relative to their preferred codon usage in the N genes. The results revealed that, overall, eighteen amino acids had different preferred codons and eight of these were over-biased. The N genes had a higher AT% over GC% and the values of their effective number of codons ranged from 40.43 to 53.85, indicating a slight codon bias. Neutrality plots and correlation analyses showed a very high level of GC3s/GC correlation in porcine epidemic diarrhea CoV (pedCoV), followed by Middle East respiratory syndrome-CoV (MERS CoV), porcine delta CoV (dCoV), bat CoV (bCoV) and feline CoV (fCoV) with r values 0.81, 0.68, -0.47, 0.98 and 0.58, respectively. These data implied a high rate of evolution of the CoV genomes and a strong influence of mutation on evolutionary selection in the CoV N genes. This type of genetic analysis would be useful for evaluating a virus's host adaptation, evolution and is thus of value to vaccine design strategies.

Shen, K., et al. (2020). "Diagnosis, treatment, and prevention of 2019 novel coronavirus infection in children: experts' consensus statement." World J Pediatr.

Since the outbreak of 2019 novel coronavirus infection (2019-nCoV) in Wuhan City, China, by January 30, 2020, a total of 9692 confirmed cases and 15,238 suspected cases have been reported around 31 provinces or cities in China. Among the confirmed cases, 1527 were severe cases, 171 had recovered and been discharged at home, and 213 died. And among these cases, a total of 28 children aged from 1 month to 17 years have been reported in China. For standardizing prevention and management of 2019-nCoV infections in children, we called up an experts' committee to formulate this experts' consensus statement. This statement is based on the Novel Coronavirus Infection Pneumonia Diagnosis and Treatment Standards (the fourth edition) (National Health Committee) and other previous diagnosis and treatment strategies for pediatric virus infections. The present consensus statement summarizes current strategies on diagnosis, treatment, and prevention of 2019-nCoV infection in children.

Shen, Z., et al. (2020). "Genomic diversity of SARS-CoV-2 in Coronavirus Disease 2019 patients." Clin Infect Dis.

BACKGROUND: A novel coronavirus (SARS-CoV-2) has infected more than 75,000 individuals and spread to over 20 countries. It is still unclear how fast the virus evolved and how the virus interacts with other microorganisms in the lung. METHODS: We have conducted metatranscriptome sequencing for the bronchoalveolar lavage fluid of eight SARS-CoV-2 patients, 25 community-acquired pneumonia (CAP) patients, and 20 healthy controls. RESULTS: The median number of intra-host variants was 1-4 in SARS-CoV-2 infected patients, which ranged between 0 and 51 in different samples. The distribution of variants on genes was similar to those observed in the population data (110 sequences). However, very few intra-host variants were observed in the population as polymorphism, implying either a bottleneck or purifying selection involved in the transmission of the virus, or a consequence of the limited diversity represented in the current polymorphism data. Although current evidence did not support the transmission of intra-host variants in a person-to-person spread, the risk should not be overlooked. The microbiota in SARS-CoV-2 infected patients was similar to those in CAP, either dominated by the pathogens or with elevated levels of oral and upper respiratory commensal bacteria. CONCLUSION: SARS-CoV-2 evolves in vivo after infection, which may affect its virulence, infectivity, and transmissibility. Although how the intra-host variant spreads in the population is still elusive, it is necessary to strengthen the surveillance of the viral evolution in the population and associated clinical changes.

Singh, S., et al. (2020). "Immunohistochemical and molecular detection of natural cases of bovine rotavirus and coronavirus infection causing enteritis in dairy calves." Microb Pathog **138**: 103814.

Bovine rotavirus (BRoV) and bovine coronavirus (BCoV) are major enteric viral pathogens responsible for calve diarrhoea. They are widespread both in dairy and beef cattle throughout the world and causing huge economic losses. The diagnosis of these agents is very difficult due to non-specific nature of lesions and the involvement of some intrinsic and extrinsic risk factors. We performed postmortem of 45 calves, which was below three months of age. Out of 45 necropscid calves, three (6.66%) cases were positive for BRoV and four (8.88%) cases were found positive for BCoV, screened by reverse transcriptase polymerase chain reaction (RT-PCR). Further RT-PCR positive cases were confirmed by immunohistochemistry (IHC) in paraffin-embedded intestinal tissue sections. Three cases of enteritis caused by BRoV showed the hallmark lesions of the shortening and fusion of villi, denudation and infiltration of mononuclear cells in the lamina propria. The BRoV antigen distribution was prominent within the lining epithelium of the villi, peyer's patches in the ileum and strong immunoreactions in the lymphocytes and some macrophages of the mesenteric lymph nodes. Four cases in which BCoV was detected, grossly lesions characterized by colonic mucosa covered with thick, fibrinous and diphtheritic membrane. Histopathologically, jejunum showed skipping lesion of micro-abscesses in crypts. The BCoV antigen distribution was prominent within the necrotic crypts in the jejunum and cryptic micro-abscesses in the colon and ileum. It is the first report of BRoV and BCoV antigen demonstration in the jejunum, colon, ileum, Peyer's patches and mesenteric lymph nodes of naturally infected calves from India by using IHC.

Singhal, T. (2020). "A Review of Coronavirus Disease-2019 (COVID-19)." Indian J Pediatr **87**(4): 281-286.

There is a new public health crises threatening the world with the emergence and spread of 2019 novel coronavirus (2019-nCoV) or the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The virus originated in bats and was transmitted to humans through yet unknown intermediary animals in Wuhan, Hubei province, China in December 2019. There have been around 96,000 reported cases of coronavirus disease 2019 (COVID-2019) and 3300 reported deaths to date (05/03/2020). The disease is transmitted by inhalation or contact with infected droplets and the incubation period ranges from 2 to 14 d. The symptoms are usually fever, cough, sore throat, breathlessness, fatigue, malaise among others. The disease is mild in most people; in some (usually the elderly and those with comorbidities), it may progress to pneumonia, acute respiratory distress syndrome (ARDS) and multi organ dysfunction. Many people are asymptomatic. The case fatality rate is estimated to range from 2 to 3%. Diagnosis is by demonstration of the virus in respiratory secretions by special molecular tests. Common laboratory findings include normal/ low white cell counts with elevated C-reactive protein (CRP). The computerized tomographic chest scan is usually abnormal even in those with no symptoms or mild disease. Treatment is essentially supportive; role of antiviral agents is yet to be established. Prevention entails home isolation of suspected cases and those with mild illnesses and strict infection control measures at hospitals that include contact and droplet precautions. The virus spreads faster than its two ancestors the SARS-CoV and Middle East respiratory syndrome coronavirus (MERS-CoV), but has lower fatality. The global impact of this new epidemic is yet uncertain.

Sohrabi, C., et al. (2020). "World Health Organization declares global emergency: A review of the 2019 novel coronavirus (COVID-19)." Int J Surg **76**: 71-76.

An unprecedented outbreak of pneumonia of unknown aetiology in Wuhan City, Hubei province in China emerged in December 2019. A novel coronavirus was identified as the causative agent and was subsequently termed COVID-19 by the World Health Organization (WHO). Considered a relative of severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS), COVID-19 is caused by a betacoronavirus named SARS-CoV-2 that affects the lower respiratory tract and manifests as pneumonia in humans. Despite rigorous global containment and quarantine efforts, the incidence of COVID-19 continues to rise, with 90,870 laboratory-confirmed cases and over 3,000 deaths worldwide. In response to this global outbreak, we summarise the current state of knowledge surrounding COVID-19.

Song, F., et al. (2020). "Emerging 2019 Novel Coronavirus (2019-nCoV) Pneumonia." Radiology **295**(1): 210-217.

BackgroundThe chest CT findings of patients with 2019 Novel Coronavirus (2019-nCoV) pneumonia have not previously been described in detail.PurposeTo investigate the clinical, laboratory, and imaging findings of emerging 2019-nCoV pneumonia in humans.Materials and MethodsFifty-one patients (25 men and 26 women; age range 16-76 years) with laboratory-confirmed 2019-nCoV infection by using real-time reverse transcription polymerase chain reaction underwent thin-section CT. The imaging findings, clinical data, and laboratory data were evaluated.ResultsFifty of 51 patients (98%) had a history of contact with individuals from the endemic center in Wuhan, China. Fever (49 of 51, 96%) and cough (24 of 51, 47%) were the most common symptoms. Most patients had a normal white blood cell count (37 of 51, 73%), neutrophil count (44 of 51, 86%), and either normal (17 of 51, 35%) or reduced (33 of 51, 65%) lymphocyte count. CT images showed pure ground-glass opacity (GGO) in 39 of 51 (77%) patients and GGO with reticular and/or interlobular septal thickening in 38 of 51 (75%) patients. GGO with consolidation was present in 30 of 51 (59%) patients, and pure consolidation was present in 28 of 51 (55%) patients. Forty-four of 51 (86%) patients had bilateral lung involvement, while 41 of 51 (80%) involved the posterior part of the lungs and 44 of 51 (86%) were peripheral. There were more consolidated lung lesions in patients 5 days or more from disease onset to CT scan versus 4 days or fewer (431 of 712 lesions vs 129 of 612 lesions; P <.001). Patients older than 50 years had more consolidated lung lesions than did those aged 50 years or younger (212 of 470 vs 198 of 854; P <.001). Follow-up CT in 13 patients showed improvement in seven (54%) patients and progression in four (31%) patients.ConclusionPatients with fever and/or cough and with conspicuous ground-glass opacity lesions in the peripheral and posterior lungs on CT images, combined with normal or decreased white blood cells and a history of epidemic exposure, are highly suspected of having 2019 Novel Coronavirus (2019-nCoV) pneumonia. (c) RSNA, 2020.

Song, Q. Q., et al. (2020). "[Study on assessing early epidemiological parameters of coronavirus disease epidemic in China]." Zhonghua Liu Xing Bing Xue Za Zhi **41**(4): 461-465.

Objective: To study the early dynamics of the epidemic of coronavirus disease (COVID-19) in China from 15 to 31 January, 2020, and estimate the corresponding epidemiological parameters (incubation period, generation interval and basic reproduction number) of the epidemic. Methods: By means of Weibull, Gamma and Lognormal distributions methods, we estimated the probability distribution of the incubation period and generation interval data obtained from the reported COVID-19 cases. Moreover, the AIC criterion was used to determine the optimal distribution. Considering the epidemic is ongoing, the exponential growth model was used to fit the incidence data of COVID-19 from 10 to 31 January, 2020, and exponential growth method, maximum likelihood method and SEIR model were used to estimate the basic reproduction number. Results: Early COVID-19 cases kept an increase in exponential growth manner before 26 January, 2020, then the increase trend became slower. The average incubation period was 5.01 (95%CI: 4.31-5.69) days; the average generation interval was 6.03 (95%CI: 5.20-6.91) days. The basic reproduction number was estimated to be 3.74 (95%CI: 3.63-3.87), 3.16 (95%CI: 2.90-3.43), and 3.91 (95%CI: 3.71-4.11) by three methods, respectively. Conclusions: The Gamma distribution fits both the generation interval and incubation period best, and the mean value of generation interval is 1.02 day longer than that of incubation period. The relatively high basic reproduction number indicates that the epidemic is still serious; Based on our analysis, the turning point of the epidemic would be seen on 26 January, the growth rate would be lower afterwards.

Sun, D., et al. (2020). "Clinical features of severe pediatric patients with coronavirus disease 2019 in Wuhan: a single center's observational study." World J Pediatr.

BACKGROUND: An outbreak of coronavirus disease 2019 (COVID-19) caused by SARS-CoV-2 was first detected in Wuhan, Hubei, China. People of all ages are susceptible to SARS-CoV-2 infection. No information on severe pediatric patients with COVID-19 has been reported. We aimed to describe the clinical features of severe pediatric patients with COVID-19. METHODS: We included eight severe or critically ill patients with COVID-19 who were treated at the Intensive Care Unit (ICU), Wuhan Children's Hospital from January 24 to February 24. We collected information including demographic data, symptoms, imaging data, laboratory findings, treatments and clinical outcomes of the patients with severe COVID-19. RESULTS: The onset age of the eight patients ranged from 2 months to 15 years; six were boys. The most common symptoms were polypnea (8/8), followed by fever (6/8) and cough (6/8). Chest imaging showed multiple patch-like shadows in seven patients and ground-glass opacity in six. Laboratory findings revealed normal or increased whole blood counts (7/8), increased C-reactive protein, procalcitonin and lactate dehydrogenase (6/8), and abnormal liver function (4/8). Other findings included decreased CD16 + CD56 (4/8) and Th/Ts*(1/8), increased CD3 (2/8), CD4 (4/8) and CD8 (1/8), IL-6 (2/8), IL-10 (5/8) and IFN-gamma (2/8). Treatment modalities were focused on symptomatic and respiratory support. Two critically ill patients underwent invasive mechanical ventilation. Up to February 24, 2020, three patients remained under treatment in ICU, the other five recovered and were discharged home. CONCLUSIONS: In this series of severe pediatric patients in Wuhan, polypnea was the most common symptom, followed by fever and cough. Common imaging changes included multiple patch-like shadows and ground-glass opacity; and a cytokine storm was found in these patients, which appeared more serious in critically ill patients.

Sun, W. W., et al. (2020). "[Epidemiological characteristics of 2019 novel coronavirus family clustering in Zhejiang Province]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E027.

Objective: Family clusters of Novel coronavirus pneumonia in Zhejiang province were analyzed to provide epidemiological basis for disease control. Methods: The data of family clusters occurred from January 20 to February 10 in Zhejiang Province were collected. Descriptive analysis was used to analyze the clinical symptoms and the serial interval between the subsequent cases and the index cases. Chi-square test was used to analyze the age distribution, gender distribution and the relationship between the subsequent cases and the index cases. Results: 391 cases including 148 family index cases, 189 subsequent cases and 54 asymptomatic infected cases. The clinical symptoms between family index cases and subsequent cases are similar, fever is the most common symptoms in the two groups 114 (77.03%) and 92 (48.68%) respectively, the cases with diarrhea symptoms accounted for the least proportion, which were 7 (4.73%) and 5 (2.65%). The serial interval between the family index cases and the subsequent cases [M (P (25), P (75))] was 3.00 (1.00, 6.00) days. Family secondary attack rate for subsequent cases and asymptomatic infected cases are 31.61% and 43.20% respectively, the family secondary attack rate of the spouses of the family index cases is 63.87%, and are higher than that of their children (30.53%), parents (28.37%) and other family members (20.93%), the difference was statistically significant. Conclusion: 2019 novel coronavirus has shorter serial interval and higher family secondary attack rate, the secondary attack rate of spouses is higher than other family members.

Tang, N., et al. (2020). "Abnormal coagulation parameters are associated with poor prognosis in patients with novel coronavirus pneumonia." J Thromb Haemost.

BACKGROUND: In the recent outbreak of novel coronavirus infection in Wuhan, China, significantly abnormal coagulation parameters in severe novel coronavirus pneumonia (NCP) cases were a concern. OBJECTIVES: To describe the coagulation feature of patients with NCP. METHODS: Conventional coagulation results and outcomes of 183 consecutive patients with confirmed NCP in Tongji hospital were retrospectively analyzed. RESULTS: The overall mortality was 11.5%, the non-survivors revealed significantly higher D-dimer and fibrin degradation product (FDP) levels, longer prothrombin time and activated partial thromboplastin time compared to survivors on admission (P <.05); 71.4% of non-survivors and 0.6% survivors met the criteria of disseminated intravascular coagulation during their hospital stay. CONCLUSIONS: The present study shows that abnormal coagulation results, especially markedly elevated D-dimer and FDP are common in deaths with NCP.

Thompson, R. N. (2020). "Novel Coronavirus Outbreak in Wuhan, China, 2020: Intense Surveillance Is Vital for Preventing Sustained Transmission in New Locations." J Clin Med **9**(2).

The outbreak of pneumonia originating in Wuhan, China, has generated 24,500 confirmed cases, including 492 deaths, as of 5 February 2020. The virus (2019-nCoV) has spread elsewhere in China and to 24 countries, including South Korea, Thailand, Japan and USA. Fortunately, there has only been limited human-to-human transmission outside of China. Here, we assess the risk of sustained transmission whenever the coronavirus arrives in other countries. Data describing the times from symptom onset to hospitalisation for 47 patients infected early in the current outbreak are used to generate an estimate for the probability that an imported case is followed by sustained human-to-human transmission. Under the assumptions that the imported case is representative of the patients in China, and that the 2019-nCoV is similarly transmissible to the SARS coronavirus, the probability that an imported case is followed by sustained human-to-human transmission is 0.41 (credible interval [0.27, 0.55]). However, if the mean time from symptom onset to hospitalisation can be halved by intense surveillance, then the probability that an imported case leads to sustained transmission is only 0.012 (credible interval [0, 0.099]). This emphasises the importance of current surveillance efforts in countries around the world, to ensure that the ongoing outbreak will not become a global pandemic.

Tian, H. Y. (2020). "[2019-nCoV: new challenges from coronavirus]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(3): 235-238.

The outbreak of pneumonia caused by the novel coronavirus (2019-nCoV) in Wuhan, Hubei province of China, at the end of 2019 shaped tremendous challenges to China's public health and clinical treatment. The virus belongs to the beta genus Coronavirus in the family Corornaviridae, and is closely related to SARS-CoV and MERS-CoV, causing severe symptoms of pneumonia. The virus is transmitted through droplets, close contact, and other means, and patients in the incubation period could potentially transmit the virus to other persons. According to current observations, 2019-nCoV is weaker than SARS in pathogenesis, but has stronger transmission competence; it's mechanism of cross-species spread might be related with angiotensin-converting enzyme (ACE2), which is consistent with the receptor SARS-CoV. After the outbreak of this disease, Chinese scientists invested a lot of energy to carry out research by developing rapid diagnostic reagents, identifying the characters of the pathogen, screening out clinical drugs that may inhibit the virus, and are rapidly developing vaccines. The emergence of 2019-nCoV reminds us once again of the importance of establishing a systematic coronavirus surveillance network. It also poses new challenges to prevention and control of the emerging epidemic and rapidly responses on scientific research.

Tian, H. Y. (2020). "[2019-nCoV: new challenges from coronavirus]." Zhonghua Yu Fang Yi Xue Za Zhi **54**(0): E001.

The outbreak of pneumonia caused by the novel coronavirus 2019-nCoV in Wuhan, Hubei province of China, at the end of 2019 shaped tremendous challenges to China's public health and clinical treatment. The virus belongs to the beta genus Coronavirus in the family Corornaviridae, and is closely related to SARS-CoV and MERS-CoV, causing severe symptoms of pneumonia. The virus is transmitted through droplets, close contact, and other means, and patients in the incubation period could potentially transmit the virus to other persons. According to current observations, 2019-nCoV is weaker than SARS in pathogenesis, but has stronger transmission competence; it's mechanism of cross-species spread might be related with angiotensin-converting enzyme (ACE2), which is consistent with the receptor SARS-CoV. After the outbreak of this disease, Chinese scientists invested a lot of energy to carry out research by developing rapid diagnostic reagents, identifying the characters of the pathogen, screening out clinical drugs that may inhibit the virus, and are rapidly developing vaccines. The emergence of 2019-nCoV reminds us once again of the importance of establishing a systematic coronavirus surveillance network. It also poses new challenges to prevention and control of the emerging epidemic and rapidly responses on scientific research.

Tian, S., et al. (2020). "Pulmonary Pathology of Early-Phase 2019 Novel Coronavirus (COVID-19) Pneumonia in Two Patients With Lung Cancer." J Thorac Oncol.

There is currently a lack of pathologic data on the novel coronavirus (severe acute respiratory syndrome coronavirus 2) pneumonia, or coronavirus disease 2019 (COVID-19), from autopsy or biopsy. Two patients who recently underwent lung lobectomies for adenocarcinoma were retrospectively found to have had COVID-19 at the time of the operation. These two cases thus provide important first opportunities to study the pathology of COVID-19. Pathologic examinations revealed that apart from the tumors, the lungs of both patients exhibited edema, proteinaceous exudate, focal reactive hyperplasia of pneumocytes with patchy inflammatory cellular infiltration, and multinucleated giant cells. Hyaline membranes were not prominent. Because both patients did not exhibit symptoms of pneumonia at the time of operation, these changes likely represent an early phase of the lung pathology of COVID-19 pneumonia.

Tian, X., et al. (2020). "Potent binding of 2019 novel coronavirus spike protein by a SARS coronavirus-specific human monoclonal antibody." Emerg Microbes Infect **9**(1): 382-385.

The newly identified 2019 novel coronavirus (2019-nCoV) has caused more than 11,900 laboratory-confirmed human infections, including 259 deaths, posing a serious threat to human health. Currently, however, there is no specific antiviral treatment or vaccine. Considering the relatively high identity of receptor-binding domain (RBD) in 2019-nCoV and SARS-CoV, it is urgent to assess the cross-reactivity of anti-SARS CoV antibodies with 2019-nCoV spike protein, which could have important implications for rapid development of vaccines and therapeutic antibodies against 2019-nCoV. Here, we report for the first time that a SARS-CoV-specific human monoclonal antibody, CR3022, could bind potently with 2019-nCoV RBD (KD of 6.3 nM). The epitope of CR3022 does not overlap with the ACE2 binding site within 2019-nCoV RBD. These results suggest that CR3022 may have the potential to be developed as candidate therapeutics, alone or in combination with other neutralizing antibodies, for the prevention and treatment of 2019-nCoV infections. Interestingly, some of the most potent SARS-CoV-specific neutralizing antibodies (e.g. m396, CR3014) that target the ACE2 binding site of SARS-CoV failed to bind 2019-nCoV spike protein, implying that the difference in the RBD of SARS-CoV and 2019-nCoV has a critical impact for the cross-reactivity of neutralizing antibodies, and that it is still necessary to develop novel monoclonal antibodies that could bind specifically to 2019-nCoV RBD.

Tian, X. L., et al. (2020). "[The differential diagnosis for novel coronavirus pneumonia and similar lung diseases in general hospitals]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E035.

Novel coronavirus pneumonia was novel coronavirus infection that has dominated pulmonary infection since December 2019. The main manifestations were fever, dry cough, shortness of breath, normal or leukopenia in peripheral blood and changes in chest CT and in severe cases, multiple organ failure might occur. The National Health Commission, PRC has revised the consensus on diagnosis and treatment seven times in a short period of time, indicating the growing understanding of the disease. Patients with novel coronavirus pneumonia usually had history of travelling or living in the epidemic area including Wuhan within 14 days before onset, or have been exposed to patients who had fever or respiratory symptoms from the epidemic area, or had clustering diseases. However, novel coronavirus pneumonia was becoming more and more blurred after vanishing epidemic. The diagnosis and differential diagnosis of novel coronavirus pneumonia was facing challenges not only because of large number of tourists increasing dramatically after the relieving of epidemic, but also patients with other diseases return from different areas to search for medical care. In this article, the clinical and chest imaging features of the novel coronavirus pneumonia were reviewed and compared with other infections and non-infectious diffuse pulmonary diseases. We were trying to find the similarities and differences among them, and to identify clues to the diagnosis of novel coronavirus pneumonia, so as to ensure accurate diagnosis and treatment.

Volk, A., et al. (2020). "Coronavirus Endoribonuclease and Deubiquitinating Interferon Antagonists Differentially Modulate the Host Response during Replication in Macrophages." J Virol.

Coronaviruses encode multiple interferon antagonists that modulate the host response to virus replication. Here, we evaluated the host transcriptional response to infection with murine coronaviruses encoding independent mutations in one of two different viral antagonists: the deubiquitinase (DUB) within nonstructural protein 3 or the endoribonuclease (EndoU) within nonstructural protein 15. We used transcriptomics approaches to compare the scope and kinetics of the host response to the wild-type, DUBmut, and EndoUmut viruses in infected macrophages. We found that the EndoUmut virus activates a focused response predominantly involving type I interferons and interferon-related genes, whereas the WT and DUBmut viruses more broadly stimulate upregulation of over 2,800 genes, including networks associated with activating the unfolded protein response (UPR), and the proinflammatory response associated with viral pathogenesis. This study highlights the role of viral interferon antagonists in shaping the kinetics and magnitude of the host response during virus infection and demonstrates that inactivating a dominant viral antagonist, the coronavirus endoribonuclease, dramatically alters the host response in macrophages.ImportanceMacrophages are an important cell type during coronavirus infections because they "notice" the infection and respond by inducing type I interferons, which limits virus replication. In turn, coronaviruses encode proteins that mitigate the cell's ability to signal an interferon response. Here, we evaluated the host macrophage response to two independent mutant coronaviruses: one with reduced deubiquitinating activity (DUBmut) and the other containing an inactivated endoribonuclease (EndoUmut). We observed a rapid, robust, and focused response to the EndoUmut virus, which was characterized by enhanced expression of interferon and interferon-related genes. In contrast, wild-type virus and the DUBmut virus elicited a more limited interferon response and ultimately activated over 2,800 genes, including players in the unfolded protein response and pro-inflammatory pathways associated with progression of significant disease. This study reveals that EndoU activity substantially contributes to the ability of coronaviruses to evade the host innate response and to replicate in macrophages.

Wang, Y., et al. (2020). "Unique epidemiological and clinical features of the emerging 2019 novel coronavirus pneumonia (COVID-19) implicate special control measures." J Med Virol.

By Feb 27(th), 2020, the outbreak of COVID-19 caused 82623 confirmed cases and 2858 deaths globally, more than Severe Acute Respiratory Syndrome (SARS) (8273 cases, 775 deaths) and Middle East Respiratory Syndrome (MERS) (1139 cases, 431 deaths) caused in 2003 and 2013 respectively. COVID-19 has spread to 46 countries internationally. Total fatality rate of COVID-19 is estimated at 3.46% by far based on published data from Chinese Center for Disease Control and Prevention (China CDC). Average incubation period of COVID-19 is around 6.4 days, ranges from 0-24 days. The basic reproductive number (R0) of COVID-19 ranges from 2-3.5 at the early phase regardless of different prediction models, which is higher than SARS and MERS. A study from China CDC showed majority of patients (80.9%) were considered asymptomatic or mild pneumonia but released large amounts of viruses at the early phase of infection, which posed enormous challenges for containing the spread of COVID-19. Nosocomial transmission was another severe problem. 3019 health workers were infected by Feb 12, 2020, which accounted for 3.83% of total number of infections, and extremely burdened the health system, especially in Wuhan. Limited epidemiological and clinical data suggest that the disease spectrum of COVID-19 may differ from SARS or MERS. We summarize latest literatures on genetic, epidemiological, and clinical features of COVID-19 in comparison to SARS and MERS and emphasize special measures on diagnosis and potential interventions. This review will improve our understanding of the unique features of COVID-19 and enhance our control measures in the future. This article is protected by copyright. All rights reserved.

Whittaker, G. R. and J. K. Millet (2020). "Biochemical Characterization of Middle East Respiratory Syndrome Coronavirus Spike Protein Proteolytic Processing." Methods Mol Biol **2099**: 21-37.

The coronavirus spike envelope glycoprotein is an essential viral component that mediates virus entry events. Biochemical assessment of the spike protein is critical for understanding structure-function relationships and the roles of the protein in the viral life cycle. Coronavirus spike proteins are typically proteolytically processed and activated by host cell enzymes such as trypsin-like proteases, cathepsins, or proprotein-convertases. Analysis of coronavirus spike proteins by western blot allows the visualization and assessment of proteolytic processing by endogenous or exogenous proteases. Here, we present a method based on western blot analysis to investigate spike protein proteolytic cleavage by transient transfection of HEK-293 T cells allowing expression of the spike protein of the highly pathogenic Middle East respiratory syndrome coronavirus in the presence or absence of a cellular trypsin-like transmembrane serine protease, matriptase. Such analysis enables the characterization of cleavage patterns produced by a host protease on a coronavirus spike glycoprotein.

Wu, C., et al. (2020). "Risk Factors Associated With Acute Respiratory Distress Syndrome and Death in Patients With Coronavirus Disease 2019 Pneumonia in Wuhan, China." JAMA Intern Med.

Importance: Coronavirus disease 2019 (COVID-19) is an emerging infectious disease that was first reported in Wuhan, China, and has subsequently spread worldwide. Risk factors for the clinical outcomes of COVID-19 pneumonia have not yet been well delineated. Objective: To describe the clinical characteristics and outcomes in patients with COVID-19 pneumonia who developed acute respiratory distress syndrome (ARDS) or died. Design, Setting, and Participants: Retrospective cohort study of 201 patients with confirmed COVID-19 pneumonia admitted to Wuhan Jinyintan Hospital in China between December 25, 2019, and January 26, 2020. The final date of follow-up was February 13, 2020. Exposures: Confirmed COVID-19 pneumonia. Main Outcomes and Measures: The development of ARDS and death. Epidemiological, demographic, clinical, laboratory, management, treatment, and outcome data were also collected and analyzed. Results: Of 201 patients, the median age was 51 years (interquartile range, 43-60 years), and 128 (63.7%) patients were men. Eighty-four patients (41.8%) developed ARDS, and of those 84 patients, 44 (52.4%) died. In those who developed ARDS, compared with those who did not, more patients presented with dyspnea (50 of 84 [59.5%] patients and 30 of 117 [25.6%] patients, respectively [difference, 33.9%; 95% CI, 19.7%-48.1%]) and had comorbidities such as hypertension (23 of 84 [27.4%] patients and 16 of 117 [13.7%] patients, respectively [difference, 13.7%; 95% CI, 1.3%-26.1%]) and diabetes (16 of 84 [19.0%] patients and 6 of 117 [5.1%] patients, respectively [difference, 13.9%; 95% CI, 3.6%-24.2%]). In bivariate Cox regression analysis, risk factors associated with the development of ARDS and progression from ARDS to death included older age (hazard ratio [HR], 3.26; 95% CI 2.08-5.11; and HR, 6.17; 95% CI, 3.26-11.67, respectively), neutrophilia (HR, 1.14; 95% CI, 1.09-1.19; and HR, 1.08; 95% CI, 1.01-1.17, respectively), and organ and coagulation dysfunction (eg, higher lactate dehydrogenase [HR, 1.61; 95% CI, 1.44-1.79; and HR, 1.30; 95% CI, 1.11-1.52, respectively] and D-dimer [HR, 1.03; 95% CI, 1.01-1.04; and HR, 1.02; 95% CI, 1.01-1.04, respectively]). High fever (>/=39 degrees C) was associated with higher likelihood of ARDS development (HR, 1.77; 95% CI, 1.11-2.84) and lower likelihood of death (HR, 0.41; 95% CI, 0.21-0.82). Among patients with ARDS, treatment with methylprednisolone decreased the risk of death (HR, 0.38; 95% CI, 0.20-0.72). Conclusions and Relevance: Older age was associated with greater risk of development of ARDS and death likely owing to less rigorous immune response. Although high fever was associated with the development of ARDS, it was also associated with better outcomes among patients with ARDS. Moreover, treatment with methylprednisolone may be beneficial for patients who develop ARDS.

Wu, F., et al. (2020). "[Discussion on diagnosis and treatment of hepatobiliary malignancies during the outbreak of novel coronavirus pneumonia]." Zhonghua Zhong Liu Za Zhi **42**(0): E004.

From December 2019, the new coronavirus pneumonia (COVID-19) broke out in Wuhan, Hubei, and spread rapidly to the nationwide. On January 20, 2020, the National Health Committee classified COVID-19 pneumonia as one of B class infectious diseases and treated it as class A infectious disease. During the epidemic period, the routine diagnosis and treatment of tumor patients was affected with varying degrees. In this special period, we performed the superiority of the multi-disciplinary team of diagnosis and treatment, achieved accurate diagnosis and treatment of patients with hepatobiliary malignant tumors, provided support for these patients with limited medical resources, and helped them to survive during the epidemic period.On the basis of fully understanding the new coronavirus pneumonia, the treatment strategy should be changed timely during the epidemic, and more appropriate treatment methods should be adopted to minimize the adverse effect of the epidemic on tumor treatment.

Wu, F., et al. (2020). "A new coronavirus associated with human respiratory disease in China." Nature **579**(7798): 265-269.

Emerging infectious diseases, such as severe acute respiratory syndrome (SARS) and Zika virus disease, present a major threat to public health (1-3). Despite intense research efforts, how, when and where new diseases appear are still a source of considerable uncertainty. A severe respiratory disease was recently reported in Wuhan, Hubei province, China. As of 25 January 2020, at least 1,975 cases had been reported since the first patient was hospitalized on 12 December 2019. Epidemiological investigations have suggested that the outbreak was associated with a seafood market in Wuhan. Here we study a single patient who was a worker at the market and who was admitted to the Central Hospital of Wuhan on 26 December 2019 while experiencing a severe respiratory syndrome that included fever, dizziness and a cough. Metagenomic RNA sequencing (4) of a sample of bronchoalveolar lavage fluid from the patient identified a new RNA virus strain from the family Coronaviridae, which is designated here 'WH-Human 1' coronavirus (and has also been referred to as '2019-nCoV'). Phylogenetic analysis of the complete viral genome (29,903 nucleotides) revealed that the virus was most closely related (89.1% nucleotide similarity) to a group of SARS-like coronaviruses (genus Betacoronavirus, subgenus Sarbecovirus) that had previously been found in bats in China (5). This outbreak highlights the ongoing ability of viral spill-over from animals to cause severe disease in humans.

Wu, J., et al. (2020). "[Novel coronavirus pneumonia (COVID-19) CT distribution and sign features]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E030.

Objective: To investigate the imaging findings of 2019 novel coronavirus pneumonia (COVID-19). Methods: From January 20 to February 5, 2020, a total of 130 patients diagnosed with COVID-19 from seven hospitals in China were collected. The imaging data were reviewed and analyzed in detail. Results: (1) Distribution: the lesion detected in the lung unilaterally in 14 cases (10.7%) and bilaterally in 116 cases (89.3%). According to the distribution in the lobes of the lung, all cases could be classified into subpleural distribution (102 cases, 78.4%), centrilobular distribution (99 cases, 76.1%) and diffused distribution (8 cases, 6.1%). (2) Number of lesions: single lesion 9 cases (6.9%); multiple lesions 113 cases (86.9%), diffuse lesions 8 cases (6.1%). (3) Imaging density: 70 cases (53.8%) of ground-glass opacity (GGO), 60 cases (46.2%) of GGO + consolidation. (4) Accompanying signs: 100 cases (76.9%) with vascular thickening, 98 cases (75.3%) with "pleural parallel sign"; "intralobular septal thickening" in 100 cases (76.9%); "halo sign" in 13 cases (10%); "reversed-halo sign" in 6 cases (4.6%); pleural effusion in 3 cases (2.3 %), and pneumatocele in 2 cases (1.5%); no case with pulmonary cavity. Among 35 patients that underwent follow-up CT, 21 patients (60%) improved while 14 (40%) exacerbated. Conclusions: COVID-19 imaging characteristic mainly has subpleural, centrilobular and diffused distribution. The first two distributions can overlap or progress to diffused distribution. In the later period, it was mainly manifested as organizing pneumonia and fibrosis. The most valuable characteristic is the pleural parallel sign.

Wu, P., et al. (2020). "Real-time tentative assessment of the epidemiological characteristics of novel coronavirus infections in Wuhan, China, as at 22 January 2020." Euro Surveill **25**(3).

A novel coronavirus (2019-nCoV) causing severe acute respiratory disease emerged recently in Wuhan, China. Information on reported cases strongly indicates human-to-human spread, and the most recent information is increasingly indicative of sustained human-to-human transmission. While the overall severity profile among cases may change as more mild cases are identified, we estimate a risk of fatality among hospitalised cases at 14% (95% confidence interval: 3.9-32%).

Xiao, H., et al. (2020). "The Effects of Social Support on Sleep Quality of Medical Staff Treating Patients with Coronavirus Disease 2019 (COVID-19) in January and February 2020 in China." Med Sci Monit **26**: e923549.

BACKGROUND Coronavirus disease 2019 (COVID-19), formerly known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and 2019 novel coronavirus (2019-nCoV), was first identified in December 2019 in Wuhan City, China. Structural equation modeling (SEM) is a multivariate analysis method to determine the structural relationship between measured variables. This observational study aimed to use SEM to determine the effects of social support on sleep quality and function of medical staff who treated patients with COVID-19 in January and February 2020 in Wuhan, China. MATERIAL AND METHODS A one-month cross-sectional observational study included 180 medical staff who treated patients with COVID-19 infection. Levels of anxiety, self-efficacy, stress, sleep quality, and social support were measured using the and the Self-Rating Anxiety Scale (SAS), the General Self-Efficacy Scale (GSES), the Stanford Acute Stress Reaction (SASR) questionnaire, the Pittsburgh Sleep Quality Index (PSQI), and the Social Support Rate Scale (SSRS), respectively. Pearson's correlation analysis and SEM identified the interactions between these factors. RESULTS Levels of social support for medical staff were significantly associated with self-efficacy and sleep quality and negatively associated with the degree of anxiety and stress. Levels of anxiety were significantly associated with the levels of stress, which negatively impacted self-efficacy and sleep quality. Anxiety, stress, and self-efficacy were mediating variables associated with social support and sleep quality. CONCLUSIONS SEM showed that medical staff in China who were treating patients with COVID-19 infection during January and February 2020 had levels of anxiety, stress, and self-efficacy that were dependent on sleep quality and social support.

Xiao, H., et al. (2020). "Social Capital and Sleep Quality in Individuals Who Self-Isolated for 14 Days During the Coronavirus Disease 2019 (COVID-19) Outbreak in January 2020 in China." Med Sci Monit **26**: e923921.

BACKGROUND From the end of December 2019, coronavirus disease 2019 (COVID-19) began to spread in central China. Social capital is a measure of social trust, belonging, and participation. This study aimed to investigate the effects of social capital on sleep quality and the mechanisms involved in people who self-isolated at home for 14 days in January 2020 during the COVID-19 epidemic in central China. MATERIAL AND METHODS Individuals (n=170) who self-isolated at home for 14 days in central China, completed self-reported questionnaires on the third day of isolation. Individual social capital was assessed using the Personal Social Capital Scale 16 (PSCI-16) questionnaire. Anxiety was assessed using the Self-Rating Anxiety Scale (SAS) questionnaire, stress was assessed using the Stanford Acute Stress Reaction (SASR) questionnaire, and sleep was assessed using the Pittsburgh Sleep Quality Index (PSQI) questionnaire. Path analysis was performed to evaluate the relationships between a dependent variable (social capital) and two or more independent variables, using Pearson's correlation analysis and structural equation modeling (SEM). RESULTS Low levels of social capital were associated with increased levels of anxiety and stress, but increased levels of social capital were positively associated with increased quality of sleep. Anxiety was associated with stress and reduced sleep quality, and the combination of anxiety and stress reduced the positive effects of social capital on sleep quality. CONCLUSIONS During a period of individual self-isolation during the COVID-19 virus epidemic in central China, increased social capital improved sleep quality by reducing anxiety and stress.

Xu, X. W., et al. (2020). "Clinical findings in a group of patients infected with the 2019 novel coronavirus (SARS-Cov-2) outside of Wuhan, China: retrospective case series." BMJ **368**: m606.

OBJECTIVE: To study the clinical characteristics of patients in Zhejiang province, China, infected with the 2019 severe acute respiratory syndrome coronavirus 2 (SARS-Cov-2) responsible for coronavirus disease 2019 (covid-2019). DESIGN: Retrospective case series. SETTING: Seven hospitals in Zhejiang province, China. PARTICIPANTS: 62 patients admitted to hospital with laboratory confirmed SARS-Cov-2 infection. Data were collected from 10 January 2020 to 26 January 2020. MAIN OUTCOME MEASURES: Clinical data, collected using a standardised case report form, such as temperature, history of exposure, incubation period. If information was not clear, the working group in Hangzhou contacted the doctor responsible for treating the patient for clarification. RESULTS: Of the 62 patients studied (median age 41 years), only one was admitted to an intensive care unit, and no patients died during the study. According to research, none of the infected patients in Zhejiang province were ever exposed to the Huanan seafood market, the original source of the virus; all studied cases were infected by human to human transmission. The most common symptoms at onset of illness were fever in 48 (77%) patients, cough in 50 (81%), expectoration in 35 (56%), headache in 21 (34%), myalgia or fatigue in 32 (52%), diarrhoea in 3 (8%), and haemoptysis in 2 (3%). Only two patients (3%) developed shortness of breath on admission. The median time from exposure to onset of illness was 4 days (interquartile range 3-5 days), and from onset of symptoms to first hospital admission was 2 (1-4) days. CONCLUSION: As of early February 2020, compared with patients initially infected with SARS-Cov-2 in Wuhan, the symptoms of patients in Zhejiang province are relatively mild.

Yang, J., et al. (2020). "Prevalence of comorbidities in the novel Wuhan coronavirus (COVID-19) infection: a systematic review and meta-analysis." Int J Infect Dis.

BACKGROUND: An outbreak of Novel Coronavirus (COVID -19) in Wuhan, China, the epidemic is more widespread than initially estimated, with cases now confirmed in multiple countries. AIMS: The aim of the meta-analysis was to assess the prevalence of comorbidities in the COVID-19 infection patients and the risk of underlying diseases in severe patients compared to non-severe patients. METHODS: A literature search was conducted using the databases PubMed, EMBASE, and Web of sciences until February 25, 2020. Risk ratio (OR) and 95% confidence intervals (CIs) were pooled using random-effects models. RESULTS: Eight studies were included in the meta- analysis, including 46248 infected patients. The result showed the most prevalent clinical symptom was fever (91 +/- 3, 95% CI 86-97%), followed by cough (67 +/- 7, 95% CI 59-76%), fatigue (51 +/- 0, 95% CI 34-68%) and dyspnea (30 +/- 4, 95% CI 21-40%). The most prevalent comorbidity were hypertension (17 +/- 7, 95% CI 14-22%) and diabetes (8 +/- 6, 95% CI 6-11%), followed by cardiovascular diseases (5 +/- 4, 95% CI 4-7%) and respiratory system disease (2 +/- 0, 95% CI 1-3%). Compared with the Non-severe patient, the pooled odds ratio of hypertension, respiratory system disease, cardiovascular disease in severe patients were (OR 2.36, 95% CI: 1.46-3.83), (OR 2.46, 95% CI: 1.76-3.44) and (OR 3.42, 95% CI: 1.88-6.22)respectively. CONCLUSION: We assessed the prevalence of comorbidities in the COVID-19 infection patients and found underlying disease, including hypertension, respiratory system disease and cardiovascular, may be a risk factor for severe patients compared with Non-severe patients.

Yang, L., et al. (2020). "[Diagnostic and therapeutic strategies of lung cancer patients during the outbreak of 2019 novel coronavirus disease (COVID-19)]." Zhonghua Zhong Liu Za Zhi **42**(0): E006.

With the increasing number of cases and widening geographical spread, the 2019 novel coronavirus disease (COVID-19) has been classified as one of the class B infectious diseases but prevented and controlled as class A infectious disease by the National Health Commission of China. The diagnosis and treatment of lung cancer patients have been challenged greatly because of extraordinary public health measures since the lung cancer patients are a high-risk population during the COVID-19 outbreak period. Strict protection for lung cancer patients is needed to avoid infection. Lung cancer patients are difficult to differentiate from patients with COVID-19 in terms of clinical symptoms, which will bring great trouble to the clinical work and physical and mental health of lung cancer patients. This review will demonstrate how to applicate appropriate and individual management for lung cancer patients to protect them from COVID-19.

Yang, T. J., et al. (2020). "Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans." Proc Natl Acad Sci U S A **117**(3): 1438-1446.

Feline infectious peritonitis virus (FIPV) is an alphacoronavirus that causes a nearly 100% mortality rate without effective treatment. Here we report a 3.3-A cryoelectron microscopy (cryo-EM) structure of the serotype I FIPV spike (S) protein, which is responsible for host recognition and viral entry. Mass spectrometry provided site-specific compositions of densely distributed high-mannose and complex-type N-glycans that account for 1/4 of the total molecular mass; most of the N-glycans could be visualized by cryo-EM. Specifically, the N-glycans that wedge between 2 galectin-like domains within the S1 subunit of FIPV S protein result in a unique propeller-like conformation, underscoring the importance of glycosylation in maintaining protein structures. The cleavage site within the S2 subunit responsible for activation also showed distinct structural features and glycosylation. These structural insights provide a blueprint for a better molecular understanding of the pathogenesis of FIP.

Yang, W., et al. (2020). "Clinical characteristics and imaging manifestations of the 2019 novel coronavirus disease (COVID-19):A multi-center study in Wenzhou city, Zhejiang, China." J Infect **80**(4): 388-393.

BACKGROUND: Little is known about COVID-19 outside Hubei. The aim of this paper was to describe the clinical characteristics and imaging manifestations of hospitalized patients with confirmed

COVID-19 infection in Wenzhou, Zhejiang, China. METHODS: In this retrospective cohort study, 149 RT-PCR confirmed positive patients were consecutively enrolled from January 17th to February 10th, 2020 in three tertiary hospitals of Wenzhou. Outcomes were followed up until Feb 15th, 2020. FINDINGS: A total of 85 patients had Hubei travel/residence history, while another 49 had contact with people from Hubei and 15 had no traceable exposure history to Hubei. Fever, cough and expectoration were the most common symptoms, 14 patients had decreased oxygen saturation, 33 had leukopenia, 53 had lymphopenia, and 82 had elevated C-reactive protein. On chest computed tomography (CT), lung segments 6 and 10 were mostly involved. A total of 287 segments presented ground glass opacity, 637 presented mixed opacity and 170 presented consolidation. Lesions were more localized in the peripheral lung with a patchy form. No significant difference was found between patients with or without Hubei exposure history. Seventeen patients had normal CT on admission of these, 12 had negative findings even10 days later. INTERPRETATION: Most patients presented with a mild infection in our study. The imaging pattern of multifocal peripheral ground glass or mixed opacity with predominance in the lower lung is highly suspicious of COVID-19 in the first week of disease onset. Nevetheless, some patients can present with a normal chest finding despite testing positive for COVID-19. FUNDING: We did not receive any fundings.

Yang, Y., et al. (2020). "The deadly coronaviruses: The 2003 SARS pandemic and the 2020 novel coronavirus epidemic in China." J Autoimmun: 102434.

The 2019-nCoV is officially called SARS-CoV-2 and the disease is named COVID-19. This viral epidemic in China has led to the deaths of over 1800 people, mostly elderly or those with an underlying chronic disease or immunosuppressed state. This is the third serious Coronavirus outbreak in less than 20 years, following SARS in 2002-2003 and MERS in 2012. While human strains of Coronavirus are associated with about 15% of cases of the common cold, the SARS-CoV-2 may present with varying degrees of severity, from flu-like symptoms to death. It is currently believed that this deadly Coronavirus strain originated from wild animals at the Huanan market in Wuhan, a city in Hubei province. Bats, snakes and pangolins have been cited as potential carriers based on the sequence homology of CoV isolated from these animals and the viral nucleic acids of the virus isolated from SARS-CoV-2 infected patients. Extreme quarantine measures, including sealing off large cities, closing borders and confining people to their homes, were instituted in January 2020 to prevent spread of the virus, but by that time much of the damage had been done, as human-human transmission became evident. While these quarantine measures are necessary and have prevented a historical disaster along the lines of the Spanish flu, earlier recognition and earlier implementation of quarantine measures may have been even more effective. Lessons learned from SARS resulted in faster determination of the nucleic acid sequence and a more robust quarantine strategy. However, it is clear that finding an effective antiviral and developing a vaccine are still significant challenges. The costs of the epidemic are not limited to medical aspects, as the virus has led to significant sociological, psychological and economic effects globally. Unfortunately, emergence of SARS-CoV-2 has led to numerous reports of Asians being subjected to racist behavior and hate crimes across the world.

Yao, N., et al. (2020). "[Clinical characteristics and influencing factors of patients with novel coronavirus pneumonia combined with liver injury in Shaanxi region]." Zhonghua Gan Zang Bing Za Zhi **28**(0): E003.

Objective: To understand the clinical characteristics, change of liver function, influencing factors and prognosis in hospitalized patients with coronavirus disease-19 (COVID-19) combined with liver injury. Methods: The general conditions, biochemical indicators of liver, blood clotting mechanism, routine blood test, UGT1A1 * 28 gene polymorphism and other data of 40 cases with COVID-19 admitted to the isolation ward of Tangdu Hospital were retrospectively analyzed. The clinical characteristics, influencing factors and prognosis of liver injury in patients with liver injury group and those with normal liver function group were compared. The mean of two samples in univariate analysis was compared by t-test and analysis of variance. The counting data was measured by chi (2) tests. The non-normal distribution measurement data were described by the median, and the non-parametric test was used. Statistically significant influencing factors were used as the independent variables in univariate analysis. Multiple logistic regression analysis was used to analyze the main influencing factors of liver injury. Results: Of the 40 cases, 25 were male (62.5%) and 15 were female (37.5%), aged 22 to 83 (53.87 +/- 15.84) years. Liver injury was occurred in 22 cases (55%) during the course of the disease. Alanine aminotransferase (ALT) and aspartate aminotransferase (AST) level was initially increased (4.4 to 3.5 times of the normal value) along with decrease of albumin in the second week, and the difference was statistically significant ($P < 0.001$). Ten

cases (43.5%) had highest abnormal total blood bilirubin (54.1 mumol/ L). There was no correlation between the increase in transaminase and the increase in total blood bilirubin (R = -0.006, P = 0.972). Three cases had prothrombin activity (PTA) of </= 50%, 10 cases had elevated FDP, and 13 cases had elevated D-dimer, all of whom were severe or critically ill. Liver function injury was more likely to occur in patients who used many types of drugs and large amounts of hormones (P = 0.002, P = 0.031), and there was no correlation with the TA6TA7 mutation in the UGT1A1 * 28 gene locus. Multiple regression analysis showed that the occurrence of liver injury was only related to critical illness. The liver function of all patients had recovered within one week after conventional liver protection treatment. Conclusion: COVID-19 combined with liver function injury may be due to the slight elevation of transaminase, mostly around the second week of the disease course. Severe patients have a higher proportion of liver injury, and critical type is an independent risk factor for liver injury.

Yao, T. T., et al. (2020). "A systematic review of lopinavir therapy for SARS coronavirus and MERS coronavirus-A possible reference for coronavirus disease-19 treatment option." J Med Virol.

In the past few decades, coronaviruses have risen as a global threat to public health. Currently, the outbreak of coronavirus disease-19 (COVID-19) from Wuhan caused a worldwide panic. There are no specific antiviral therapies for COVID-19. However, there are agents that were used during the severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) epidemics. We could learn from SARS and MERS. Lopinavir (LPV) is an effective agent that inhibits the protease activity of coronavirus. In this review, we discuss the literature on the efficacy of LPV in vitro and in vivo, especially in patients with SARS and MERS, so that we might clarify the potential for the use of LPV in patients with COVID-19.

Yao, X., et al. (2020). "In Vitro Antiviral Activity and Projection of Optimized Dosing Design of Hydroxychloroquine for the Treatment of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)." Clin Infect Dis.

BACKGROUND: The Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) first broke out in Wuhan (China) and subsequently spread worldwide. Chloroquine has been sporadically used in treating SARS-CoV-2 infection. Hydroxychloroquine shares the same mechanism of action as chloroquine, but its more tolerable safety profile makes it the preferred drug to treat malaria and autoimmune conditions. We propose that the immunomodulatory effect of hydroxychloroquine also may be useful in controlling the cytokine storm that occurs late-phase in critically ill SARS-CoV-2 infected patients. Currently, there is no evidence to support the use of hydroxychloroquine in SARS-CoV-2 infection. METHODS: The pharmacological activity of chloroquine and hydroxychloroquine was tested using SARS-CoV-2 infected Vero cells. Physiologically-based pharmacokinetic models (PBPK) were implemented for both drugs separately by integrating their in vitro data. Using the PBPK models, hydroxychloroquine concentrations in lung fluid were simulated under 5 different dosing regimens to explore the most effective regimen whilst considering the drug's safety profile. RESULTS: Hydroxychloroquine (EC50=0.72 muM) was found to be more potent than chloroquine (EC50=5.47 muM) in vitro. Based on PBPK models results, a loading dose of 400 mg twice daily of hydroxychloroquine sulfate given orally, followed by a maintenance dose of 200 mg given twice daily for 4 days is recommended for SARS-CoV-2 infection, as it reached three times the potency of chloroquine phosphate when given 500 mg twice daily 5 days in advance. CONCLUSIONS: Hydroxychloroquine was found to be more potent than chloroquine to inhibit SARS-CoV-2 in vitro.

Yu, P., et al. (2020). "A familial cluster of infection associated with the 2019 novel coronavirus indicating potential person-to-person transmission during the incubation period." J Infect Dis.

An ongoing outbreak of pneumonia associated with 2019 novel coronavirus (2019-nCoV) was reported in China. It is unclear if the infectivity exists during the incubation period, although a person-to-person transmission has been reported in previous studies. We report the epidemiological features of a familial cluster of four patients in Shanghai, of which one was 88 years old man with moving difficulties and was only exposed to his asymptomatic family members who developed symptoms later. The epidemiological evidence has shown a potential transmission of the 2019-nCoV during the incubation period.

Yu, Y. X., et al. (2020). "[Consideration and prevention for the aerosol transmission of 2019 novel coronavirus]." Zhonghua Yan Ke Za Zhi **56**(0): E008.

Novel coronavirus pneumonia broke out from Wuhan, and spreading to the whole nation and world since Dec, 2019. It is now the critical stage to fight against the virus. Previous epidemiological investigations and animal experiments suggest aerosol could perform as virus transmitter. Based on the clinical observation, the possibility of aerosol transmission of 2019 novel coronavirus has aroused a

lot of attention. This study focuses on the feature of aerosol transmission, and the pathogens involved in. We analyzed the possibility of aerosol transmission for the novel coronavirus. Relevant strategies to prevent novel coronavirus pneumonia are established, serving as references to the medical personnel and general public during their work or daily life. (Chin J Ophthalmol, 2020, 56:).

Yuan, M., et al. (2020). "Association of radiologic findings with mortality of patients infected with 2019 novel coronavirus in Wuhan, China." PLoS One **15**(3): e0230548.

Radiologic characteristics of 2019 novel coronavirus (2019-nCoV) infected pneumonia (NCIP) which had not been fully understood are especially important for diagnosing and predicting prognosis. We retrospective studied 27 consecutive patients who were confirmed NCIP, the clinical characteristics and CT image findings were collected, and the association of radiologic findings with mortality of patients was evaluated. 27 patients included 12 men and 15 women, with median age of 60 years (IQR 47-69). 17 patients discharged in recovered condition and 10 patients died in hospital. The median age of mortality group was higher compared to survival group (68 (IQR 63-73) vs 55 (IQR 35-60), P = 0.003). The comorbidity rate in mortality group was significantly higher than in survival group (80% vs 29%, P = 0.018). The predominant CT characteristics consisted of ground glass opacity (67%), bilateral sides involved (86%), both peripheral and central distribution (74%), and lower zone involvement (96%). The median CT score of mortality group was higher compared to survival group (30 (IQR 7-13) vs 12 (IQR 11-43), P = 0.021), with more frequency of consolidation (40% vs 6%, P = 0.047) and air bronchogram (60% vs 12%, P = 0.025). An optimal cutoff value of a CT score of 24.5 had a sensitivity of 85.6% and a specificity of 84.5% for the prediction of mortality. 2019-nCoV was more likely to infect elderly people with chronic comorbidities. CT findings of NCIP were featured by predominant ground glass opacities mixed with consolidations, mainly peripheral or combined peripheral and central distributions, bilateral and lower lung zones being mostly involved. A simple CT scoring method was capable to predict mortality.

Yuan, Y., et al. (2020). "Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species." J Virol **94**(5).

Continued reports of Middle East respiratory syndrome coronavirus (MERS-CoV) infecting humans have occurred since the identification of this virus in 2012. MERS-CoV is prone to cause endemic disease in the Middle East, with several dozen spillover infections to other continents. It is hypothesized that MERS-CoV originated from bat coronaviruses and that dromedary camels are its natural reservoir. Although gene segments identical to MERS-CoV were sequenced from certain species of bats and one species experimentally shed the virus, it is still unknown whether other bats can transmit the virus. Here, at the molecular level, we found that all purified bat CD26s (bCD26s) from a diverse range of species interact with the receptor binding domain (RBD) of MERS-CoV, with equilibrium dissociation constant values ranging from several to hundreds at the micromolar level. Moreover, all bCD26s expressed in this study mediated the entry of pseudotyped MERS-CoV to receptor-expressing cells, indicating the broad potential engagement of bCD26s as MERS-CoV receptors. Further structural analysis indicated that in the bat receptor, compared to the human receptor, substitutions of key residues and their adjacent amino acids leads to decreased binding affinity to the MERS-RBD. These results add more evidence to the existing belief that bats are the original source of MERS-CoV and suggest that bCD26s in many species can mediate the entry of the virus, which has significant implications for the surveillance and control of MERS-CoV infection.IMPORTANCE In this study, we found that bat CD26s (bCD26s) from different species exhibit large diversities, especially in the region responsible for binding to the receptor binding domain (RBD) of Middle East respiratory syndrome coronavirus (MERS-CoV). However, they maintain the interaction with MERS-RBD at varied affinities and support the entry of pseudotyped MERS-CoV. These bat receptors polymorphisms seem to confer evolutionary pressure for the adaptation of CD26-binding virus, such as the ancestor of MERS-CoV, and led to the generation of diversified CD26-engaging CoV strains. Thus, our data add more evidence to support that bats are the reservoir of MERS-CoV and similar viruses, as well as further emphasize the necessity to survey MERS-CoV and other CoVs among bats.

Zhang, J., et al. (2020). "Swine acute diarrhea syndrome coronavirus-induced apoptosis is caspase- and cyclophilin D- dependent." Emerg Microbes Infect **9**(1): 439-456.

Swine acute diarrhea syndrome coronavirus (SADS-CoV), a newly discovered enteric coronavirus, is the aetiological agent that causes severe clinical diarrhea and intestinal pathological damage in piglets. To understand the effect of SADS-CoV on host cells, we characterized the apoptotic pathways and elucidated mechanisms underlying the process of apoptotic cell death after SADS-CoV infection.

SADS-CoV-infected cells showed evidence of apoptosis in vitro and in vivo. The use of a pan-caspase inhibitor resulted in the inhibition of SADS-CoV-induced apoptosis and reduction in SADS-CoV replication, suggestive of the association of a caspase-dependent pathway. Furthermore, SADS-CoV infection activated the initiators caspase-8 and -9 and upregulated FasL and Bid cleavage, demonstrating a crosstalk between the extrinsic and intrinsic pathways. However, the proapoptotic proteins Bax and Cytochrome c (Cyt c) relocalized to the mitochondria and cytoplasm, respectively, after infection by SADS-CoV. Moreover, Vero E6 and IPI-2I cells treated with cyclosporin A (CsA), an inhibitor of mitochondrial permeability transition pore (MPTP) opening, were completely protected from SADS-CoV-induced apoptosis and viral replication, suggesting the involvement of cyclophilin D (CypD) in these processes. Altogether, our results indicate that caspase-dependent FasL (extrinsic)- and mitochondria (intrinsic)- mediated apoptotic pathways play a central role in SADS-CoV-induced apoptosis that facilitates viral replication. In summary, these findings demonstrate mechanisms by which SADS-CoV induces apoptosis and improve our understanding of SADS-CoV pathogenesis.

Zhang, L., et al. (2020). "alpha-Ketoamides as Broad-Spectrum Inhibitors of Coronavirus and Enterovirus Replication: Structure-Based Design, Synthesis, and Activity Assessment." J Med Chem.

The main protease of coronaviruses and the 3C protease of enteroviruses share a similar active-site architecture and a unique requirement for glutamine in the P1 position of the substrate. Because of their unique specificity and essential role in viral polyprotein processing, these proteases are suitable targets for the development of antiviral drugs. In order to obtain near-equipotent, broad-spectrum antivirals against alphacoronaviruses, betacoronaviruses, and enteroviruses, we pursued a structure-based design of peptidomimetic alpha-ketoamides as inhibitors of main and 3C proteases. Six crystal structures of protease-inhibitor complexes were determined as part of this study. Compounds synthesized were tested against the recombinant proteases as well as in viral replicons and virus-infected cell cultures; most of them were not cell-toxic. Optimization of the P2 substituent of the alpha-ketoamides proved crucial for achieving near-equipotency against the three virus genera. The best near-equipotent inhibitors, 11u (P2 = cyclopentylmethyl) and 11r (P2 = cyclohexylmethyl), display low-micromolar EC50 values against enteroviruses, alphacoronaviruses, and betacoronaviruses in cell cultures. In Huh7 cells, 11r exhibits three-digit picomolar activity against the Middle East Respiratory Syndrome coronavirus.

Zhang, L. and Y. Liu (2020). "Potential interventions for novel coronavirus in China: A systematic review." J Med Virol **92**(5): 479-490.

An outbreak of a novel coronavirus (COVID-19 or 2019-CoV) infection has posed significant threats to international health and the economy. In the absence of treatment for this virus, there is an urgent need to find alternative methods to control the spread of disease. Here, we have conducted an online search for all treatment options related to coronavirus infections as well as some RNA-virus infection and we have found that general treatments, coronavirus-specific treatments, and antiviral treatments should be useful in fighting COVID-19. We suggest that the nutritional status of each infected patient should be evaluated before the administration of general treatments and the current children's RNA-virus vaccines including influenza vaccine should be immunized for uninfected people and health care workers. In addition, convalescent plasma should be given to COVID-19 patients if it is available. In conclusion, we suggest that all the potential interventions be implemented to control the emerging COVID-19 if the infection is uncontrollable.

Zhang, M. C., et al. (2020). "[Suggestions for disinfection of ophthalmic examination equipment and protection of ophthalmologist against 2019 novel coronavirus infection]." Zhonghua Yan Ke Za Zhi **56**(0): E001.

At present, the prevention and treatment of 2019 Novel Coronavirus (2019-nCoV) in China has reached a critical stage. It is extremely important to disinfect ophthalmic examination instruments and protect ophthalmic medical care during the epidemic period to reduce cross-infection in clinical practice and reduce the infection risk of ophthalmic medical staff. (Chin J Ophthalmol, 2020, 56: 0001).

Zhang, M. Q., et al. (2020). "[Clinical features of 2019 novel coronavirus pneumonia in the early stage from a fever clinic in Beijing]." Zhonghua Jie He He Hu Xi Za Zhi **43**(3): 215-218.

Objective: To summarize and analyze the clinical and imaging characteristics of patients with 2019 novel coronavirus pneumonia in the early stage in Beijing. Methods: A retrospective analysis of clinical and imaging data of 9 patients with 2019 novel coronavirus infection diagnosed in one fever clinicic in Beijing from January 18, 2020 to February 3, 2020. Results: 5 male and 4 female was included in those 9 patients, whose median age was 36 years, and the age range from 15 to 49 years. 8 of these patients had no underlying disease and one suffered from diabetes. 7 patients had a history of travel to Wuhan City or Hubei Province, and one patient was a medical staff. Two family clustered was found. The incubation period was 1 to 6 days. The clinical manifestations were fever in 8 cases (8/9), dry cough in 5 cases (5/9), pharyngalgia in 4 cases (4/9), fatigue in 4 cases (4/9), body soreness in 4 cases (4/9), and blocked or watery nose in 1 case (1/9). Six patients (6/9) had abnormal cell peripheral blood, of which 3 (3/9) had an increased monocyte count, 2 (2/9) had a reduced lymphocyte, and 1 (1/9) had an increased leukocyte count, while the 3 patients had normal cell blood routines. The median of CRP was 16.3 mg/L, including 5 patients with slightly elevated (5/9), 4 patients with normal values (4/9). the results of procalcitonin test were negative in5 patients. Three patients were examined by chest X-ray examination, one of which was normal, one case showed infiltrates of right upper lung, and another showed in right lower lung. All patients underwent chest HRCT. And 7 cases (7/9) showed multiple ground glass exudation, including 5 cases (5/7) involved bilateral lungs, 2 cases (2/7) involved unilateral lung, 3 cases (3/7) with patchy consolidation, and 2 cases (2/9) showed no abnormality. Conclusions: The patents with 2019 novel coronavirus pneumonia in this study generally have an epidemiological history. The clinical manifestations are fever and cough. Peripheral white blood cell counts were most normal And PCT were all negative. Chest HRCT manifested as multiple ground-glass opacities with partly consolidation. Some patients had normal chest radiographs but HRCT showed pneumonia. Some patients had no pneumonia on chest HRCT.

Zhang, M. Q., et al. (2020). "[Clinical features of 2019 novel coronavirus pneumonia in the early stage from a fever clinic in Beijing]." Zhonghua Jie He He Hu Xi Za Zhi **43**(0): E013.

Objective: To summarize and analyze the clinical and imaging characteristics of patients with 2019 novel coronavirus pneumonia in the early stage in Beijing. Methods: A retrospective analysis of clinical and imaging data of 9 patients with 2019 novel coronavirus infection diagnosed in one fever clinicic in Beijing from January 18, 2020 to February 3, 2020. Results: 5 male and 4 female was included in those 9 patients, whose median age was 36 years, and the age range from 15 to 49 years. 8 of these patients had no underlying disease and one suffered from diabetes. 7 patients had a history of travel to Wuhan City or Hubei Province, and one patient was a medical staff. Two family clustered was found. The incubation period was 1 to 6 days. The clinical manifestations were fever in 8 cases (8/9), dry cough in 5 cases (5/9), pharyngalgia in 4 cases (4/9), fatigue in 4 cases (4/9), body soreness in 4 cases (4/9), and blocked or watery nose in 1 case (1/9). Six patients (6/9) had abnormal cell peripheral blood, of which 3 (3/9) had an increased monocyte count, 2 (2/9) had a reduced lymphocyte, and 1 (1/9) had an increased leukocyte count, while the 3 patients had normal cell blood routines. The median of CRP was 16.3 mg/L, including 5 patients with slightly elevated (5/9), 4 patients with normal values (4/9). the results of procalcitonin test were negative in5 patients. Three patients were examined by chest X-ray examination, one of which was normal, one case showed infiltrates of right upper lung, and another showed in right lower lung. All patients underwent chest HRCT. And 7 cases (7/9) showed multiple ground glass exudation, including 5 cases (5/7) involved bilateral lungs, 2 cases (2/7) involved unilateral lung, 3 cases (3/7) with patchy consolidation, and 2 cases (2/9) showed no abnormality. Conclusions: The patents with 2019 novel coronavirus pneumonia in this study generally have an epidemiological history. The clinical manifestations are fever and cough. Peripheral white blood cell counts were most normal And PCT were all negative. Chest HRCT manifested as multiple ground-glass opacities with partly consolidation. Some patients had normal chest radiographs but HRCT showed pneumonia. Some patients had no pneumonia on chest HRCT.

Zhao, S., et al. (2020). "Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak." Int J Infect Dis **92**: 214-217.

BACKGROUNDS: An ongoing outbreak of a novel coronavirus (2019-nCoV) pneumonia hit a major city in China, Wuhan, December 2019 and subsequently reached other provinces/regions of China and other countries. We present estimates of the basic reproduction number, R0, of 2019-nCoV in the early phase of the outbreak. METHODS: Accounting for the impact of the variations in disease reporting rate, we modelled the epidemic curve of 2019-nCoV cases time series, in mainland China from January 10 to January 24, 2020, through the exponential growth. With the estimated intrinsic growth rate (gamma), we estimated R0 by using the serial intervals (SI) of two other well-known coronavirus diseases, MERS and SARS, as approximations for the true unknown SI. FINDINGS: The early outbreak data largely follows the exponential growth. We estimated that the mean R0 ranges from 2.24 (95%CI: 1.96-2.55) to 3.58 (95%CI: 2.89-4.39) associated with 8-fold to 2-fold increase in the reporting rate. We demonstrated that changes in reporting rate substantially affect estimates of R0. CONCLUSION: The mean estimate of R0 for the 2019-nCoV ranges from 2.24 to 3.58, and is significantly larger than 1. Our findings indicate the potential of 2019-nCoV to cause outbreaks.

Zhao, S., et al. (2020). "Anesthetic Management of Patients With Suspected or Confirmed 2019 Novel Coronavirus Infection During Emergency Procedures." J Cardiothorac Vasc Anesth.

OBJECTIVES: The aim of the present study was to prevent cross-infection in the operating room during emergency procedures for patients with confirmed or suspected 2019 novel coronavirus (2019-nCoV) by following anesthesia management protocols, and to document clinical- and anesthesia-related characteristics of these patients. DESIGN: This was a retrospective, multicenter clinical study. SETTING: This study used a multicenter dataset from 4 hospitals in Wuhan, China. PARTICIPANTS: Patients and health care providers with confirmed or suspected 2019-nCoV from January 23 to 31, 2020, at the Wuhan Union Hospital, the Wuhan Children's Hospital, The Central Hospital of Wuhan, and the Wuhan Fourth Hospital in Wuhan, China. INTERVENTIONS: Anesthetic management and infection control guidelines for emergency procedures for patients with suspected 2019-nCoV were drafted and applied in 4 hospitals in Wuhan. MEASUREMENTS AND MAIN RESULTS: Cross-infection in the operating rooms of the 4 hospitals was effectively reduced by implementing the new measures and procedures. The majority of patients with laboratory-confirmed 2019-nCoV infection or suspected infection were female (23 [62%] of 37), and the mean age was 41.0 years old (standard deviation 19.6; range 4-78). 10 (27%) patients had chronic medical illnesses, including 4 (11%) with diabetes, 8 (22%) with hypertension, and 8 (22%) with digestive system disease. Twenty-five (68%) patients presented with lymphopenia, and 23 (62%) patients exhibited multiple mottling and ground-glass opacity on computed tomography scanning. CONCLUSIONS: The present study indicates that COVID 19-specific guidelines for emergency procedures for patients with confirmed or suspected 2019-nCoV may effectively prevent cross-infection in the operating room. Most patients with confirmed or suspected COVID 19 presented with fever and dry cough and demonstrated bilateral multiple mottling and ground-glass opacity on chest computed tomography scans.

Zhao, S., et al. (2020). "Estimating the Unreported Number of Novel Coronavirus (2019-nCoV) Cases in China in the First Half of January 2020: A Data-Driven Modelling Analysis of the Early Outbreak." J Clin Med **9**(2).

BACKGROUND: In December 2019, an outbreak of respiratory illness caused by a novel coronavirus (2019-nCoV) emerged in Wuhan, China and has swiftly spread to other parts of China and a number of foreign countries. The 2019-nCoV cases might have been under-reported roughly from 1 to 15 January 2020, and thus we estimated the number of unreported cases and the basic reproduction number, R0, of 2019-nCoV. METHODS: We modelled the epidemic curve of 2019-nCoV cases, in mainland China from 1 December 2019 to 24 January 2020 through the exponential growth. The number of unreported cases was determined by the maximum likelihood estimation. We used the serial intervals (SI) of infection caused by two other well-known coronaviruses (CoV), Severe Acute Respiratory Syndrome (SARS) and Middle East Respiratory Syndrome (MERS) CoVs, as approximations of the unknown SI for 2019-nCoV to estimate R0. RESULTS: We confirmed that the initial growth phase followed an exponential growth pattern. The under-reporting was likely to have resulted in 469 (95% CI: 403-540) unreported cases from 1 to 15 January 2020. The reporting rate after 17 January 2020 was likely to have increased 21-fold (95% CI: 18-25) in comparison to the situation from 1 to 17 January 2020 on average. We estimated the R0 of 2019-nCoV at 2.56 (95% CI: 2.49-2.63). CONCLUSION: The under-reporting was likely to have occurred during the first half of January 2020 and should be considered in future investigation.

Zhou, Y., et al. (2020). "Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2." Cell Discov **6**: 14.

Human coronaviruses (HCoVs), including severe acute respiratory syndrome coronavirus (SARS-CoV) and 2019 novel coronavirus (2019-nCoV, also known as SARS-CoV-2), lead global epidemics with high morbidity and mortality. However, there are currently no effective drugs targeting 2019-nCoV/SARS-CoV-2. Drug repurposing, representing as an effective drug discovery strategy from existing drugs, could shorten the time and reduce the cost compared to de novo drug discovery. In this study, we present an integrative, antiviral drug repurposing methodology implementing a systems pharmacology-based network medicine platform, quantifying the interplay between the HCoV-host interactome and drug targets in the human protein-protein interaction network. Phylogenetic analyses of 15 HCoV whole genomes reveal that 2019-nCoV/SARS-CoV-2 shares the highest nucleotide sequence identity with SARS-CoV (79.7%). Specifically, the envelope and nucleocapsid proteins of 2019-nCoV/SARS-CoV-2 are two evolutionarily conserved regions, having the sequence identities of 96% and 89.6%, respectively, compared to SARS-CoV. Using network proximity analyses of drug targets and HCoV-host interactions in the human

interactome, we prioritize 16 potential anti-HCoV repurposable drugs (e.g., melatonin, mercaptopurine, and sirolimus) that are further validated by enrichment analyses of drug-gene signatures and HCoV-induced transcriptomics data in human cell lines. We further identify three potential drug combinations (e.g., sirolimus plus dactinomycin, mercaptopurine plus melatonin, and toremifene plus emodin) captured by the "Complementary Exposure" pattern: the targets of the drugs both hit the HCoV-host subnetwork, but target separate neighborhoods in the human interactome network. In summary, this study offers powerful network-based methodologies for rapid identification of candidate repurposable drugs and potential drug combinations targeting 2019-nCoV/SARS-CoV-2.

Zhou, Y., et al. (2020). "[Clinical features and chest CT findings of coronavirus disease 2019 in infants and young children]." Zhongguo Dang Dai Er Ke Za Zhi **22**(3): 215-220.

OBJECTIVE: To study the clinical features and chest CT findings of coronavirus disease 2019 (COVID-19) in infants and young children. METHODS: A retrospective analysis was performed for the clinical data and chest CT images of 9 children, aged 0 to 3 years, who were diagnosed with COVID-19 by nucleic acid detection between January 20 and February 10, 2020. RESULTS: All 9 children had an epidemiological history, and family clustering was observed for all infected children. Among the 9 children with COVID-19, 5 had no symptoms, 4 had fever, 2 had cough, and 1 had rhinorrhea. There were only symptoms of the respiratory system. Laboratory examination showed no reductions in leukocyte or lymphocyte count. Among the 9 children, 6 had an increase in lymphocyte count and 2 had an increase in leukocyte count. CT examination showed that among the 9 children, 8 had pulmonary inflammation located below the pleura or near the interlobar fissure and 3 had lesions distributed along the bronchovascular bundles. As for the morphology of the lesions, 6 had nodular lesions and 7 had patchy lesions; ground glass opacity with consolidation was observed in 6 children, among whom 3 had halo sign, and there was no typical paving stone sign. CONCLUSIONS: Infants and young children with COVID-19 tend to have mild clinical symptoms and imaging findings not as typical as those of adults, and therefore, the diagnosis of COVID-19 should be made based on imaging findings along with epidemiological history and nucleic acid detection. Chest CT has guiding significance for the early diagnosis of asymptomatic children.

Zhou, Y. H., et al. (2020). "Effectiveness of glucocorticoid therapy in patients with severe novel coronavirus pneumonia: protocol of a randomized controlled trial." Chin Med J (Engl).

BACKGROUND: At the end of 2019, a novel coronavirus outbreak emerged in Wuhan, China, and its causative organism has been subsequently designated the 2019 novel coronavirus (2019-nCoV). The virus has since rapidly spread to all provinces and autonomous regions of China, and to countries outside of China. Patients who become infected with 2019-nCoV may initially develop mild upper respiratory tract symptoms. However, a significant fraction of these patients goes on to subsequently develop serious lower respiratory disease. The effectiveness of adjunctive glucocorticoid therapy uses in the management of 2019-nCoV infected patients with severe lower respiratory tract infections is not clear, and warrants further investigation. METHODS: The present study will be conducted as an open-labelled, randomised controlled trial. We will enrol 48 subjects from Chongqing Public Health Medical Center. Each eligible subject will be assigned to an intervention group (methylprednisolone via intravenous injection at a dose of 1-2mg/kg/day for 3 days) or a control group (no glucocorticoid use) randomly, at a 1:1 ratio. Subjects in both groups will be invited for 28 days of follow-up which will be scheduled at 4 consecutive visit points. We will use the clinical improvement rate as our primary endpoint. Secondary endpoints include the timing of clinical improvement after intervention, duration of mechanical ventilation, duration of hospitalization, overall incidence of adverse events, as well as rate of adverse events at each visit, and mortality at 2 and 4 weeks. DISCUSSION: The present coronavirus outbreak is the third serious global coronavirus outbreak in the past two decades. Oral and parenteral glucocorticoids have been used in the management of severe respiratory symptoms in coronavirus-infected patients in the past. However, there remains no definitive evidence in the literature for or against the utilization of systemic glucocorticoids in seriously ill patients with coronavirus-related severe respiratory disease, or indeed in other types of severe respiratory disease. In this study, we hope to discover evidence either supporting or opposing the systemic therapeutic administration of glucocorticoids in severe coronavirus disease 2019 (COVID-19) patients. TRIAL REGISTRATION: ClinicalTrials.gov, ChiCTR2000029386, http://www.chictr.org.cn/showproj.aspx?proj=48777.

Zhou, Z., et al. (2020). "Swine acute diarrhea syndrome coronavirus (SADS-CoV) antagonizes interferon-beta production via blocking IPS-1 and RIG-I." Virus Res **278**: 197843.

Swine acute diarrhea syndrome coronavirus (SADS-CoV), a newly emerging enteric coronavirus, is considered to be associated with swine acute diarrhea syndrome (SADS) which has caused significantly economic losses to the porcine industry. Interactions between SADS-CoV and the host innate immune response is unclear yet. In this study, we used IPEC-J2 cells as a model to explore potential evasion strategies employed by SADS-CoV. Our results showed that SADS-CoV infection failed to induce IFN-beta production, and inhibited poly (I:C) and Sendai virus (SeV)-triggered IFN-beta expression. SADS-CoV also blocked poly (I:C)-induced phosphorylation and nuclear translocation of IRF-3 and NF-kappaB. Furthermore, SADS-CoV did not interfere with the activity of IFN-beta promoter stimulated by IRF3, TBK1 and IKKepsilon, but counteracted its activation induced by IPS-1 and RIG-I. Collectively, this study is the first investigation that shows interactions between SADS-CoV and the host innate immunity, which provides information of the molecular mechanisms underlying SASD-CoV infection.

Zhu, G. D. and J. Cao (2020). "[Challenges and countermeasures on Chinese malaria elimination programme during the coronavirus disease 2019 (COVID-19) outbreak]." Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi **32**(1): 7-9.

Since the end of 2019, the coronavirus disease 2019 (COVID-19) has been extensively epidemic in China, which not only seriously threatens the safety and health of Chinese people, but also challenges the management of other infectious diseases. Currently, there are still approximately three thousand malaria cases imported into China every year. If the diagnosis and treatment of malaria cases as well as the investigation and response of the epidemic foci are not carried out timely, it may endanger patients'lives and cause the possible of secondary transmission, which threatens the achievements of malaria elimination in China. Due to the extensive spread and high transmission ability of the COVID-19, there is a possibility of virus infections among malaria cases during the medical care-seeking behaviors and among healthcare professionals during clinical diagnosis and treatment, sample collection and testing and epidemiological surveys. This paper analyzes the challenges of the COVID-19 for Chinese malaria elimination programme, and proposes the countermeasures in response to the COVID-19 outbreak, so as to provide the reference for healthcare professionals.

Zhu, N., et al. (2020). "A Novel Coronavirus from Patients with Pneumonia in China, 2019." N Engl J Med **382**(8): 727-733.

In December 2019, a cluster of patients with pneumonia of unknown cause was linked to a seafood wholesale market in Wuhan, China. A previously unknown betacoronavirus was discovered through the use of unbiased sequencing in samples from patients with pneumonia. Human airway epithelial cells were used to isolate a novel coronavirus, named 2019-nCoV, which formed a clade within the subgenus sarbecovirus, Orthocoronavirinae subfamily. Different from both MERS-CoV and SARS-CoV, 2019-nCoV is the seventh member of the family of coronaviruses that infect humans. Enhanced surveillance and further investigation are ongoing. (Funded by the National Key Research and Development Program of China and the National Major Project for Control and Prevention of Infectious Disease in China.).

Zhu, Z. W., et al. (2020). "[Comparison of heart failure and 2019 novel coronavirus pneumonia in chest CT features and clinical characteristics]." Zhonghua Xin Xue Guan Bing Za Zhi **48**(0): E007.

Objective: To identify the characteristics including clinical features and pulmonary computed tomography (CT) features of heart failure and novel coronavirus pneumonia (COVID-19). Methods: This study was a retrospective study. A total of 7 patients with Heart failure and 12 patients with COVID-19 in the Second Xiangya Hospital of Central South University between December 1, 2019 and February 15, 2020 were enrolled. The baseline clinical and imaging features of the two groups were statistically analyzed. Results: There was no significant difference in age and sex between the two groups, but the incidence of epidemiological contact history, fever or respiratory symptoms in the COVID-19 group was significantly higher than that in the heart failure group (12/12 vs. 2/7, P=0.001; 12/12 vs. 4/7, P<0.001). While the proportion of cardiovascular diseases and impaired cardiac function was significantly less than that of the heart failure group (2/12 vs.7/7, P<0.001; 0/12 vs.7/7, P<0.001). For imaging features, both groups had ground-glass opacity and thickening of interlobular septum, but the ratio of central and gradient distribution was higher in patients with heart failure than that in patients with COVID-19 (4/7 vs. 1/12, P=0.04). In heart failure group, the ratio of the expansion of small pulmonary veins was also higher (3/7 vs. 0, P=0.013), and the lung lesions can be significantly improved after effective anti-heart failure treatment. Besides, there are more disease with rounded morphology in COVID-19 (9/12 vs. 2/7, P=0.048). Conclusions: More patients with COVID-19 have epidemiological history and fever or respiratory symptoms. There are significant differences in chest CT features, such as enlargement of pulmonary veins, lesions distribution and morphology between heart failure and COVID-19.

Zhuang, Q., et al. (2020). "Surveillance and Taxonomic Analysis of the Coronavirus Dominant in Pigeons in China." Transbound Emerg Dis.

Coronaviruses (CoVs) are found in humans and a wide variety of wild and domestic animals, and of substantial impact on human and animal health. In poultry, the genetic diversity, evolution, distribution, and taxonomy of CoVs dominant in birds other than chickens remain enigmatic. In our previous study, we proposed that the CoVs dominant (i.e., mainly circulating) in ducks (DdCoVs) should represent a novel species, which was different from the one represented by the CoVs dominant in chickens (CdCoVs). In this study, we conducted a large-scale surveillance of CoVs in chickens, ducks, geese, pigeons and other birds (quails, sparrows and partridges) using a conserved RT-PCR assay. The surveillance demonstrated that CdCoVs, DdCoVs and the CoVs dominant in pigeons (PdCoVs) belong to different lineages, and they are all prevalent in live poultry markets and the backyard flocks in some regions of China. We further sequenced seven Coronaviridae-wide conserved domains in their replicase polyprotein pp1ab of seven PdCoVs, and found that the genetic distances in these domains between PdCoVs and DdCoVs or CdCoVs are large enough to separate PdCoVs into a novel species, which were different from the ones represented by DdCoVs or CdCoVs within the genus Gammacoronavirus, per the species demarcation criterion of International Committee on Taxonomy of Viruses. This report shed novel insight into the genetic diversity, distribution, evolution, and taxonomy of avian CoVs.

Zhuang, Z., et al. (2020). "Preliminary estimation of the novel coronavirus disease (COVID-19) cases in Iran: A modelling analysis based on overseas cases and air travel data." Int J Infect Dis.

As of 1 March 2020, Iran has reported 987 COVID-19 cases and including 54 associated deaths. At least six neighboring countries (Bahrain, Iraq, Kuwait, Oman, Afghanistan and Pakistan) have reported imported COVID-19 cases from Iran. We used air travel data and the cases from Iran to other Middle East countries and estimated 16533 (95% CI: 5925, 35538) COVID-19 cases in Iran by 25 February, before UAE and other Gulf Cooperation Council countries suspended inbound and outbound flights from Iran.

Zu, Z. Y., et al. (2020). "Coronavirus Disease 2019 (COVID-19): A Perspective from China." Radiology: 200490.

In December 2019, an outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection occurred in Wuhan, Hubei Province, China and spread across China and beyond. On February 12, 2020, WHO officially named the disease caused by the novel coronavirus as Coronavirus Disease 2019 (COVID-19). Since most COVID-19 infected patients were diagnosed with pneumonia and characteristic CT imaging patterns, radiological examinations have become vital in early diagnosis and assessment of disease course. To date, CT findings have been recommended as major evidence for clinical diagnosis of COVID-19 in Hubei, China. This review focuses on the etiology, epidemiology, and clinical symptoms of COVID-19, while highlighting the role of chest CT in prevention and disease control. A full translation of this article in Chinese is available.

Zuo, M. Z., et al. (2020). "Expert Recommendations for Tracheal Intubation in Critically ill Patients with Noval Coronavirus Disease 2019." Chin Med Sci J.

Coronavirus Disease 2019 (COVID-19), caused by a novel coronavirus (SARS-CoV-2), is a highly contagious disease. It firstly appeared in Wuhan, Hubei province of China in December 2019. During the next two months, it moved rapidly throughout China and spread to multiple countries through infected persons travelling by air. Most of the infected patients have mild symptoms including fever, fatigue and cough. But in severe cases, patients can progress rapidly and develop to the acute respiratory distress syndrome, septic shock, metabolic acidosis and coagulopathy. The new coronavirus was reported to spread via droplets, contact and natural aerosols from human-to-human. Therefore, high-risk aerosol-producing procedures such as endotracheal intubation may put the anesthesiologists at high risk of nosocomial infections. In fact, SARS-CoV-2 infection of anesthesiologists after endotracheal intubation for confirmed COVID-19 patients have been reported in hospitals in Wuhan. The expert panel of airway management in Chinese Society of Anaesthesiology has deliberated and drafted this recommendation, by which we hope to guide the performance of endotracheal intubation by frontline anesthesiologists and critical care physicians. During the airway management, enhanced droplet/airborne PPE should be applied to the health care providers. A good airway assessment before airway intervention is of vital importance. For patients with normal airway, awake intubation should be avoided and modified rapid sequence induction is strongly recommended.

Sufficient muscle relaxant should be assured before intubation. For patients with difficult airway, good preparation of airway devices and detailed intubation plans should be made.

The above contents are the collected information from Internet and public resources to offer to the people for the convenient reading and information disseminating and sharing.

References

1. Adhikari, S. P., et al. (2020). "Epidemiology, causes, clinical manifestation and diagnosis, prevention and control of coronavirus disease (COVID-19) during the early outbreak period: a scoping review." Infect Dis Poverty 9(1): 29.
2. Agarwal, A., et al. (2020). "Guidance for building a dedicated health facility to contain the spread of the 2019 novel coronavirus outbreak." Indian J Med Res.
3. Ahmed, S. F., et al. (2020). "Preliminary Identification of Potential Vaccine Targets for the COVID-19 Coronavirus (SARS-CoV-2) Based on SARS-CoV Immunological Studies." Viruses 12(3).
4. Ai, T., et al. (2020). "Correlation of Chest CT and RT-PCR Testing in Coronavirus Disease 2019 (COVID-19) in China: A Report of 1014 Cases." Radiology: 200642.
5. Al-Ahmadi, K., et al. (2020). "Spatial association between primary Middle East respiratory syndrome coronavirus infection and exposure to dromedary camels in Saudi Arabia." Zoonoses Public Health.
6. Albarello, F., et al. (2020). "2019-novel Coronavirus severe adult respiratory distress syndrome in two cases in Italy: An uncommon radiological presentation." Int J Infect Dis 93: 192-197.
7. Alderman, C. (2020). "Pharmacy Services and the Novel Coronavirus." Sr Care Pharm 35(4): 146-147.
8. Alfano, F., et al. (2020). "Circulation of pantropic canine coronavirus in autochthonous and imported dogs, Italy." Transbound Emerg Dis.
9. Algaissi, A., et al. (2020). "Quantification of the Middle East Respiratory Syndrome-Coronavirus RNA in Tissues by Quantitative Real-Time RT-PCR." Methods Mol Biol 2099: 99-106.
10. Allam, Z. and D. S. Jones (2020). "On the Coronavirus (COVID-19) Outbreak and the Smart City Network: Universal Data Sharing Standards Coupled with Artificial Intelligence (AI) to Benefit Urban Health Monitoring and Management." Healthcare (Basel) 8(1).
11. Al-Mandhari, A., et al. (2020). "Coronavirus Disease 2019 outbreak: preparedness and readiness of countries in the Eastern Mediterranean Region." East Mediterr Health J 26(2): 136-137.
12. An, P., et al. (2020). "CT Manifestations of Novel Coronavirus Pneumonia: A Case Report." Balkan Med J.
13. Andrea, G., et al. (2020). "Coronavirus Disease 2019 and Transplantation: a view from the inside." Am J Transplant.
14. Anzai, A., et al. (2020). "Assessing the Impact of Reduced Travel on Exportation Dynamics of Novel Coronavirus Infection (COVID-19)." J Clin Med 9(2).
15. Arshad Ali, S., et al. (2020). "The outbreak of Coronavirus Disease 2019 (COVID-19)-An emerging global health threat." J Infect Public Health.
16. Ashour, H. M., et al. (2020). "Insights into the Recent 2019 Novel Coronavirus (SARS-CoV-2) in Light of Past Human Coronavirus Outbreaks." Pathogens 9(3).
17. Baglivo, M., et al. (2020). "Natural small molecules as inhibitors of coronavirus lipid-dependent attachment to host cells: a possible strategy for reducing SARS-COV-2 infectivity?" Acta Biomed 91(1): 161-164.
18. Bai, S. L., et al. (2020). "[Analysis of the first cluster of cases in a family of novel coronavirus pneumonia in Gansu Province]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E005.
19. Baidu. http://www.baidu.com. 2020.
20. Bajema, K. L., et al. (2020). "Persons Evaluated for 2019 Novel Coronavirus - United States, January 2020." MMWR Morb Mortal Wkly Rep 69(6): 166-170.
21. Benvenuto, D., et al. (2020). "The 2019-new coronavirus epidemic: Evidence for virus evolution." J Med Virol 92(4): 455-459.
22. Bernard Stoecklin, S., et al. (2020). "First cases of coronavirus disease 2019 (COVID-19) in France: surveillance, investigations and control measures, January 2020." Euro Surveill 25(6).
23. Bernheim, A., et al. (2020). "Chest CT Findings in Coronavirus Disease-19 (COVID-19): Relationship to Duration of Infection." Radiology: 200463.
24. Bhatnagar, T., et al. (2020). "Lopinavir/ritonavir combination therapy amongst symptomatic coronavirus disease 2019 patients in India: Protocol for restricted public health emergency use." Indian J Med Res.
25. Bhattacharya, M., et al. (2020). "Development of epitope-based peptide vaccine against novel

coronavirus 2019 (SARS-COV-2): Immunoinformatics approach." J Med Virol.

26. Boldog, P., et al. (2020). "Risk Assessment of Novel Coronavirus COVID-19 Outbreaks Outside China." J Clin Med 9(2).
27. Bonilla-Aldana, D. K., et al. (2020). "Coronavirus infections reported by ProMED, February 2000-January 2020." Travel Med Infect Dis: 101575.
28. Bordi, L., et al. (2020). "Differential diagnosis of illness in patients under investigation for the novel coronavirus (SARS-CoV-2), Italy, February 2020." Euro Surveill 25(8).
29. Bouwman, K. M., et al. (2020). "Three Amino Acid Changes in Avian Coronavirus Spike Protein Allow Binding to Kidney Tissue." J Virol 94(2).
30. Cancer Biology. http://www.cancerbio.net. 2020.
31. Cardenas-Conejo, Y., et al. (2020). "An exclusive 42 amino acid signature in pp1ab protein provides insights into the evolutive history of the 2019 novel human-pathogenic coronavirus (SARS-CoV-2)." J Med Virol.
32. Ceraolo, C. and F. M. Giorgi (2020). "Genomic variance of the 2019-nCoV coronavirus." J Med Virol 92(5): 522-528.
33. Chan, J. F., et al. (2020). "A familial cluster of pneumonia associated with the 2019 novel coronavirus indicating person-to-person transmission: a study of a family cluster." Lancet 395(10223): 514-523.
34. Chan, J. F., et al. (2020). "Genomic characterization of the 2019 novel human-pathogenic coronavirus isolated from a patient with atypical pneumonia after visiting Wuhan." Emerg Microbes Infect 9(1): 221-236.
35. Chen, L., et al. (2020). "[Analysis of clinical features of 29 patients with 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 203-208.
36. Chen, L., et al. (2020). "[Analysis of clinical features of 29 patients with 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E005.
37. Chen, L., et al. (2020). "RNA based mNGS approach identifies a novel human coronavirus from two individual pneumonia cases in 2019 Wuhan outbreak." Emerg Microbes Infect 9(1): 313-319.
38. Chen, N., et al. (2020). "Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study." Lancet 395(10223): 507-513.
39. Chen, X. and B. Yu (2020). "First two months of the 2019 Coronavirus Disease (COVID-19) epidemic in China: real-time surveillance and evaluation with a second derivative model." Glob Health Res Policy 5: 7.
40. Chen, X., et al. (2020). "Application of a Risk Analysis Tool to Middle East Respiratory Syndrome Coronavirus (MERS-CoV) Outbreak in Saudi Arabia." Risk Anal.
41. Chen, X., et al. (2020). "Perioperative Management of Patients Infected with the Novel Coronavirus: Recommendation from the Joint Task Force of the Chinese Society of Anesthesiology and the Chinese Association of Anesthesiologists." Anesthesiology.
42. Cheng, V. C. C., et al. (2020). "Escalating infection control response to the rapidly evolving epidemiology of the Coronavirus disease 2019 (COVID-19) due to SARS-CoV-2 in Hong Kong." Infect Control Hosp Epidemiol: 1-24.
43. Chronic obstructive pulmonary disease group of Chinese Thoracic, S. and P. Chronic obstructive pulmonary disease committee of Chinese Association of Chest (2020). "[Medical management and prevention instruction of chronic obstructive pulmonary disease during the coronavirus disease 2019 epidemic]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E034.
44. Chu, D. K. W., et al. (2020). "Molecular Diagnosis of a Novel Coronavirus (2019-nCoV) Causing an Outbreak of Pneumonia." Clin Chem.
45. Deng, S. Q. and H. J. Peng (2020). "Characteristics of and Public Health Responses to the Coronavirus Disease 2019 Outbreak in China." J Clin Med 9(2).
46. Deng, X., et al. (2020). "Structure-Guided Mutagenesis Alters Deubiquitinating Activity and Attenuates Pathogenesis of a Murine Coronavirus." J Virol.
47. Devaux, C. A., et al. (2020). "New insights on the antiviral effects of chloroquine against coronavirus: what to expect for COVID-19?" Int J Antimicrob Agents: 105938.
48. Dhama, K., et al. (2020). "COVID-19, an emerging coronavirus infection: advances and prospects in designing and developing vaccines, immunotherapeutics, and therapeutics." Hum Vaccin Immunother: 1-7.
49. Ding, Q., et al. (2020). "The clinical characteristics of pneumonia patients co-infected with 2019 novel coronavirus and influenza virus in Wuhan, China." J Med Virol.
50. Driggin, E., et al. (2020). "Cardiovascular Considerations for Patients, Health Care Workers, and Health Systems During the Coronavirus Disease 2019 (COVID-19) Pandemic." J Am Coll Cardiol.

51. Du, B., et al. (2020). "[Pharmacotherapeutics for the new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 173-176.
52. Du, B., et al. (2020). "[Pharmacotherapeutics for the New Coronavirus Pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E012.
53. Fan, C., et al. (2020). "Prediction of Epidemic Spread of the 2019 Novel Coronavirus Driven by Spring Festival Transportation in China: A Population-Based Study." Int J Environ Res Public Health 17(5).
54. Fan, H. H., et al. (2020). "Repurposing of clinically approved drugs for treatment of coronavirus disease 2019 in a 2019-novel coronavirus (2019-nCoV) related coronavirus model." Chin Med J (Engl).
55. Frieden, T. R. and C. T. Lee (2020). "Identifying and Interrupting Superspreading Events-Implications for Control of Severe Acute Respiratory Syndrome Coronavirus 2." Emerg Infect Dis 26(6).
56. Fung, J., et al. (2020). "Antigen Capture Enzyme-Linked Immunosorbent Assay for Detecting Middle East Respiratory Syndrome Coronavirus in Humans." Methods Mol Biol 2099: 89-97.
57. Google. http://www.google.com. 2020.
58. Gordon, C. J., et al. (2020). "The antiviral compound remdesivir potently inhibits RNA-dependent RNA polymerase from Middle East respiratory syndrome coronavirus." J Biol Chem.
59. Gorse, G. J., et al. (2020). "Antibodies to coronaviruses are higher in older compared with younger adults and binding antibodies are more sensitive than neutralizing antibodies in identifying coronavirus-associated illnesses." J Med Virol 92(5): 512-517.
60. Group of Interventional Respiratory Medicine, C. T. S. (2020). "[Expert consensus for bronchoscopy during the epidemic of 2019 novel coronavirus infection (Trial version)]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 199-202.
61. Group of Interventional Respiratory Medicine, C. T. S. (2020). "[Expert consensus for bronchoscopy during the epidemic of 2019 Novel Coronavirus infection (Trial version)]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E006.
62. Grunewald, M. E., et al. (2020). "Murine Coronavirus Infection Activates the Aryl Hydrocarbon Receptor in an Indoleamine 2,3-Dioxygenase-Independent Manner, Contributing to Cytokine Modulation and Proviral TCDD-Inducible-PARP Expression." J Virol 94(3).
63. Guan, C. S., et al. (2020). "Imaging Features of Coronavirus disease 2019 (COVID-19): Evaluation on Thin-Section CT." Acad Radiol.
64. Guan, G. W., et al. (2020). "[Exploring the mechanism of liver enzyme abnormalities in patients with novel coronavirus-infected pneumonia]." Zhonghua Gan Zang Bing Za Zhi 28(2): E002.
65. Han, R., et al. (2020). "Early Clinical and CT Manifestations of Coronavirus Disease 2019 (COVID-19) Pneumonia." AJR Am J Roentgenol: 1-6.
66. Hu, X. H., et al. (2020). "[Thinking of treatment strategies for colorectal cancer patients in tumor hospitals under the background of coronavirus pneumonia]." Zhonghua Wei Chang Wai Ke Za Zhi 23(3): E002.
67. Huan, C., et al. (2020). "Characterization and evolution of the coronavirus porcine epidemic diarrhoea virus HLJBY isolated in China." Transbound Emerg Dis 67(1): 65-79.
68. Huang, C., et al. (2020). "Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China." Lancet 395(10223): 497-506.
69. Jang, K. J., et al. (2020). "A high ATP concentration enhances the cooperative translocation of the SARS coronavirus helicase nsP13 in the unwinding of duplex RNA." Sci Rep 10(1): 4481.
70. Jang, W. M., et al. (2020). "Influence of trust on two different risk perceptions as an affective and cognitive dimension during Middle East respiratory syndrome coronavirus (MERS-CoV) outbreak in South Korea: serial cross-sectional surveys." BMJ Open 10(3): e033026.
71. Jazieh, A. R., et al. (2020). "Outcome of Oncology Patients Infected With Coronavirus." JCO Glob Oncol 6: 471-475.
72. Jernigan, D. B. and C. C.-R. Team (2020). "Update: Public Health Response to the Coronavirus Disease 2019 Outbreak - United States, February 24, 2020." MMWR Morb Mortal Wkly Rep 69(8): 216-219.
73. Ji, W., et al. (2020). "Cross-species transmission of the newly identified coronavirus 2019-nCoV." J Med Virol 92(4): 433-440.
74. Journal of American Science. http://www.jofamericanscience.org. 2020.
75. Kang, X., et al. (2020). "[Anesthesia management in cesarean section for a patient with coronavirus disease 2019]." Zhejiang Da Xue Xue Bao Yi Xue Ban 49(1): 0.
76. Kannan, S., et al. (2020). "COVID-19 (Novel Coronavirus 2019) - recent trends." Eur Rev Med Pharmacol Sci 24(4): 2006-2011.
77. Killerby, M. E., et al. (2020). "Middle East Respiratory Syndrome Coronavirus Transmission." Emerg Infect Dis 26(2): 191-198.

78. Kim, J. M., et al. (2020). "Identification of Coronavirus Isolated from a Patient in Korea with COVID-19." Osong Public Health Res Perspect 11(1): 3-7.
79. Kim, J. Y., et al. (2020). "The First Case of 2019 Novel Coronavirus Pneumonia Imported into Korea from Wuhan, China: Implication for Infection Prevention and Control Measures." J Korean Med Sci 35(5): e61.
80. Kinross, P., et al. (2020). "Rapidly increasing cumulative incidence of coronavirus disease (COVID-19) in the European Union/European Economic Area and the United Kingdom, 1 January to 15 March 2020." Euro Surveill 25(11).
81. Koonin, L. M. (2020). "Novel coronavirus disease (COVID-19) outbreak: Now is the time to refresh pandemic plans." J Bus Contin Emer Plan 13(4): 1-15.
82. Kooraki, S., et al. (2020). "Coronavirus (COVID-19) Outbreak: What the Department of Radiology Should Know." J Am Coll Radiol.
83. Korean Society of Infectious, D., et al. (2020). "Report on the Epidemiological Features of Coronavirus Disease 2019 (COVID-19) Outbreak in the Republic of Korea from January 19 to March 2, 2020." J Korean Med Sci 35(10): e112.
84. Kritas, S. K., et al. (2020). "Mast cells contribute to coronavirus-induced inflammation: new anti-inflammatory strategy." J Biol Regul Homeost Agents 34(1).
85. Kruse, R. L. (2020). "Therapeutic strategies in an outbreak scenario to treat the novel coronavirus originating in Wuhan, China." F1000Res 9: 72.
86. Kumar, S., et al. (2020). "Structural, glycosylation and antigenic variation between 2019 novel coronavirus (2019-nCoV) and SARS coronavirus (SARS-CoV)." Virusdisease 31(1): 13-21.
87. Lai, C. C., et al. (2020). "Asymptomatic carrier state, acute respiratory disease, and pneumonia due to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): Facts and myths." J Microbiol Immunol Infect.
88. Lai, C. C., et al. (2020). "Global epidemiology of coronavirus disease 2019: disease incidence, daily cumulative index, mortality, and their association with country healthcare resources and economic status." Int J Antimicrob Agents: 105946.
89. Lai, C. C., et al. (2020). "Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): The epidemic and the challenges." Int J Antimicrob Agents 55(3): 105924.
90. Lai, J., et al. (2020). "Factors Associated With Mental Health Outcomes Among Health Care Workers Exposed to Coronavirus Disease 2019." JAMA Netw Open 3(3): e203976.
91. Lai, T. H. T., et al. (2020). "Stepping up infection control measures in ophthalmology during the novel coronavirus outbreak: an experience from Hong Kong." Graefes Arch Clin Exp Ophthalmol.
92. Leung, C. (2020). "Clinical features of deaths in the novel coronavirus epidemic in China." Rev Med Virol: e2103.
93. Li, G., et al. (2020). "Coronavirus infections and immune responses." J Med Virol 92(4): 424-432.
94. Li, H., et al. (2020). "[Potential antiviral therapeutics for 2019 Novel Coronavirus]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 170-172.
95. Li, H., et al. (2020). "The novel coronavirus outbreak: what can be learned from China in public reporting?" Glob Health Res Policy 5: 9.
96. Li, K. and P. B. McCray, Jr. (2020). "Development of a Mouse-Adapted MERS Coronavirus." Methods Mol Biol 2099: 161-171.
97. Li, L. H., et al. (2020). "[Treatment strategies of Budd-Chiari syndrome during the epidemic period of 2019 coronavirus disease]." Zhonghua Wai Ke Za Zhi 58(0): E007.
98. Li, L. Q., et al. (2020). "2019 novel coronavirus patients' clinical characteristics, discharge rate, and fatality rate of meta-analysis." J Med Virol.
99. Li, X. Y., et al. (2020). "[The keypoints in treatment of the critical coronavirus disease 2019 patient]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E026.
100. Li, X., et al. (2020). "[Preliminary Recommendations for Lung Surgery during 2019 Novel Coronavirus Disease (COVID-19) Epidemic Period]." Zhongguo Fei Ai Za Zhi 23(3): 133-135.
101. Li, Y. and L. Xia (2020). "Coronavirus Disease 2019 (COVID-19): Role of Chest CT in Diagnosis and Management." AJR Am J Roentgenol: 1-7.
102. Li, Z. Y. and L. Y. Meng (2020). "[The prevention and control of a new coronavirus infection in department of stomatology]." Zhonghua Kou Qiang Yi Xue Za Zhi 55(0): E001.
103. Life Science Journal. http://www.lifesciencesite.com. 2020.
104. Ling, Y., et al. (2020). "Persistence and clearance of viral RNA in 2019 novel coronavirus disease rehabilitation patients." Chin Med J (Engl).
105. Linton, N. M., et al. (2020). "Incubation Period and Other Epidemiological Characteristics of 2019 Novel Coronavirus Infections with Right Truncation: A Statistical Analysis of Publicly Available Case Data." J Clin Med 9(2).

106. Liu, C., et al. (2020). "[Preliminary study of the relationship between novel coronavirus pneumonia and liver function damage: a multicenter study]." Zhonghua Gan Zang Bing Za Zhi 28(2): 148-152.
107. Liu, D., et al. (2020). "Pregnancy and Perinatal Outcomes of Women With Coronavirus Disease (COVID-19) Pneumonia: A Preliminary Analysis." AJR Am J Roentgenol: 1-6.
108. Liu, J., et al. (2019). "Comprehensive Genomic Characterization Analysis of lncRNAs in Cells With Porcine Delta Coronavirus Infection." Front Microbiol 10: 3036.
109. Liu, J., et al. (2020). "Community Transmission of Severe Acute Respiratory Syndrome Coronavirus 2, Shenzhen, China, 2020." Emerg Infect Dis 26(6).
110. Liu, M., et al. (2020). "[Clinical characteristics of 30 medical workers infected with new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 209-214.
111. Liu, M., et al. (2020). "[Clinical characteristics of 30 medical workers infected with new coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E016.
112. Lu, R., et al. (2020). "Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding." Lancet 395(10224): 565-574.
113. Lu, S., et al. (2020). "Alert for non-respiratory symptoms of Coronavirus Disease 2019 (COVID-19) patients in epidemic period: A case report of familial cluster with three asymptomatic COVID-19 patients." J Med Virol.
114. Lu, T. and H. Pu (2020). "Computed Tomography Manifestations of 5 Cases of the Novel Coronavirus Disease 2019 (COVID-19) Pneumonia From Patients Outside Wuhan." J Thorac Imaging.
115. Ma H, Chen G. Stem cell. The Journal of American Science 2005;1(2):90-92. doi:10.7537/marsjas010205.14. http://www.jofamericanscience.org/journals/am-sci/0102/14-mahongbao.pdf.
116. Ma H, Cherng S. Eternal Life and Stem Cell. Nature and Science. 2007;5(1):81-96. doi:10.7537/marsnsj050107.10. http://www.sciencepub.net/nature/0501/10-0247-mahongbao-eternal-ns.pdf.
117. Ma H, Cherng S. Nature of Life. Life Science Journal 2005;2(1):7-15. doi:10.7537/marslsj020105.03. http://www.lifesciencesite.com/lsj/life0201/life-0201-03.pdf.
118. Ma H, Yang Y. Turritopsis nutricula. Nature and Science 2010;8(2):15-20. doi:10.7537/marsnsj080210.03. http://www.sciencepub.net/nature/ns0802/03_1279_hongbao_turritopsis_ns0802_15_20.pdf.
119. Ma H. The Nature of Time and Space. Nature and science 2003;1(1):1-11. doi:10.7537/marsnsj010103.01. http://www.sciencepub.net/nature/0101/01-ma.pdf.
120. Mandal, S., et al. (2020). "Prudent public health intervention strategies to control the coronavirus disease 2019 transmission in India: A mathematical model-based approach." Indian J Med Res.
121. Marsland Press. http://www.sciencepub.net. 2020.
122. Marsland Press. http://www.sciencepub.org. 2020.
123. Martinez, M. A. (2020). "Compounds with therapeutic potential against novel respiratory 2019 coronavirus." Antimicrob Agents Chemother.
124. Menachery, V. D., et al. (2020). "Trypsin Treatment Unlocks Barrier for Zoonotic Bat Coronavirus Infection." J Virol 94(5).
125. Meng, L., et al. (2020). "Coronavirus Disease 2019 (COVID-19): Emerging and Future Challenges for Dental and Oral Medicine." J Dent Res: 22034520914246.
126. Meo, S. A., et al. (2020). "Novel coronavirus 2019-nCoV: prevalence, biological and clinical characteristics comparison with SARS-CoV and MERS-CoV." Eur Rev Med Pharmacol Sci 24(4): 2012-2019.
127. National Center for Biotechnology Information, U.S. National Library of Medicine. http://www.ncbi.nlm.nih.gov/pubmed. 2020.
128. Nature and Science. http://www.sciencepub.net/nature. 2020.
129. Novel Coronavirus Pneumonia Emergency Response Epidemiology, T. (2020). "[The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (COVID-19) in China]." Zhonghua Liu Xing Bing Xue Za Zhi 41(2): 145-151.
130. Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Health protection guideline of mobile cabin hospitals during Novel Coronavirus Pneumonia (NPC) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E006.
131. Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Health protection guideline of passenger transport stations and transportation facilities during novel coronavirus pneumonia (NCP) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E007.

132. Novel Coronavirus Pneumonia Emergency Response Key Places, P., et al. (2020). "[Technologies and requirements of protection and disinfection in key places during the novel coronavirus pneumonia (NCP) outbreak]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E008.
133. Patel, A., et al. (2020). "Initial Public Health Response and Interim Clinical Guidance for the 2019 Novel Coronavirus Outbreak - United States, December 31, 2019-February 4, 2020." MMWR Morb Mortal Wkly Rep 69(5): 140-146.
134. Pullano, G., et al. (2020). "Novel coronavirus (2019-nCoV) early-stage importation risk to Europe, January 2020." Euro Surveill 25(4).
135. Ralph, R., et al. (2020). "2019-nCoV (Wuhan virus), a novel Coronavirus: human-to-human transmission, travel-related cases, and vaccine readiness." J Infect Dev Ctries 14(1): 3-17.
136. Respiratory care committee of Chinese Thoracic, S. (2020). "[Expert consensus on preventing nosocomial transmission during respiratory care for critically ill patients infected by 2019 novel coronavirus pneumonia]." Zhonghua Jie He He Hu Xi Za Zhi 17(0): E020.
137. Reusken, C., et al. (2020). "Laboratory readiness and response for novel coronavirus (2019-nCoV) in expert laboratories in 30 EU/EEA countries, January 2020." Euro Surveill 25(6).
138. Runfeng, L., et al. (2020). "Lianhuaqingwen exerts anti-viral and anti-inflammatory activity against novel coronavirus (SARS-CoV-2)." Pharmacol Res: 104761.
139. Ryu, S., et al. (2020). "An interim review of the epidemiological characteristics of 2019 novel coronavirus." Epidemiol Health 42: e2020006.
140. Sekimukai, H., et al. (2020). "Gold nanoparticle-adjuvanted S protein induces a strong antigen-specific IgG response against severe acute respiratory syndrome-related coronavirus infection, but fails to induce protective antibodies and limit eosinophilic infiltration in lungs." Microbiol Immunol 64(1): 33-51.
141. Shang, J., et al. (2020). "Structure of mouse coronavirus spike protein complexed with receptor reveals mechanism for viral entry." PLoS Pathog 16(3): e1008392.
142. Shanmugaraj, B., et al. (2020). "Emergence of Novel Coronavirus 2019-nCoV: Need for Rapid Vaccine and Biologics Development." Pathogens 9(2).
143. Shanmugaraj, B., et al. (2020). "Perspectives on monoclonal antibody therapy as potential therapeutic intervention for Coronavirus disease-19 (COVID-19)." Asian Pac J Allergy Immunol 38(1): 10-18.
144. She, J., et al. (2020). "2019 novel coronavirus of pneumonia in Wuhan, China: emerging attack and management strategies." Clin Transl Med 9(1): 19.
145. Sheikh, A., et al. (2020). "Analysis of preferred codon usage in the coronavirus N genes and their implications for genome evolution and vaccine design." J Virol Methods 277: 113806.
146. Shen, K., et al. (2020). "Diagnosis, treatment, and prevention of 2019 novel coronavirus infection in children: experts' consensus statement." World J Pediatr.
147. Shen, Z., et al. (2020). "Genomic diversity of SARS-CoV-2 in Coronavirus Disease 2019 patients." Clin Infect Dis.
148. Singh, S., et al. (2020). "Immunohistochemical and molecular detection of natural cases of bovine rotavirus and coronavirus infection causing enteritis in dairy calves." Microb Pathog 138: 103814.
149. Singhal, T. (2020). "A Review of Coronavirus Disease-2019 (COVID-19)." Indian J Pediatr 87(4): 281-286.
150. Sohrabi, C., et al. (2020). "World Health Organization declares global emergency: A review of the 2019 novel coronavirus (COVID-19)." Int J Surg 76: 71-76.
151. Song, F., et al. (2020). "Emerging 2019 Novel Coronavirus (2019-nCoV) Pneumonia." Radiology 295(1): 210-217.
152. Song, Q. Q., et al. (2020). "[Study on assessing early epidemiological parameters of coronavirus disease epidemic in China]." Zhonghua Liu Xing Bing Xue Za Zhi 41(4): 461-465.
153. Stem Cell. http://www.sciencepub.net/stem. 2020.
154. Sun, D., et al. (2020). "Clinical features of severe pediatric patients with coronavirus disease 2019 in Wuhan: a single center's observational study." World J Pediatr.
155. Sun, W. W., et al. (2020). "[Epidemiological characteristics of 2019 novel coronavirus family clustering in Zhejiang Province]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E027.
156. Tang, N., et al. (2020). "Abnormal coagulation parameters are associated with poor prognosis in patients with novel coronavirus pneumonia." J Thromb Haemost.
157. Thompson, R. N. (2020). "Novel Coronavirus Outbreak in Wuhan, China, 2020: Intense Surveillance Is Vital for Preventing Sustained Transmission in New Locations." J Clin Med 9(2).
158. Tian, H. Y. (2020). "[2019-nCoV: new challenges from coronavirus]." Zhonghua Yu Fang Yi Xue Za Zhi 54(3): 235-238.

159. Tian, H. Y. (2020). "[2019-nCoV: new challenges from coronavirus]." Zhonghua Yu Fang Yi Xue Za Zhi 54(0): E001.
160. Tian, S., et al. (2020). "Pulmonary Pathology of Early-Phase 2019 Novel Coronavirus (COVID-19) Pneumonia in Two Patients With Lung Cancer." J Thorac Oncol.
161. Tian, X. L., et al. (2020). "[The differential diagnosis for novel coronavirus pneumonia and similar lung diseases in general hospitals]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E035.
162. Tian, X., et al. (2020). "Potent binding of 2019 novel coronavirus spike protein by a SARS coronavirus-specific human monoclonal antibody." Emerg Microbes Infect 9(1): 382-385.
163. Volk, A., et al. (2020). "Coronavirus Endoribonuclease and Deubiquitinating Interferon Antagonists Differentially Modulate the Host Response during Replication in Macrophages." J Virol.
164. Wang, Y., et al. (2020). "Unique epidemiological and clinical features of the emerging 2019 novel coronavirus pneumonia (COVID-19) implicate special control measures." J Med Virol.
165. Whittaker, G. R. and J. K. Millet (2020). "Biochemical Characterization of Middle East Respiratory Syndrome Coronavirus Spike Protein Proteolytic Processing." Methods Mol Biol 2099: 21-37.
166. Wikipedia. The free encyclopedia. http://en.wikipedia.org. 2020.
167. Wu, C., et al. (2020). "Risk Factors Associated With Acute Respiratory Distress Syndrome and Death in Patients With Coronavirus Disease 2019 Pneumonia in Wuhan, China." JAMA Intern Med.
168. Wu, F., et al. (2020). "[Discussion on diagnosis and treatment of hepatobiliary malignancies during the outbreak of novel coronavirus pneumonia]." Zhonghua Zhong Liu Za Zhi 42(0): E004.
169. Wu, F., et al. (2020). "A new coronavirus associated with human respiratory disease in China." Nature 579(7798): 265-269.
170. Wu, J., et al. (2020). "[Novel coronavirus pneumonia (COVID-19) CT distribution and sign features]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E030.
171. Wu, P., et al. (2020). "Real-time tentative assessment of the epidemiological characteristics of novel coronavirus infections in Wuhan, China, as at 22 January 2020." Euro Surveill 25(3).
172. Xiao, H., et al. (2020). "Social Capital and Sleep Quality in Individuals Who Self-Isolated for 14 Days During the Coronavirus Disease 2019 (COVID-19) Outbreak in January 2020 in China." Med Sci Monit 26: e923921.
173. Xiao, H., et al. (2020). "The Effects of Social Support on Sleep Quality of Medical Staff Treating Patients with Coronavirus Disease 2019 (COVID-19) in January and February 2020 in China." Med Sci Monit 26: e923549.
174. Xu, X. W., et al. (2020). "Clinical findings in a group of patients infected with the 2019 novel coronavirus (SARS-Cov-2) outside of Wuhan, China: retrospective case series." BMJ 368: m606.
175. Yang, J., et al. (2020). "Prevalence of comorbidities in the novel Wuhan coronavirus (COVID-19) infection: a systematic review and meta-analysis." Int J Infect Dis.
176. Yang, L., et al. (2020). "[Diagnostic and therapeutic strategies of lung cancer patients during the outbreak of 2019 novel coronavirus disease (COVID-19)]." Zhonghua Zhong Liu Za Zhi 42(0): E006.
177. Yang, T. J., et al. (2020). "Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans." Proc Natl Acad Sci U S A 117(3): 1438-1446.
178. Yang, W., et al. (2020). "Clinical characteristics and imaging manifestations of the 2019 novel coronavirus disease (COVID-19):A multi-center study in Wenzhou city, Zhejiang, China." J Infect 80(4): 388-393.
179. Yang, Y., et al. (2020). "The deadly coronaviruses: The 2003 SARS pandemic and the 2020 novel coronavirus epidemic in China." J Autoimmun: 102434.
180. Yao, N., et al. (2020). "[Clinical characteristics and influencing factors of patients with novel coronavirus pneumonia combined with liver injury in Shaanxi region]." Zhonghua Gan Zang Bing Za Zhi 28(0): E003.
181. Yao, T. T., et al. (2020). "A systematic review of lopinavir therapy for SARS coronavirus and MERS coronavirus-A possible reference for coronavirus disease-19 treatment option." J Med Virol.
182. Yao, X., et al. (2020). "In Vitro Antiviral Activity and Projection of Optimized Dosing Design of Hydroxychloroquine for the Treatment of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)." Clin Infect Dis.
183. Yu, P., et al. (2020). "A familial cluster of infection associated with the 2019 novel coronavirus indicating potential person-to-person transmission during the incubation period." J Infect Dis.
184. Yu, Y. X., et al. (2020). "[Consideration and prevention for the aerosol transmission of 2019 novel coronavirus]." Zhonghua Yan Ke Za Zhi 56(0): E008.

185. Yuan, M., et al. (2020). "Association of radiologic findings with mortality of patients infected with 2019 novel coronavirus in Wuhan, China." PLoS One 15(3): e0230548.
186. Yuan, Y., et al. (2020). "Molecular Basis of Binding between Middle East Respiratory Syndrome Coronavirus and CD26 from Seven Bat Species." J Virol 94(5).
187. Zhang, J., et al. (2020). "Swine acute diarrhea syndrome coronavirus-induced apoptosis is caspase- and cyclophilin D- dependent." Emerg Microbes Infect 9(1): 439-456.
188. Zhang, L. and Y. Liu (2020). "Potential interventions for novel coronavirus in China: A systematic review." J Med Virol 92(5): 479-490.
189. Zhang, L., et al. (2020). "alpha-Ketoamides as Broad-Spectrum Inhibitors of Coronavirus and Enterovirus Replication: Structure-Based Design, Synthesis, and Activity Assessment." J Med Chem.
190. Zhang, M. C., et al. (2020). "[Suggestions for disinfection of ophthalmic examination equipment and protection of ophthalmologist against 2019 novel coronavirus infection]." Zhonghua Yan Ke Za Zhi 56(0): E001.
191. Zhang, M. Q., et al. (2020). "[Clinical features of 2019 novel coronavirus pneumonia in the early stage from a fever clinic in Beijing]." Zhonghua Jie He He Hu Xi Za Zhi 43(3): 215-218.
192. Zhang, M. Q., et al. (2020). "[Clinical features of 2019 novel coronavirus pneumonia in the early stage from a fever clinic in Beijing]." Zhonghua Jie He He Hu Xi Za Zhi 43(0): E013.
193. Zhao, S., et al. (2020). "Anesthetic Management of Patients With Suspected or Confirmed 2019 Novel Coronavirus Infection During Emergency Procedures." J Cardiothorac Vasc Anesth.
194. Zhao, S., et al. (2020). "Estimating the Unreported Number of Novel Coronavirus (2019-nCoV) Cases in China in the First Half of January 2020: A Data-Driven Modelling Analysis of the Early Outbreak." J Clin Med 9(2).
195. Zhao, S., et al. (2020). "Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak." Int J Infect Dis 92: 214-217.
196. Zhou, Y. H., et al. (2020). "Effectiveness of glucocorticoid therapy in patients with severe novel coronavirus pneumonia: protocol of a randomized controlled trial." Chin Med J (Engl).
197. Zhou, Y., et al. (2020). "[Clinical features and chest CT findings of coronavirus disease 2019 in infants and young children]." Zhongguo Dang Dai Er Ke Za Zhi 22(3): 215-220.
198. Zhou, Y., et al. (2020). "Network-based drug repurposing for novel coronavirus 2019-nCoV/SARS-CoV-2." Cell Discov 6: 14.
199. Zhou, Z., et al. (2020). "Swine acute diarrhea syndrome coronavirus (SADS-CoV) antagonizes interferon-beta production via blocking IPS-1 and RIG-I." Virus Res 278: 197843.
200. Zhu, G. D. and J. Cao (2020). "[Challenges and countermeasures on Chinese malaria elimination programme during the coronavirus disease 2019 (COVID-19) outbreak]." Zhongguo Xue Xi Chong Bing Fang Zhi Za Zhi 32(1): 7-9.
201. Zhu, N., et al. (2020). "A Novel Coronavirus from Patients with Pneumonia in China, 2019." N Engl J Med 382(8): 727-733.
202. Zhu, Z. W., et al. (2020). "[Comparison of heart failure and 2019 novel coronavirus pneumonia in chest CT features and clinical characteristics]." Zhonghua Xin Xue Guan Bing Za Zhi 48(0): E007.
203. Zhuang, Q., et al. (2020). "Surveillance and Taxonomic Analysis of the Coronavirus Dominant in Pigeons in China." Transbound Emerg Dis.
204. Zhuang, Z., et al. (2020). "Preliminary estimation of the novel coronavirus disease (COVID-19) cases in Iran: A modelling analysis based on overseas cases and air travel data." Int J Infect Dis.
205. Zu, Z. Y., et al. (2020). "Coronavirus Disease 2019 (COVID-19): A Perspective from China." Radiology: 200490.
206. Zuo, M. Z., et al. (2020). "Expert Recommendations for Tracheal Intubation in Critically ill Patients with Noval Coronavirus Disease 2019." Chin Med Sci J.

3/25/2020