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Wu, Z., McGoogan, J.M.
(2020) JAMA - Journal of the American Medical Association

Wu, J.T., Leung, K., Leung, G.M.
Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study

Abstract:
Background: Since Dec 31, 2019, the Chinese city of Wuhan has reported an outbreak of atypical pneumonia caused by the 2019 novel coronavirus (2019-nCoV). Cases have been exported to other Chinese cities, as well as internationally, threatening to trigger a global outbreak. Here, we provide an estimate of the size of the epidemic in Wuhan on the basis of the number of cases exported from Wuhan to cities outside mainland China and forecast the extent of the domestic and global public health risks of epidemics, accounting for social and non-pharmaceutical prevention interventions.

Methods: We used data from Dec 31, 2019, to Jan 28, 2020, on the number of cases exported from Wuhan internationally (known days of symptom onset from Dec 25, 2019, to Jan 19, 2020) to infer the number of infections in Wuhan from Dec 1, 2019, to Jan 25, 2020. Cases exported domestically were then estimated. We forecasted the national and global spread of 2019-nCoV, accounting for the effect of the metropolitan-wide quarantine of Wuhan and surrounding cities, which began Jan 23–24, 2020. We used data on monthly flight bookings from the Official Aviation Guide and data on human mobility across more than 300 prefecture-level cities in mainland China from the Tencent database. Data on confirmed cases were obtained from the reports published by the Chinese Center for Disease Control and Prevention. Serial interval estimates were based on previous studies of severe acute respiratory syndrome coronavirus (SARS-CoV). A susceptible-exposed-infectious-recovered metapopulation model was used to simulate the epidemics across all major cities in China. The basic reproductive number was estimated using Markov Chain Monte Carlo methods and presented using the resulting posterior mean and 95% credible interval (CrI). Findings: In our baseline scenario, we estimated that the basic reproductive number for 2019-nCoV was 2.68 (95% CrI 2.47–2.86) and that 75,815 individuals (95% CrI 37,304–130,330) have been infected in Wuhan as of Jan 25, 2020. The epidemic doubling time was 6–4 days (95% CrI 5.8–7.1). We estimated that in the baseline scenario, Chongqing, Beijing, Shanghai, Guangzhou, and Shenzhen had imported 461 (95% CrI 227–805), 113 (57–193), 98 (49–168), 111 (56–191), and 80 (40–139) infections from Wuhan, respectively. If the transmissibility of 2019-nCoV were similar everywhere domestically and over time, we inferred that epidemics are already growing exponentially in multiple major cities of China with a lag time behind the Wuhan outbreak of about 1–2 weeks. Interpretation: Given that 2019-nCoV is no longer contained within Wuhan, other major Chinese cities are probably sustaining localised outbreaks. Large cities overseas with close transport links to China could also become outbreak epicentres, unless substantial public health interventions at both the population and personal levels are implemented immediately. Independent self-sustaining outbreaks in major cities globally could become inevitable because of substantial exportation of presymptomatic cases and in the absence of large-scale public health interventions. Preparedness plans and mitigation interventions should be readied for quick deployment globally. Funding: Health and Medical Research Fund (Hong Kong, China).
Clinical characteristics and intrauterine vertical transmission potential of COVID-19 infection in nine pregnant women: a retrospective review of medical records

Abstract:
Background: Previous studies on the pneumonia outbreak caused by the 2019 novel coronavirus disease (COVID-19) were based on information from the general population. Limited data are available for pregnant women with COVID-19 pneumonia. This study aimed to evaluate the clinical characteristics of COVID-19 in pregnancy and the intrauterine vertical transmission potential of COVID-19 infection. Methods: Clinical records, laboratory results, and chest CT scans were retrospectively reviewed for nine pregnant women with laboratory-confirmed COVID-19 pneumonia (ie, with maternal throat swab samples that were positive for severe acute respiratory syndrome coronavirus 2 [SARS-CoV-2]) who were admitted to Zhongnan Hospital of Wuhan University, Wuhan, China, from Jan 20 to Jan 31, 2020. Evidence of intrauterine vertical transmission was assessed by testing for the presence of SARS-CoV-2 in amniotic fluid, cord blood, and neonatal throat swab samples. Breastmilk samples were also collected and tested from patients after the first lactation. Findings: All nine patients had a caesarean section in their third trimester. Seven patients presented with a fever. Other symptoms, including cough (in four of nine patients), myalgia (in three), sore throat (in two), and malaise (in two), were also observed. Fetal distress was monitored in two cases. Five of nine patients had lymphopenia (<1·0 × 10⁹ cells per L). Three patients had increased aminotransferase concentrations. None of the patients developed severe COVID-19 pneumonia or died, as of Feb 4, 2020. Nine livebirths were recorded. No neonatal asphyxia was observed in newborn babies. All nine livebirths had a 1-min Apgar score of 8–9 and a 5-min Apgar score of 9–10. Amniotic fluid, cord blood, neonatal throat swab, and breastmilk samples from six patients were tested for SARS-CoV-2, and all samples tested negative for the virus. Interpretation: The clinical characteristics of COVID-19 pneumonia in pregnant women were similar to those reported for non-pregnant adult patients who developed COVID-19 pneumonia. Findings from this small group of cases suggest that there is currently no evidence for intrauterine infection caused by vertical transmission in women who develop COVID-19 pneumonia in late pregnancy. Funding: Hubei Science and Technology Plan, Wuhan University Medical Development Plan.

Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR
(2020) Eurosurveillance, 25 (3), art. no. 2000045

Abstract:
Background: The ongoing outbreak of the recently emerged novel coronavirus (2019-nCoV) poses a challenge for public health laboratories as virus isolates are unavailable while there is growing evidence that the outbreak is more widespread than initially thought, and international spread through travellers does already occur. Aim: We aimed to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available. Methods: Here we present a validated diagnostic workflow for 2019-nCoV, its design relying on close genetic relatedness of 2019-nCoV with SARS coronavirus, making use of synthetic nucleic
acid technology. Results: The workflow reliably detects 2019-nCoV, and further discriminates 2019-nCoV from SARS-CoV. Through coordination between academic and public laboratories, we confirmed assay exclusivity based on 297 original clinical specimens containing a full spectrum of human respiratory viruses. Control material is made available through European Virus Archive Global (EVAg), a European Union infrastructure project. Conclusion: The present study demonstrates the enormous response capacity achieved through coordination of academic and public laboratories in national and European research networks. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Pathological findings of COVID-19 associated with acute respiratory distress syndrome

Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: a retrospective cohort study
(2020) The Lancet

Abstract:
Background: Since December, 2019, Wuhan, China, has experienced an outbreak of coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Epidemiological and clinical characteristics of patients with COVID-19 have been reported but risk factors for mortality and a detailed clinical course of illness, including viral shedding, have not been well described. Methods: In this retrospective, multicentre cohort study, we included all adult inpatients (≥18 years old) with laboratory-confirmed COVID-19 from Jinyintan Hospital and Wuhan Pulmonary Hospital (Wuhan, China) who had been discharged or had died by Jan 31, 2020. Demographic, clinical, treatment, and laboratory data, including serial samples for viral RNA detection, were extracted from electronic medical records and compared between survivors and non-survivors. We used univariable and multivariable logistic regression methods to explore the risk factors associated with in-hospital death. Findings: 191 patients (135 from Jinyintan Hospital and 56 from Wuhan Pulmonary Hospital) were included in this study, of whom 137 were discharged and 54 died in hospital. 91 (48%) patients had a comorbidity, with hypertension being the most common (58 [30%] patients), followed by diabetes (36 [19%] patients) and coronary heart disease (15 [8%] patients). Multivariable regression showed increasing odds of in-hospital death associated with older age (odds ratio 1·10, 95% CI 1·03–1·17, per year increase; p=0·0043), higher Sequential Organ Failure Assessment (SOFA) score (5·65, 2·61–12·23; p<0·0001), and d-dimer greater than 1 μg/mL (18·42, 2·64–128·55; p=0·0033) on admission. Median duration of viral shedding was 20·0 days (IQR 17·0–24·0) in survivors, but SARS-CoV-2 was detectable until death in non-survivors. The longest observed duration of viral shedding in survivors was 37 days. Interpretation: The potential risk factors of older age, high SOFA score, and d-dimer greater than 1 μg/mL could help clinicians to identify patients with poor prognosis at an early stage. Prolonged viral shedding provides the rationale for a strategy of isolation of infected patients and optimal antiviral interventions in the future. Funding: Chinese Academy of Medical Sciences Innovation Fund for Medical Sciences; National Science Grant for Distinguished Young Scholars; National Key Research and Development Program of China; The Beijing Science and Technology Project; and Major Projects of National Science and Technology on New Drug Creation and Development.
Chung, M., Bernheim, A., Mei, X., Zhang, N., Huang, M., Zeng, X., Cui, J., Xu, W., Yang, Y., Fayad, Z.A., Jacobi, A., Li, K., Li, S., Shan, H.

**CT imaging features of 2019 novel coronavirus (2019-nCoV)**

**Abstract:**
In this retrospective case series, chest CT scans of 21 symptomatic patients from China infected with the 2019 novel coronavirus (2019-nCoV) were reviewed, with emphasis on identifying and characterizing the most common findings. Typical CT findings included bilateral pulmonary parenchymal ground-glass and consolidative pulmonary opacities, sometimes with a rounded morphology and a peripheral lung distribution. Notably, lung cavitation, discrete pulmonary nodules, pleural effusions, and lymphadenopathy were absent. Follow-up imaging in a subset of patients during the study time window often demonstrated mild or moderate progression of disease, as manifested by increasing extent and density of lung opacities. © RSNA, 2020.

Ji, W., Wang, W., Zhao, X., Zai, J., Li, X.

**Cross-species transmission of the newly identified coronavirus 2019-nCoV**

**Abstract:**
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 coronavirus 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. © 2020 Wiley Periodicals, Inc.

Zhao, S., Lin, Q., Ran, J., Musa, S.S., Yang, G., Wang, W., Lou, Y., Gao, D., Yang, L., He, D., Wang, M.H.

**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**

**Abstract:**
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 (γ), 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. © 2020 The Author(s)

Wang, W., Tang, J., Wei, F.

Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China

Abstract:
To help health workers and the public recognize and deal with the 2019 novel coronavirus (2019-nCoV) quickly, effectively, and calmly with an updated understanding. A comprehensive search from Chinese and worldwide official websites and announcements was performed between 1 December 2019 and 9:30 am 26 January 2020 (Beijing time). A latest summary of 2019-nCoV and the current outbreak was drawn. Up to 24 pm, 25 January 2020, a total of 1975 cases of 2019-nCoV infection were confirmed in mainland China with a total of 56 deaths having occurred. The latest mortality was approximately 2.84% with a total of 2684 cases still suspected. The China National Health Commission reported the details of the first 17 deaths up to 24 pm, 22 January 2020. The deaths included 13 males and 4 females. The median age of the people who died was 75 (range 48-89) years. Fever (64.7%) and cough (52.9%) were the most common first symptoms among those who died. The median number of days from the occurrence of the first symptom to death was 14.0 (range 6-41) days, and it tended to be shorter among people aged 70 years or more (11.5 [range 6-19] days) than those aged less than 70 years (20 [range 10-41] days; P =.033). The 2019-nCoV infection is spreading and its incidence is increasing nationwide. The first deaths occurred mostly in elderly people, among whom the disease might progress faster. The public should still be cautious in dealing with the virus and pay more attention to protecting the elderly people from the virus. © 2020 Wiley Periodicals, Inc.


Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes

Abstract:
In December 2019, a novel coronavirus (2019-nCoV) caused an outbreak in Wuhan, China, and soon spread to other parts of the world. It was believed that 2019-nCoV was transmitted through respiratory tract and then induced pneumonia, thus molecular diagnosis based on oral swabs was used for confirmation of this disease. Likewise, patient will be released upon two times of negative detection from oral swabs. However, many coronaviruses can also be transmitted through oral–fecal route by infecting intestines. Whether 2019-nCoV infected patients also carry virus in other organs like intestine need to be tested. We conducted investigation on patients in a local hospital who were infected with this virus. We found the presence of 2019-nCoV in anal swabs and blood as well, and more anal swab positives than oral swab positives in a later stage of infection, suggesting shedding and thereby transmitted through oral–fecal route. We also showed serology test can improve detection positive rate thus should be used in future epidemiology. Our report provides a cautionary
warning that 2019-nCoV may be shed through multiple routes. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.

Initial CT findings and temporal changes in patients with the novel coronavirus pneumonia (2019-nCoV): a study of 63 patients in Wuhan, China (2020) European Radiology
Abstract:
Objectives: The purpose of this study was to observe the imaging characteristics of the novel coronavirus pneumonia. Methods: Sixty-three confirmed patients were enrolled from December 30, 2019 to January 31, 2020. High-resolution CT (HRCT) of the chest was performed. The number of affected lobes, ground glass nodules (GGO), patchy/punctate ground glass opacities, patchy consolidation, fibrous stripes and irregular solid nodules in each patient's chest CT image were recorded. Additionally, we performed imaging follow-up of these patients. Results: CT images of 63 confirmed patients were collected. M/F ratio: 33/30. The mean age was 44.9 ± 15.2 years. The mean number of affected lobes was 3.3 ± 1.8. Nineteen (30.2%) patients had one affected lobe, five (7.9%) patients had two affected lobes, four (6.3%) patients had three affected lobes, seven (11.1%) patients had four affected lobes while 28 (44.4%) patients had 5 affected lobes. Fifty-four (85.7%) patients had patchy/punctate ground glass opacities, 14 (22.2%) patients had GGO, 12 (19.0%) patients had patchy consolidation, 11 (17.5%) patients had fibrous stripes and 8 (12.7%) patients had irregular solid nodules. Fifty-four (85.7%) patients progressed, including single GGO increased, enlarged and consolidated; fibrous stripe enlarged, while solid nodules increased and enlarged. Conclusions: Imaging changes in novel viral pneumonia are rapid. The manifestations of the novel coronavirus pneumonia are diverse. Imaging changes of typical viral pneumonia and some specific imaging features were observed. Therefore, we need to strengthen the recognition of image changes to help clinicians to diagnose quickly and accurately. Key Points: • High-resolution CT (HRCT) of the chest is critical for early detection, evaluation of disease severity and follow-up of patients with the novel coronavirus pneumonia. • The manifestations of the novel coronavirus pneumonia are diverse and change rapidly. • Radiologists should be aware of the various features of the disease and temporal changes. © 2020, European Society of Radiology.

Shi, H., Han, X., Jiang, N., Cao, Y., Alwalid, O., Gu, J., Fan, Y., Zheng, C.
Abstract:
Background: A cluster of patients with coronavirus disease 2019 (COVID-19) pneumonia caused by infection with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) were successively reported in Wuhan, China. We aimed to describe the CT findings across different timepoints throughout the disease course. Methods: Patients with COVID-19 pneumonia (confirmed by next-generation sequencing or RT-PCR) who were admitted to one of two hospitals in Wuhan and who underwent serial chest CT scans were retrospectively enrolled. Patients were grouped on the basis of the interval between symptom onset and the first CT scan: group 1 (subclinical patients; scans done before symptom onset), group 2 (scans done ≤1 week after symptom onset), group 3 (>1 week to 2 weeks), and group 4 (>2 weeks to 3 weeks). Imaging features and their distribution were analysed and compared across the four groups. Findings: 81 patients admitted to hospital between Dec 20, 2019, and Jan 23, 2020, were retrospectively enrolled. The cohort included 42 (52%) men
and 39 (48%) women, and the mean age was 49·5 years (SD 11·0). The mean number of involved lung segments was 10·5 (SD 6·4) overall, 2·8 (3·3) in group 1, 11·1 (5·4) in group 2, 13·0 (5·7) in group 3, and 12·1 (5·9) in group 4. The predominant pattern of abnormality observed was bilateral (64 [79%] patients), peripheral (44 [54%]), ill-defined (66 [81%]), and ground-glass opacification (53 [65%]), mainly involving the right lower lobes (225 [27%] of 849 affected segments). In group 1 (n=15), the predominant pattern was unilateral (nine [60%]) and multifocal (eight [53%]) ground-glass opacities (14 [93%]). Lesions quickly evolved to bilateral (19 [90%]), diffuse (11 [52%]) ground-glass opacity predominance (17 [81%]) in group 2 (n=21). Thereafter, the prevalence of ground-glass opacities continued to decrease (17 [57%] of 30 patients in group 3, and five [33%] of 15 in group 4), and consolidation and mixed patterns became more frequent (12 [40%] in group 3, eight [53%] in group 4). Interpretation: COVID-19 pneumonia manifests with chest CT imaging abnormalities, even in asymptomatic patients, with rapid evolution from focal unilateral to diffuse bilateral ground-glass opacities that progressed to or co-existed with consolidations within 1–3 weeks. Combining assessment of imaging features with clinical and laboratory findings could facilitate early diagnosis of COVID-19 pneumonia. Funding: None.


Abstract:
Background: The chest CT findings of patients with 2019 Novel Coronavirus (2019-nCoV) pneumonia have not previously been described in detail. Purpose: To investigate the clinical, laboratory, and imaging findings of emerging 2019-nCoV pneumonia in humans. Materials and Methods: Fifty-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. Results: Fifty 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. Conclusion: Patients 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. © RSNA, 2020.


Abstract:
Background: The newly identified 2019-nCoV, which appears to have originated in Wuhan, the capital city of Hubei province in central China, is spreading rapidly nationwide. A number of cases of neonates born to mothers with 2019-nCoV pneumonia have been recorded. However, the clinical features of these cases have not been reported, and there is no sufficient evidence for the proper prevention and control of 2019-nCoV infections in neonates. Methods: The clinical features and outcomes of 10 neonates (including 2 twins) born to 9 mothers with confirmed 2019-nCoV infection in 5 hospitals from January 20 to February 5, 2020 were retrospectively analyzed. Results: Among these 9 pregnant women with confirmed 2019-nCoV infection, onset of clinical symptoms occurred before delivery in 4 cases, on the day of delivery in 2 cases, and after delivery in 3 cases. In most cases, fever and a cough were the first symptoms experienced, and 1 patient also had diarrhea. Of the newborns born to these mothers, 8 were male and 2 were female; 4 were full-term infants and 6 were born premature; 2 were small-for-gestational-age (SGA) infants and 1 was a large-for-gestational-age (LGA) infant; there were 8 singletons and 2 twins. Of the neonates, 6 had a Pediatric Critical Illness Score (PCIS) score of less than 90. Clinically, the first symptom in the neonates was shortness of breath (n=6), but other initial symptoms such as fever (n=2), thrombocytopenia accompanied by abnormal liver function (n=2), rapid heart rate (n=1), vomiting (n=1), and pneumothorax (n=1) were observed. Up to now, 5 neonates have been cured and discharged, 1 has died, and 4 neonates remain in hospital in a stable condition. Pharyngeal swab specimens were collected from 9 of the 10 neonates 1 to 9 days after birth for nucleic acid amplification tests for 2019-nCoV, all of which showed negative results. Conclusions: Perinatal 2019-nCoV infection may have adverse effects on newborns, causing problems such as fetal distress, premature labor, respiratory distress, thrombocytopenia accompanied by abnormal liver function, and even death. However, vertical transmission of 2019-nCoV is yet to be confirmed.

Chen, J.
Pathogenicity and transmissibility of 2019-nCoV—A quick overview and comparison with other emerging viruses

Abstract:
A zoonotic coronavirus, tentatively labeled as 2019-nCoV by the World Health Organization (WHO), has been identified as the causative agent of the viral pneumonia outbreak in Wuhan, China, at the end of 2019. Although 2019-nCoV can cause a severe respiratory illness like SARS and MERS, evidence from clinics suggested that 2019-nCoV is generally less pathogenic than SARS-CoV, and much less than MERS-CoV. The transmissibility of 2019-nCoV is still debated and needs to be further assessed. To avoid the 2019-nCoV outbreak turning into an epidemic or even a pandemic and to minimize the mortality rate, China activated emergency response procedures, but much remains to be learned about the features of the virus to refine the risk assessment and response. Here, the current knowledge in 2019-nCoV pathogenicity and transmissibility is summarized in comparison with several commonly known emerging viruses, and information urgently needed for a better control of the disease is highlighted. © 2020 The Author(s)

Paraskevis, D., Kostaki, E.G., Magiorkinis, G., Panayiotakopoulos, G., Sourvinos, G., Tsiodras, S.
Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event
(2020) Infection, Genetics and Evolution, 79, art. no. 104212

Abstract:
Background: A novel coronavirus (2019-nCoV) associated with human to human transmission and severe human infection has been recently reported from the city of Wuhan in China. Our objectives
were to characterize the genetic relationships of the 2019-nCoV and to search for putative recombination within the subgenus of sarbecovirus. Methods: Putative recombination was investigated by RDP4 and Simplot v3.5.1 and discordant phylogenetic clustering in individual genomic fragments was confirmed by phylogenetic analysis using maximum likelihood and Bayesian methods. Results: Our analysis suggests that the 2019-nCoV although closely related to BatCoV RaTG13 sequence throughout the genome (sequence similarity 96.3%), shows discordant clustering with the Bat_SARS-like coronavirus sequences. Specifically, in the 5′-part spanning the first 11,498 nucleotides and the last 3′-part spanning 24,341–30,696 positions, 2019-nCoV and RaTG13 formed a single cluster with Bat_SARS-like coronavirus sequences, whereas in the middle region spanning the 3′-end of ORF1a, the ORF1b and almost half of the spike regions, 2019-nCoV and RaTG13 grouped in a separate distant lineage within the sarbecovirus branch. Conclusions: The levels of genetic similarity between the 2019-nCoV and RaTG13 suggest that the latter does not provide the exact variant that caused the outbreak in humans, but the hypothesis that 2019-nCoV has originated from bats is very likely. We show evidence that the novel coronavirus (2019-nCoV) is not-mosaic consisting in almost half of its genome of a distinct lineage within the betacoronavirus. These genomic features and their potential association with virus characteristics and virulence in humans need further attention. © 2020 Elsevier B.V.


Abstract:
Background: Isolation of cases and contact tracing is used to control outbreaks of infectious diseases, and has been used for coronavirus disease 2019 (COVID-19). Whether this strategy will achieve control depends on characteristics of both the pathogen and the response. Here we use a mathematical model to assess if isolation and contact tracing are able to control onwards transmission from imported cases of COVID-19. Methods: We developed a stochastic transmission model, parameterised to the COVID-19 outbreak. We used the model to quantify the potential effectiveness of contact tracing and isolation of cases at controlling a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-like pathogen. We considered scenarios that varied in the number of initial cases, the basic reproduction number (R0), the delay from symptom onset to isolation, the probability that contacts were traced, the proportion of transmission that occurred before symptom onset, and the proportion of subclinical infections. We assumed isolation prevented all further transmission in the model. Outbreaks were deemed controlled if transmission ended within 12 weeks or before 5000 cases in total. We measured the success of controlling outbreaks using isolation and contact tracing, and quantified the weekly maximum number of cases traced to measure feasibility of public health effort. Findings: Simulated outbreaks starting with five initial cases, an R0 of 1·5, and 0% transmission before symptom onset could be controlled even with low contact tracing probability; however, the probability of controlling an outbreak decreased with the number of initial cases, when R0 was 2·5 or 3·5 and with more transmission before symptom onset. Across different initial numbers of cases, the majority of scenarios with an R0 of 1·5 were controllable with less than 50% of contacts successfully traced. To control the majority of outbreaks, for R0 of 2·5 more than 70% of contacts had to be traced, and for an R0 of 3·5 more than 90% of contacts had to be traced. The delay between symptom onset and isolation had the largest role in determining whether an outbreak was controllable when R0 was 1·5. For R0 values of 2·5 or 3·5, if
there were 40 initial cases, contact tracing and isolation were only potentially feasible when less than 1% of transmission occurred before symptom onset. Interpretation: In most scenarios, highly effective contact tracing and case isolation is enough to control a new outbreak of COVID-19 within 3 months. The probability of control decreases with long delays from symptom onset to isolation, fewer cases ascertained by contact tracing, and increasing transmission before symptoms. This model can be modified to reflect updated transmission characteristics and more specific definitions of outbreak control to assess the potential success of local response efforts. Funding: Wellcome Trust, Global Challenges Research Fund, and Health Data Research UK. © 2020 The Author(s). Published by Elsevier Ltd. This is an Open Access article under the CC BY-NC-ND 4.0 license


**Preparedness and vulnerability of African countries against importations of COVID-19: a modelling study**

**Abstract:**
Background: The novel coronavirus disease 2019 (COVID-19) epidemic has spread from China to 25 countries. Local cycles of transmission have already occurred in 12 countries after case importation. In Africa, Egypt has so far confirmed one case. The management and control of COVID-19 importations heavily rely on a country’s health capacity. Here we evaluate the preparedness and vulnerability of African countries against their risk of importation of COVID-19.

Methods: We used data on the volume of air travel departing from airports in the infected provinces in China and directed to Africa to estimate the risk of importation per country. We determined the country’s capacity to detect and respond to cases with two indicators: preparedness, using the WHO International Health Regulations Monitoring and Evaluation Framework; and vulnerability, using the Infectious Disease Vulnerability Index. Countries were clustered according to the Chinese regions contributing most to their risk. Findings: Countries with the highest importation risk (ie, Egypt, Algeria, and South Africa) have moderate to high capacity to respond to outbreaks. Countries at moderate risk (ie, Nigeria, Ethiopia, Sudan, Angola, Tanzania, Ghana, and Kenya) have variable capacity and high vulnerability. We identified three clusters of countries that share the same exposure to the risk originating from the provinces of Guangdong, Fujian, and the city of Beijing, respectively. Interpretation: Many countries in Africa are stepping up their preparedness to detect and cope with COVID-19 importations. Resources, intensified surveillance, and capacity building should be urgently prioritised in countries with moderate risk that might be ill-prepared to detect imported cases and to limit onward transmission. Funding: EU Framework Programme for Research and Innovation Horizon 2020, Agence Nationale de la Recherche.


**Case of the index patient who caused tertiary transmission of coronavirus disease 2019 in Korea: The application of lopinavir/ritonavir for the treatment of COVID-19 pneumonia monitored by quantitative RT-PCR**
(2020) Journal of Korean Medical Science, 35 (6), art. no. e79

**Abstract:**
Since mid-December of 2019, coronavirus disease 2019 (COVID-19) has been spreading from Wuhan, China. The confirmed COVID-19 patients in South Korea are those who came from or visited China. As secondary transmissions have occurred and the speed of transmission is accelerating, there are rising concerns about community infections. The 54-year old male is the third
patient diagnosed with COVID-19 in Korea. He is a worker for a clothing business and had mild respiratory symptoms and intermittent fever in the beginning of hospitalization, and pneumonia symptoms on chest computerized tomography scan on day 6 of admission. This patient caused one case of secondary transmission and three cases of tertiary transmission. Hereby, we report the clinical findings of the index patient who was the first to cause tertiary transmission outside China. Interestingly, after lopinavir/ritonavir (Kaletra, AbbVie) was administered, β-coronavirus viral loads significantly decreased and no or little coronavirus titers were observed. © 2020 The Korean Academy of Medical Sciences.


Characteristics of COVID-19 infection in Beijing

Abstract:
Background: Since the first case of a novel coronavirus (COVID-19) infection pneumonia was detected in Wuhan, China, a series of confirmed cases of the COVID-19 were found in Beijing. We analyzed the data of 262 confirmed cases to determine the clinical and epidemiological characteristics of COVID-19 in Beijing. Methods: We collected patients who were transferred by Beijing Emergency Medical Service to the designated hospitals. The information on demographic, epidemiological, clinical, laboratory test for the COVID-19 virus, diagnostic classification, cluster case and outcome were obtained. Furthermore we compared the characteristics between severe and common confirmed cases which including mild cases, no-pneumonia cases and asymptomatic cases, and we also compared the features between COVID-19 and 2003 SARS. Findings: By Feb 10, 2020, 262 patients were transferred from the hospitals across Beijing to the designated hospitals for special treatment of the COVID-19 infected by Beijing emergency medical service. Among of 262 patients, 46 (17.6%) were severe cases, 216 (82.4%) were common cases, which including 192 (73.3%) mild cases, 11(4.2%) non-pneumonia cases and 13 (5.0%) asymptomatic cases respectively. The median age of patients was 47.5 years old and 48.5% were male. 192 (73.3%) patients were residents of Beijing, 50 (26.0%) of which had been to Wuhan, 116 (60.4%) had close contact with confirmed cases, 21 (10.9%) had no contact history. The most common symptoms at the onset of illness were fever (82.1%), cough (45.8%), fatigue (26.3%), dyspnea (6.9%) and headache (6.5%). The median incubation period was 6.7 days, the interval time from between illness onset and seeing a doctor was 4.5 days. As of Feb 10, 17.2% patients have discharged and 81.7% patients remain in hospital in our study, the fatality of COVID-19 infection in Beijing was 0.9%. Interpretation: On the basis of this study, we provided the ratio of the COVID-19 infection on the severe cases to the mild, asymptomatic and non-pneumonia cases in Beijing. Population was generally susceptible, and with a relatively low fatality rate. The measures to prevent transmission was very successful at early stage, the next steps on the COVID-19 infection should be focused on early isolation of patients and quarantine for close contacts in families and communities in Beijing. Funding: Beijing Municipal Science and Technology Commission and Ministry of Science and Technology.

Tang, B., Bragazzi, N.L., Li, Q., Tang, S., Xiao, Y., Wu, J.

An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov)
(2020) Infectious Disease Modelling, 5, pp. 248-255.

Abstract:
The basic reproduction number of an infectious agent is the average number of infections one case can generate over the course of the infectious period, in a naïve, uninfected population. It is well-
known that the estimation of this number may vary due to several methodological issues, including different assumptions and choice of parameters, utilized models, used datasets and estimation period. With the spreading of the novel coronavirus (2019-nCoV) infection, the reproduction number has been found to vary, reflecting the dynamics of transmission of the coronavirus outbreak as well as the case reporting rate. Due to significant variations in the control strategies, which have been changing over time, and thanks to the introduction of detection technologies that have been rapidly improved, enabling to shorten the time from infection/symptoms onset to diagnosis, leading to faster confirmation of the new coronavirus cases, our previous estimations on the transmission risk of the 2019-nCoV need to be revised. By using time-dependent contact and diagnose rates, we refit our previously proposed dynamics transmission model to the data available until January 29th, 2020 and re-estimated the effective daily reproduction ratio that better quantifies the evolution of the interventions. We estimated when the effective daily reproduction ratio has fallen below 1 and when the epidemics will peak. Our updated findings suggest that the best measure is persistent and strict self-isolation. The epidemics will continue to grow, and can peak soon with the peak time depending highly on the public health interventions practically implemented. © 2020 The Authors

Zhang, S., Diao, M., Yu, W., Pei, L., Lin, Z., Chen, D.

Estimation of the reproductive number of novel coronavirus (COVID-19) and the probable outbreak size on the Diamond Princess cruise ship: A data-driven analysis
(2020) International Journal of Infectious Diseases, 93, pp. 201-204.

Abstract:

Backgrounds: Up to February 16, 2020, 355 cases have been confirmed as having COVID-19 infection on the Diamond Princess cruise ship. It is of crucial importance to estimate the reproductive number (R0) of the novel virus in the early stage of outbreak and make a prediction of daily new cases on the ship.

Method: We fitted the reported serial interval (mean and standard deviation) with a gamma distribution and applied “earlyR” package in R to estimate the R0 in the early stage of COVID-19 outbreak. We applied “projections” package in R to simulate the plausible cumulative epidemic trajectories and future daily incidence by fitting the data of existing daily incidence, a serial interval distribution, and the estimated R0 into a model based on the assumption that daily incidence obeys approximately Poisson distribution determined by daily infectiousness.

Results: The Maximum-Likelihood (ML) value of R0 was 2.28 for COVID-19 outbreak at the early stage on the ship. The median with 95% confidence interval (CI) of R0 values was 2.28 (2.06–2.52) estimated by the bootstrap resampling method. The probable number of new cases for the next ten days would gradually increase, and the estimated cumulative cases would reach 1514 (1384–1656) at the tenth day in the future. However, if R0 value was reduced by 25% and 50%, the estimated total number of cumulative cases would be reduced to 1081 (981–1177) and 758 (697–817), respectively. Conclusion: The median with 95% CI of R0 of COVID-19 was about 2.28 (2.06–2.52) during the early stage experienced on the Diamond Princess cruise ship. The future daily incidence and probable outbreak size is largely dependent on the change of R0. Unless strict infection management and control are taken, our findings indicate the potential of COVID-19 to cause greater outbreak on the ship. © 2020 The Author(s)

Wilder-Smith, A., Freedman, D.O.

Isolation, quarantine, social distancing and community containment: pivotal role for old-style public health measures in the novel coronavirus (2019-nCoV) outbreak
(2020) Journal of travel medicine, 27 (2)
Malik, Y.S., Sircar, S., Bhat, S., Sharun, K., Dhama, K., Dadar, M., Tiwari, R., Chaicumpa, W.  
Emerging novel coronavirus (2019-nCoV)—current scenario, evolutionary perspective based on genome analysis and recent developments  
Abstract:  
Coronaviruses are the well-known cause of severe respiratory, enteric and systemic infections in a wide range of hosts including man, mammals, fish, and avian. The scientific interest on coronaviruses increased after the emergence of Severe Acute Respiratory Syndrome coronavirus (SARS-CoV) outbreaks in 2002-2003 followed by Middle East Respiratory Syndrome CoV (MERS-CoV). This decade’s first CoV, named 2019-nCoV, emerged from Wuhan, China, and declared as ‘Public Health Emergency of International Concern’ on January 30th, 2020 by the World Health Organization (WHO). As on February 4, 2020, 425 deaths reported in China only and one death outside China (Philippines). In a short span of time, the virus spread has been noted in 24 countries. The zoonotic transmission (animal-to-human) is suspected as the route of disease origin. The genetic analyses predict bats as the most probable source of 2019-nCoV though further investigations needed to confirm the origin of the novel virus. The ongoing nCoV outbreak highlights the hidden wild animal reservoir of the deadly viruses and possible threat of spillover zoonoses as well. The successful virus isolation attempts have made doors open for developing better diagnostics and effective vaccines helping in combating the spread of the virus to newer areas. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.

Ceraolo, C., Giorgi, F.M.  
Genomic variance of the 2019-nCoV coronavirus  
Abstract:  
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. © 2020 Wiley Periodicals, Inc.

Luo, H., Tang, Q.-L., Shang, Y.-X., Liang, S.-B., Yang, M., Robinson, N., Liu, J.-P.  
Can Chinese Medicine Be Used for Prevention of Corona Virus Disease 2019 (COVID-19)? A Review of Historical Classics, Research Evidence and Current Prevention Programs  
Abstract:
Objective: Since December 2019, an outbreak of coronavirus disease 2019 (COVID-19) occurred in Wuhan, and rapidly spread to almost all parts of China. This was followed by prevention programs recommending Chinese medicine (CM) for the prevention. In order to provide evidence for CM recommendations, we reviewed ancient classics and human studies. Methods: Historical records on prevention and treatment of infections in CM classics, clinical evidence of CM on the prevention of severe acute respiratory syndrome (SARS) and H1N1 influenza, and CM prevention programs issued by health authorities in China since the COVID-19 outbreak were retrieved from different databases and websites till 12 February, 2020. Research evidence included data from clinical trials, cohort or other population studies using CM for preventing contagious respiratory virus diseases. Results: The use of CM to prevent epidemics of infectious diseases was traced back to ancient Chinese practice cited in Huangdi’s Internal Classic (Huang Di Nei Jing) where preventive effects were recorded. There were 3 studies using CM for prevention of SARS and 4 studies for H1N1 influenza. None of the participants who took CM contracted SARS in the 3 studies. The infection rate of H1N1 influenza in the CM group was significantly lower than the non-CM group (relative risk 0.36, 95% confidence interval 0.24–0.52; n=4). For prevention of COVID-19, 23 provinces in China issued CM programs. The main principles of CM use were to tonify qi to protect from external pathogens, disperse wind and discharge heat, and resolve dampness. The most frequently used herbs included Radix astragali (Huangqi), Radix glycyrrhizae (Gancao), Radix saposhnikoviae (Fangfeng), Rhizoma Atractylodis Macrocephalae (Baizhu), Lonicerae Japonicae Flos (Jinyinhua), and Fructus forsythia (Lianqiao). Conclusions: Based on historical records and human evidence of SARS and H1N1 influenza prevention, Chinese herbal formula could be an alternative approach for prevention of COVID-19 in high-risk population. Prospective, rigorous population studies are warranted to confirm the potential preventive effect of CM. © 2020, The Chinese Journal of Integrated Traditional and Western Medicine Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Li, X., Zai, J., Wang, X., Li, Y.  
Potential of large “first generation” human-to-human transmission of 2019-nCoV  
Abstract:  
To investigate the genetic diversity, time origin, and evolutionary history of the 2019-nCoV outbreak in China and Thailand, a total of 12 genome sequences of the virus with known sampling date (24 December 2019 and 13 January 2020) and geographic location (primarily Wuhan city, Hubei Province, China, but also Bangkok, Thailand) were analyzed. Phylogenetic and likelihood-mapping analyses of these genome sequences were performed. On the basis of our results, the star-like signal and topology of 2019-nCoV may be indicative of potentially large “first generation” human-to-human virus transmission. We estimated that 2019-nCoV likely originated in Wuhan on 9 November 2019 (95% credible interval: 25 September 2019 and 19 December 2019), and that Wuhan is the major hub for the spread of the 2019-nCoV outbreak in China and elsewhere. Our results could be useful for designing effective prevention strategies for 2019-nCoV in China and beyond. © 2020 Wiley Periodicals, Inc.

Mahase, E.  
Coronavirus covid-19 has killed more people than SARS and MERS combined, despite lower case fatality rate  
(2020) BMJ (Clinical research ed.), 368, p. m641.

**Pulmonary Pathology of Early-Phase 2019 Novel Coronavirus (COVID-19) Pneumonia in Two Patients With Lung Cancer**

(2020) Journal of Thoracic Oncology

**Abstract:**

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. © 2020 International Association for the Study of Lung Cancer

Sun, P., Qie, S., Liu, Z., Ren, J., Li, K., Xi, J.

**Clinical characteristics of 50 466 hospitalized patients with 2019-nCoV infection**

(2020) Journal of Medical Virology

**Abstract:**

We aim to summarize reliable evidence of evidence-based medicine for the treatment and prevention of the 2019 novel coronavirus (2019-nCoV) by analyzing all the published studies on the clinical characteristics of patients with 2019-nCoV. PubMed, Cochrane Library, Embase, and other databases were searched. Several studies on the clinical characteristics of 2019-nCoV infection were collected for meta-analysis. Ten studies were included in the meta-analysis, including a total number of 50 466 patients with 2019-nCoV infection. Meta-analysis shows that among these patients, the incidence of fever was 89.1%, the incidence of cough was 72.2%, and the incidence of muscle soreness or fatigue was 42.5%. The incidence of acute respiratory distress syndrome (ARDS) was 14.8%, the incidence of abnormal chest computer tomography (CT) was 96.6%, the percentage of severe cases in all infected cases was 18.1%, and the case fatality rate of patients with 2019-nCoV infection was 4.3%. Fever and cough are the most common symptoms in patients with 2019-nCoV infection, and most of these patients have abnormal chest CT examination. Several people have muscle soreness or fatigue as well as ARDS. Diarrhea, hemoptysis, headache, sore throat, shock, and other symptoms only occur in a small number of patients. The case fatality rate of patients with 2019-nCoV infection is lower than that of the severe acute respiratory syndrome and Middle East respiratory syndrome. © 2020 Wiley Periodicals, Inc.

Lee, P.-I., Hsueh, P.-R.

**Emerging threats from zoonotic coronaviruses-from SARS and MERS to 2019-nCoV**

(2020) Journal of Microbiology, Immunology and Infection

Giovanetti, M., Benvenuto, D., Angeletti, S., Ciccozzi, M.

**The first two cases of 2019-nCoV in Italy: Where they come from?**

Abstract:
A novel Coronavirus, 2019-nCoV, has been identified as the causal pathogen of an ongoing epidemic, with the first cases reported in Wuhan, China, last December 2019, and has since spread to other countries worldwide, included Europe and very recently Italy. In this short report, phylogenetic reconstruction was used to better understand the transmission dynamics of the virus from its first introduction in China focusing on the more recent evidence of infection in a couple of Chinese tourists arrived in Italy on 23rd January 2020 and labeled as Coronavirus Italian cases. A maximum clade credibility tree has been built using a dataset of 54 genome sequences of 2019-nCoV plus two closely related bat strains (SARS-like CoV) available in GenBank. Bayesian timescaled phylogenetic analysis was implemented in BEAST 1.10.4. The Bayesian phylogenetic reconstruction showed that 2019-2020 nCoV firstly introduced in Wuhan on 25 November 2019, started epidemic transmission reaching many countries worldwide, including Europe and Italy where the two strains isolated dated back 19 January 2020, the same that the Chinese tourists arrived in Italy. Strains isolated outside China were intermixed with strains isolated in China as evidence of likely imported cases in Rome, Italy, and Europe, as well. In conclusion, this report suggests that further spread of 2019-nCoV epidemic was supported by human mobility and that quarantine of suspected or diagnosed cases is useful to prevent further transmission. Viral genome phylogenetic analysis represents a useful tool for the evaluation of transmission dynamics and preventive action. © 2020 Wiley Periodicals, Inc.

CDC COVID-19 Response Team
Severe Outcomes Among Patients with Coronavirus Disease 2019 (COVID-19) - United States, February 12-March 16, 2020

Abstract:
Globally, approximately 170,000 confirmed cases of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) have been reported, including an estimated 7,000 deaths in approximately 150 countries (1). On March 11, 2020, the World Health Organization declared the COVID-19 outbreak a pandemic (2). Data from China have indicated that older adults, particularly those with serious underlying health conditions, are at higher risk for severe COVID-19-associated illness and death than are younger persons (3). Although the majority of reported COVID-19 cases in China were mild (81%), approximately 80% of deaths occurred among adults aged ≥60 years; only one (0.1%) death occurred in a person aged ≤19 years (3). In this report, COVID-19 cases in the United States that occurred during February 12-March 16, 2020 and severity of disease (hospitalization, admission to intensive care unit [ICU], and death) were analyzed by age group. As of March 16, a total of 4,226 COVID-19 cases in the United States had been reported to CDC, with multiple cases reported among older adults living in long-term care facilities (4). Overall, 31% of cases, 45% of hospitalizations, 53% of ICU admissions, and 80% of deaths associated with COVID-19 were among adults aged ≥65 years with the highest percentage of severe outcomes among persons aged ≥85 years. In contrast, no ICU admissions or deaths were reported among persons aged ≤19 years. Similar to reports from other countries, this finding suggests that the risk for serious disease and death from COVID-19 is higher in older age groups.

Devaux, C.A., Rolain, J.-M., Colson, P., Raoult, D.
New insights on the antiviral effects of chloroquine against coronavirus: what to expect for COVID-19?
(2020) International Journal of Antimicrobial Agents, art. no. 105938

Abstract:
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. © 2020 The Authors

Zou, X., Chen, K., Zou, J., Han, P., Hao, J., Han, Z.

Single-cell RNA-seq data analysis on the receptor ACE2 expression reveals the potential risk of different human organs vulnerable to 2019-nCoV infection (2020) Frontiers of Medicine

Abstract:
It has been known that, the novel Coronavirus, 2019-nCoV, which is considered similar to SARS-CoV and originated from Wuhan (China), invades human cells via the receptor angiotensin converting enzyme II (ACE2). Moreover, lung cells that have ACE2 expression may be the main target cells during 2019-nCoV infection. However, some patients also exhibit non-respiratory symptoms, such as kidney failure, implying that 2019-nCoV could also invade other organs. To construct a risk map of different human organs, we analyzed the single-cell RNA sequencing (scRNA-seq) datasets derived from major human physiological systems, including the respiratory, cardiovascular, digestive, and urinary systems. Through scRNA-seq data analyses, we identified the organs at risk, such as lung, heart, esophagus, kidney, bladder, and ileum, and located specific cell types (i.e., type II alveolar cells (AT2), myocardial cells, proximal tubule cell of the kidney, ileum and esophagus epithelial cells, and bladder urothelial cells), which are vulnerable to 2019-nCoV infection. Based on the findings, we constructed a risk map indicating the vulnerability of different organs to 2019-nCoV infection. This study may provide potential clues for further investigation of the pathogenesis and route of 2019-nCoV infection. © 2020, The Author(s).

Qin, C., Liu, F., Yen, T.-C., Lan, X.


Abstract:
Purpose: The aim of this case series is to illustrate the 18F-FDG PET/CT findings of patients with acute respiratory disease caused by COVID-19 in Wuhan, Hubei province of China. Methods: We describe the 18F-FDG PET/CT results from four patients who were admitted to the hospital with respiratory symptoms and fever between January 13 and January 20, 2020, when the COVID-19 outbreak was still unrecognized and the virus infectivity was unknown. A retrospective review of the patients’ medical history, clinical and laboratory data, as well as imaging findings strongly suggested a diagnosis of COVID-19. Results: All patients had peripheral ground-glass opacities and/or lung consolidations in more than two pulmonary lobes. Lung lesions were characterized by a high 18F-FDG uptake and there was evidence of lymph node involvement. Conversely, disseminated disease was absent, a finding suggesting that COVID-19 has pulmonary tropism. Conclusions: Although 18F-FDG PET/CT cannot be routinely used in an emergency setting and is
generally not recommended for infectious diseases, our pilot data shed light on the potential clinical utility of this imaging technique in the differential diagnosis of complex cases. © 2020, Springer-Verlag GmbH Germany, part of Springer Nature.


Abstract:
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 even 10 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. Nevertheless, some patients can present with a normal chest finding despite testing positive for COVID-19. Funding: We did not receive any fundings. © 2020


Abstract:
An outbreak of respiratory illness proved to be infected by a 2019 novel coronavirus, officially named Coronavirus Disease 2019 (COVID-19), was notified first in Wuhan, China, and has spread rapidly in China and to other parts of the world. Herein, we reported the first confirmed case of novel coronavirus pneumonia (NCP) imported from China in Taiwan. This case report revealed a natural course of NCP with self-recovery, which may be a good example in comparison with medical treatments. © 2020

Eurosurveillance Editorial Team

Cardiac Involvement in a Patient with Coronavirus Disease 2019 (COVID-19) (2020) JAMA Cardiology

Abstract:
Importance: Virus infection has been widely described as one of the most common causes of myocarditis. However, less is known about the cardiac involvement as a complication of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. Objective: To describe the presentation of acute myocardial inflammation in a patient with coronavirus disease 2019 (COVID-19) who recovered from the influenzalike syndrome and developed fatigue and signs and symptoms of heart failure a week after upper respiratory tract symptoms. Design, Setting, and Participant: This case report describes an otherwise healthy 53-year-old woman who tested positive for COVID-19 and was admitted to the cardiac care unit in March 2020 for acute myopericarditis with systolic dysfunction, confirmed on cardiac magnetic resonance imaging, the week after onset of fever and dry cough due to COVID-19. The patient did not show any respiratory involvement during the clinical course. Exposure: Cardiac involvement with COVID-19. Main Outcomes and Measures: Detection of cardiac involvement with an increase in levels of N-terminal pro-brain natriuretic peptide (NT-proBNP) and high-sensitivity troponin T, echocardiography changes, and diffuse biventricular myocardial edema and late gadolinium enhancement on cardiac magnetic resonance imaging. Results: An otherwise healthy 53-year-old white woman presented to the emergency department with severe fatigue. She described fever and dry cough the week before. She was afebrile but hypotensive; electrocardiography showed diffuse ST elevation, and elevated high-sensitivity troponin T and NT-proBNP levels were detected. Findings on chest radiography were normal. There was no evidence of obstructive coronary disease on coronary angiography. Based on the COVID-19 outbreak, a nasopharyngeal swab was performed, with a positive result for SARS-CoV-2 on real-time reverse transcriptase-polymerase chain reaction assay. Cardiac magnetic resonance imaging showed increased wall thickness with diffuse biventricular hypokinesis, especially in the apical segments, and severe left ventricular dysfunction (left ventricular ejection fraction of 35%). Short tau inversion recovery and T2-mapping sequences showed marked biventricular myocardial interstitial edema, and there was also diffuse late gadolinium enhancement involving the entire biventricular wall. There was a circumferential pericardial effusion that was most notable around the right cardiac chambers. These findings were all consistent with acute myopericarditis. She was treated with dobutamine, antiviral drugs (lopinavir/ritonavir), steroids, chloroquine, and medical treatment for heart failure, with progressive clinical and instrumental stabilization. Conclusions and Relevance: This case highlights cardiac involvement as a complication associated with COVID-19, even without symptoms and signs of interstitial pneumonia. © 2020 Cambridge University Press. All rights reserved.


Cardiovascular Implications of Fatal Outcomes of Patients with Coronavirus Disease 2019 (COVID-19) (2020) JAMA Cardiology

Abstract:
Importance: Increasing numbers of confirmed cases and mortality rates of coronavirus disease 2019 (COVID-19) are occurring in several countries and continents. Information regarding the impact of cardiovascular complication on fatal outcome is scarce. Objective: To evaluate the association of underlying cardiovascular disease (CVD) and myocardial injury with fatal outcomes in patients with
COVID-19. Design, Setting, and Participants: This retrospective single-center case series analyzed patients with COVID-19 at the Seventh Hospital of Wuhan City, China, from January 23, 2020, to February 23, 2020. Analysis began February 25, 2020. Main Outcomes and Measures: Demographic data, laboratory findings, comorbidities, and treatments were collected and analyzed in patients with and without elevation of troponin T (TnT) levels. Result: Among 187 patients with confirmed COVID-19, 144 patients (77%) were discharged and 43 patients (23%) died. The mean (SD) age was 58.50 (14.66) years. Overall, 66 (35.3%) had underlying CVD including hypertension, coronary heart disease, and cardiomyopathy, and 52 (27.8%) exhibited myocardial injury as indicated by elevated TnT levels. The mortality during hospitalization was 7.62% (8 of 105) for patients without underlying CVD and normal TnT levels, 13.33% (4 of 30) for those with underlying CVD and normal TnT levels, 37.50% (6 of 16) for those without underlying CVD but elevated TnT levels, and 69.44% (25 of 36) for those with underlying CVD and elevated TnTs. Patients with underlying CVD were more likely to exhibit elevation of TnT levels compared with the patients without CVD (36 [54.5%] vs 16 [13.2%]). Plasma TnT levels demonstrated a high and significantly positive linear correlation with plasma high-sensitivity C-reactive protein levels ($\beta = 0.530$, $P < .001$) and N-terminal pro-brain natriuretic peptide (NT-proBNP) levels ($\beta = 0.613$, $P < .001$). Plasma TnT and NT-proBNP levels during hospitalization (median [interquartile range (IQR)], 0.307 [0.094-0.600]; 1902.00 [728.35-8100.00]) and impending death (median [IQR], 0.141 [0.058-0.860]; 5375 [1179.50-25695.25]) increased significantly compared with admission values (median [IQR], 0.0355 [0.015-0.102]; 796.90 [401.93-1742.25]) in patients who died ($P = .001$; $P < .001$), while no significant dynamic changes of TnT (median [IQR], 0.010 [0.007-0.019]; 0.013 [0.007-0.022]; 0.011 [0.007-0.016]) and NT-proBNP (median [IQR], 352.20 [174.70-636.70]; 433.80 [155.80-1272.60]; 145.40 [63.4-526.50]) was observed in survivors ($P = .96$; $P = .16$). During hospitalization, patients with elevated TnT levels had more frequent malignant arrhythmias, and the use of glucocorticoid therapy (37 [71.2%] vs 69 [51.1%]) and mechanical ventilation (41 [59.6%] vs 14 [10.4%]) were higher compared with patients with normal TnT levels. The mortality rates of patients with and without use of angiotensin-converting enzyme inhibitors/angiotensin receptor blockers was 36.8% (7 of 19) and 25.6% (43 of 168). Conclusions and Relevance: Myocardial injury is significantly associated with fatal outcome of COVID-19, while the prognosis of patients with underlying CVD but without myocardial injury is relatively favorable. Myocardial injury is associated with cardiac dysfunction and arrhythmias. Inflammation may be a potential mechanism for myocardial injury. Aggressive treatment may be considered for patients at high risk of myocardial injury.. © 2020 Cambridge University Press. All rights reserved.

Cortegiani, A., Ingoglia, G., Ippolito, M., Giarratano, A., Einav, S.

A systematic review on the efficacy and safety of chloroquine for the treatment of COVID-19

(2020) Journal of Critical Care

Abstract:

Purpose: COVID-19 (coronavirus disease 2019) is a public health emergency of international concern. As of this time, there is no known effective pharmaceutical treatment, although it is much needed for patient contracting the severe form of the disease. The aim of this systematic review was to summarize the evidence regarding chloroquine for the treatment of COVID-19. Methods: PubMed, EMBASE, and three trial Registries were searched for studies on the use of chloroquine in patients with COVID-19. Results: We included six articles (one narrative letter, one in-vitro study, one editorial, expert consensus paper, two national guideline documents) and 23 ongoing clinical trials in China. Chloroquine seems to be effective in limiting the replication of SARS-CoV-2 (virus causing COVID-19) in vitro. Conclusions: There is rationale, pre-clinical evidence of
effectiveness and evidence of safety from long-time clinical use for other indications to justify clinical research on chloroquine in patients with COVID-19. However, clinical use should either adhere to the Monitored Emergency Use of Unregistered Interventions (MEURI) framework or be ethically approved as a trial as stated by the World Health Organization. Safety data and data from high-quality clinical trials are urgently needed. © 2020 Elsevier Inc.

Xia, W., Shao, J., Guo, Y., Peng, X., Li, Z., Hu, D.  
**Clinical and CT features in pediatric patients with COVID-19 infection: Different points from adults**  
(2020) Pediatric Pulmonology  
**Abstract:**  
Purpose: To discuss the different characteristics of clinical, laboratory, and chest computed tomography (CT) in pediatric patients from adults with 2019 novel coronavirus (COVID-19) infection. Methods: The clinical, laboratory, and chest CT features of 20 pediatric inpatients with COVID-19 infection confirmed by pharyngeal swab COVID-19 nucleic acid test were retrospectively analyzed during 23 January and 8 February 2020. The clinical and laboratory information was obtained from inpatient records. All the patients were undergone chest CT in our hospital. Results: Thirteen pediatric patients (13/20, 65%) had an identified history of close contact with COVID-19 diagnosed family members. Fever (12/20, 60%) and cough (13/20, 65%) were the most common symptoms. For laboratory findings, procalcitonin elevation (16/20, 80%) should be pay attention to, which is not common in adults. Coinfection (8/20, 40%) is common in pediatric patients. A total of 6 patients presented with unilateral pulmonary lesions (6/20, 30%), 10 with bilateral pulmonary lesions (10/20, 50%), and 4 cases showed no abnormality on chest CT (4/20, 20%). Consolidation with surrounding halo sign was observed in 10 patients (10/20, 50%), ground-glass opacities were observed in 12 patients (12/20, 60%), fine mesh shadow was observed in 4 patients (4/20, 20%), and tiny nodules were observed in 3 patients (3/20, 15%). Conclusion: Procalcitonin elevation and consolidation with surrounding halo signs were common in pediatric patients which were different from adults. It is suggested that underlying coinfection may be more common in pediatrics, and the consolidation with surrounding halo sign which is considered as a typical sign in pediatric patients. © 2020 Wiley Periodicals, Inc.

Porcheddu, R., Serra, C., Kelvin, D., Kelvin, N., Rubino, S.  
**Similarity in Case Fatality Rates (CFR) of COVID-19/SARS-COV-2 in Italy and China**  
**Abstract:**  
As of 28 February 2020, Italy had 888 cases of SARS-CoV-2 infections, with most cases in Northern Italy in the Lombardia and Veneto regions. Travel-related cases were the main source of COVID-19 cases during the early stages of the current epidemic in Italy. The month of February, however, has been dominated by two large clusters of outbreaks in Northern Italy, south of Milan, with mainly local transmission the source of infections. Contact tracing has failed to identify patient zero in one of the outbreaks. As of 28 February 2020, twenty-one cases of COVID-19 have died. Comparison between case fatality rates in China and Italy are identical at 2.3. Additionally, deaths are similar in both countries with fatalities in mostly the elderly with known comorbidities. It will be important to develop point-of-care devices to aid clinicians in stratifying elderly patients as early as possible to determine the potential level of care they will require to improve their chances of survival from COVID-19 disease. © 2020 Porcheddu et al.
Xie, J., Tong, Z., Guan, X., Du, B., Qiu, H., Slutsky, A.S.
Critical care crisis and some recommendations during the COVID-19 epidemic in China
(2020) Intensive Care Medicine

Al-Tawfiq, J.A.
Asymptomatic coronavirus infection: MERS-CoV and SARS-CoV-2 (COVID-19)
(2020) Travel Medicine and Infectious Disease, art. no. 101608

Baruah, V., Bose, S.
Immunoinformatics-aided identification of T cell and B cell epitopes in the surface glycoprotein of 2019-nCoV
Abstract:
The 2019 novel coronavirus (2019-nCoV) outbreak has caused a large number of deaths with thousands of confirmed cases worldwide, especially in East Asia. This study took an immunoinformatics approach to identify significant cytotoxic T lymphocyte (CTL) and B cell epitopes in the 2019-nCoV surface glycoprotein. Also, interactions between identified CTL epitopes and their corresponding major histocompatibility complex (MHC) class I supertype representatives prevalent in China were studied by molecular dynamics simulations. We identified five CTL epitopes, three sequential B cell epitopes and five discontinuous B cell epitopes in the viral surface glycoprotein. Also, during simulations, the CTL epitopes were observed to be binding MHC class I peptide-binding grooves via multiple contacts, with continuous hydrogen bonds and salt bridge anchors, indicating their potential in generating immune responses. Some of these identified epitopes can be potential candidates for the development of 2019-nCoV vaccines. © 2020 Wiley Periodicals, Inc.

Transplantation of ACE2- Mesenchymal stem cells improves the outcome of patients with covid-19 pneumonia
Abstract:
A coronavirus (HCoV-19) has caused the novel coronavirus disease (COVID-19) outbreak in Wuhan, China. Preventing and reversing the cytokine storm may be the key to save the patients with severe COVID-19 pneumonia. Mesenchymal stem cells (MSCs) have been shown to possess a comprehensive powerful immunomodulatory function. This study aims to investigate whether MSC transplantation improves the outcome of 7 enrolled patients with COVID-19 pneumonia in Beijing YouAn Hospital, China, from Jan 23, 2020 to Feb 16, 2020. The clinical outcomes, as well as changes of inflammatory and immune function levels and adverse effects of 7 enrolled patients were assessed for 14 days after MSC injection. MSCs could cure or significantly improve the functional
outcomes of seven patients without observed adverse effects. The pulmonary function and symptoms of these seven patients were significantly improved in 2 days after MSC transplantation. Among them, two common and one severe patient were recovered and discharged in 10 days after treatment. After treatment, the peripheral lymphocytes were increased, the C-reactive protein decreased, and the overactivated cytokine-secreting immune cells CXCR3+CD4+ T cells, CXCR3+CD8+ T cells, and CXCR3+ NK cells disappeared in 3-6 days. In addition, a group of CD14+CD11c+CD11bmid regulatory DC cell population dramatically increased. Meanwhile, the level of TNF-α was significantly decreased, while IL-10 increased in MSC treatment group compared to the placebo control group. Furthermore, the gene expression profile showed MSCs were ACE2- and TMPRSS2- which indicated MSCs are free from COVID-19 infection. Thus, the intravenous transplantation of MSCs was safe and effective for treatment in patients with COVID-19 pneumonia, especially for the patients in critically severe condition. © 2020 Leng Z et al. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.


Early dynamics of transmission and control of COVID-19: a mathematical modelling study

(2020) The Lancet Infectious Diseases

Abstract:
Background: An outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has led to 95,333 confirmed cases as of March 5, 2020. Understanding the early transmission dynamics of the infection and evaluating the effectiveness of control measures is crucial for assessing the potential for sustained transmission to occur in new areas. Combining a mathematical model of severe SARS-CoV-2 transmission with four datasets from within and outside Wuhan, we estimated how transmission in Wuhan varied between December, 2019, and February, 2020. We used these estimates to assess the potential for sustained human-to-human transmission to occur in locations outside Wuhan if cases were introduced. Methods: We combined a stochastic transmission model with data on cases of coronavirus disease 2019 (COVID-19) in Wuhan and international cases that originated in Wuhan to estimate how transmission had varied over time during January, 2020, and February, 2020. Based on these estimates, we then calculated the probability that newly introduced cases might generate outbreaks in other areas. To estimate the early dynamics of transmission in Wuhan, we fitted a stochastic transmission dynamic model to multiple publicly available datasets on cases in Wuhan and internationally exported cases from Wuhan. The four datasets we fitted to were: daily number of new internationally exported cases (or lack thereof), by date of onset, as of Jan 26, 2020; daily number of new cases in Wuhan with no market exposure, by date of onset, between Dec 1, 2019, and Jan 1, 2020; daily number of new cases in China, by date of onset, between Dec 29, 2019, and Jan 23, 2020; and proportion of infected passengers on evacuation flights between Jan 29, 2020, and Feb 4, 2020. We used an additional two datasets for comparison with model outputs: daily number of new exported cases from Wuhan (or lack thereof) in countries with high connectivity to Wuhan (ie, top 20 most at-risk countries), by date of confirmation, as of Feb 10, 2020; and data on new confirmed cases reported in Wuhan between Jan 16, 2020, and Feb 11, 2020. Findings: We estimated that the median daily reproduction number (Rt) in Wuhan declined from 2.35 (95% CI 1.15–4.77) 1 week before travel restrictions were introduced on Jan 23, 2020,
to 1.05 (0.41–2.39) 1 week after. Based on our estimates of Rt, assuming SARS-like variation, we calculated that in locations with similar transmission potential to Wuhan in early January, once there are at least four independently introduced cases, there is a more than 50% chance the infection will establish within that population. Interpretation: Our results show that COVID-19 transmission probably declined in Wuhan during late January, 2020, coinciding with the introduction of travel control measures. As more cases arrive in international locations with similar transmission potential to Wuhan before these control measures, it is likely many chains of transmission will fail to establish initially, but might lead to new outbreaks eventually. Funding: Wellcome Trust, Health Data Research UK, Bill & Melinda Gates Foundation, and National Institute for Health Research.

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Contact transmission of Covid-19 in South Korea: Novel investigation techniques for tracing contacts

Abstract:
In the epidemiological investigation of an infectious disease, investigating, classifying, tracking, and managing contacts by identifying the patient’s route are important for preventing further transmission of the disease. However, omissions and errors in previous activities can occur when the investigation is performed through only a proxy interview with the patient. To overcome these limitations, methods that can objectively verify the patient’s claims (medical facility records, Global Positioning System, card transactions, and closed-circuit television) were used for the recent ongoing coronavirus disease 2019 contact investigations in South Korea. © 2020 Korea Centers for Disease Control and Prevention.

Lee, P.-I., Hu, Y.-L., Chen, P.-Y., Huang, Y.-C., Hsueh, P.-R.

Are children less susceptible to COVID-19?
(2020) Journal of Microbiology, Immunology and Infection


2019-nCoV (Wuhan virus), a novel Coronavirus: Human-to-human transmission, travel-related cases, and vaccine readiness

Abstract:
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 prevalent. 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.

Copyright © 2020 Ralph et al.

Wang, A., Zhao, W., Xu, Z., Gu, J.

Timely blood glucose management for the outbreak of 2019 novel coronavirus disease (COVID-19) is urgently needed
(2020) Diabetes Research and Clinical Practice, 162, art. no. 108118


Corona Virus International Public Health Emergencies: Implications for Radiology Management

Abstract:
The outbreak of 2019 novel coronavirus (2019-nCoV) pneumonia was reported in Wuhan, Hubei Province, China in December 2019 and has spread internationally. This article discusses how radiology departments can most effectively respond to this public health emergency. © 2020 The Association of University Radiologists


Covid-19: How doctors and healthcare systems are tackling coronavirus worldwide
(2020) The BMJ, 368, art. no. m1086

Korean Society of Infectious Diseases

Report on the epidemiological features of coronavirus disease 2019 (covid-19) outbreak in the republic of korea from january 19 to march 2, 2020
(2020) Journal of Korean Medical Science, 35 (10), art. no. e112

Abstract:
Since the first case of coronavirus disease (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. © 2020 The Korean Academy of Medical Sciences.

Day, M.

Covid-19: surge in cases in Italy and South Korea makes pandemic look more likely
(2020) BMJ (Clinical research ed.), 368, p. m751.

Zhou, T., Liu, Q., Yang, Z., Liao, J., Yang, K., Bai, W., Lu, X., Zhang, W.

Preliminary prediction of the basic reproduction number of the Wuhan novel coronavirus 2019-nCoV

Abstract:
Objectives: To estimate the basic reproduction number of the Wuhan novel coronavirus (2019-nCoV). Methods: Based on the susceptible-exposed-infected-removed (SEIR) compartment model and the assumption that the infectious cases with symptoms occurred before 26 January, 2020 are resulted from free propagation without intervention, we estimate the basic reproduction number of 2019-nCoV according to the reported confirmed cases and suspected cases, as well as the theoretical estimated number of infected cases by other research teams, together with some epidemiological determinants learned from the severe acute respiratory syndrome (SARS). Results: The basic reproduction number fall between 2.8 and 3.3 by using the real-time reports on the number of 2019-nCoV-infected cases from People's Daily in China and fall between 3.2 and 3.9 on the basis of the predicted number of infected cases from international colleagues. Conclusions: The early transmission ability of 2019-nCoV is close to or slightly higher than SARS. It is a controllable disease with moderate to high transmissibility. Timely and effective control measures are needed to prevent the further transmissions. © 2020 Chinese Cochrane Center, West China Hospital of Sichuan University and John Wiley & Sons Australia, Ltd


CT Imaging and Differential Diagnosis of COVID-19
(2020) Canadian Association of Radiologists Journal

Abstract:
Since the beginning of 2020, coronavirus disease 2019 (COVID-19) has spread throughout China. This study explains the findings from lung computed tomography images of some patients with COVID-19 treated in this medical institution and discusses the difference between COVID-19 and other lung diseases. © The Author(s) 2020.

Sahraei, Z., Shabani, M., Shokouhi, S., Saffaei, A.

Aminoquinolines against coronavirus disease 2019 (COVID-19): chloroquine or hydroxychloroquine
(2020) International Journal of Antimicrobial Agents, art. no. 105945
Surviving Sepsis Campaign: guidelines on the management of critically ill adults with Coronavirus Disease 2019 (COVID-19)
(2020) Intensive Care Medicine

Abstract:
Background: The novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the cause of a rapidly spreading illness, Coronavirus Disease 2019 (COVID-19), affecting thousands of people around the world. Urgent guidance for clinicians caring for the sickest of these patients is needed. Methods: We formed a panel of 36 experts from 12 countries. All panel members completed the World Health Organization conflict of interest disclosure form. The panel proposed 53 questions that are relevant to the management of COVID-19 in the ICU. We searched the literature for direct and indirect evidence on the management of COVID-19 in critically ill patients in the ICU. We identified relevant and recent systematic reviews on most questions relating to supportive care. We assessed the certainty in the evidence using the Grading of Recommendations, Assessment, Development and Evaluation (GRADE) approach, then generated recommendations based on the balance between benefit and harm, resource and cost implications, equity, and feasibility. Recommendations were either strong or weak, or in the form of best practice recommendations. Results: The Surviving Sepsis Campaign COVID-19 panel issued 54 statements, of which 4 are best practice statements, 9 are strong recommendations, and 35 are weak recommendations. No recommendation was provided for 6 questions. The topics were: (1) infection control, (2) laboratory diagnosis and specimens, (3) hemodynamic support, (4) ventilatory support, and (5) COVID-19 therapy. Conclusion: The Surviving Sepsis Campaign COVID-19 panel issued several recommendations to help support healthcare workers caring for critically ill ICU patients with COVID-19. When available, we will provide new recommendations in further releases of these guidelines. © 2020, European Society of Intensive Care Medicine and the Society of Critical Care Medicine.

Association of Cardiac Injury with Mortality in Hospitalized Patients with COVID-19 in Wuhan, China
(2020) JAMA Cardiology

Abstract:
Importance: Coronavirus disease 2019 (COVID-19) has resulted in considerable morbidity and mortality worldwide since December 2019. However, information on cardiac injury in patients affected by COVID-19 is limited. Objective: To explore the association between cardiac injury and mortality in patients with COVID-19. Design, Setting, and Participants: This cohort study was conducted from January 20, 2020, to February 10, 2020, in a single center at Renmin Hospital of Wuhan University, Wuhan, China; the final date of follow-up was February 15, 2020. All consecutive inpatients with laboratory-confirmed COVID-19 were included in this study. Main Outcomes and Measures: Clinical laboratory, radiological, and treatment data were collected and analyzed. Outcomes of patients with and without cardiac injury were compared. The association between cardiac injury and mortality was analyzed. Results: A total of 416 hospitalized patients with COVID-19 were included in the final analysis; the median age was 64 years (range, 21-95
years), and 211 (50.7%) were female. Common symptoms included fever (334 patients [80.3%]), cough (144 [34.6%]), and shortness of breath (117 [28.1%]). A total of 82 patients (19.7%) had cardiac injury, and compared with patients without cardiac injury, these patients were older (median [range] age, 74 [34-95] vs 60 [21-90] years; P <.001); had more comorbidities (eg, hypertension in 49 of 82 [59.8%] vs 78 of 334 [23.4%]; P <.001); had higher leukocyte counts (median [interquartile range (IQR)], 9400 [6900-13800] vs 5500 [4200-7400] cells/μL) and levels of C-reactive protein (median [IQR], 10.2 [6.4-17.0] vs 3.7 [1.0-7.3] mg/dL), procalcitonin (median [IQR], 0.27 [0.10-1.22] vs 0.06 [0.03-0.10] ng/mL), creatinine kinase-myocardial band (median [IQR], 3.2 [1.8-6.2] vs 0.9 [0.6-1.3] ng/mL), myoglobin (median [IQR], 128 [68-305] vs 39 [27-65] μg/L), high-sensitivity troponin I (median [IQR], 0.19 [0.08-1.12] vs <0.006 [<0.006-0.009] μg/L), N-terminal pro-B-type natriuretic peptide (median [IQR], 1689 [698-3327] vs 139 [51-335] pg/mL), aspartate aminotransferase (median [IQR], 40 [27-60] vs 29 [21-40] U/L), and creatinine (median [IQR], 1.15 [0.72-1.92] vs 0.64 [0.54-0.78] mg/dL); and had a higher proportion of multiple mottling and ground-glass opacity in radiographic findings (53 of 82 patients [64.6%] vs 15 of 334 patients [4.5%]). Greater proportions of patients with cardiac injury required noninvasive mechanical ventilation (38 of 82 [46.3%] vs 13 of 334 [3.9%]; P <.001) or invasive mechanical ventilation (18 of 82 [22.0%] vs 14 of 334 [4.2%]; P <.001) than those without cardiac injury. Complications were more common in patients with cardiac injury than those without cardiac injury and included acute respiratory distress syndrome (48 of 82 [58.5%] vs 49 of 334 [14.7%]; P <.001), acute kidney injury (7 of 82 [8.5%] vs 1 of 334 [0.3%]; P <.001), electrolyte disturbances (13 of 82 [15.9%] vs 17 of 334 [5.1%]; P =.003), hypoproteinemia (11 of 82 [13.4%] vs 16 of 334 [4.8%]; P =.01), and coagulation disorders (6 of 82 [7.3%] vs 6 of 334 [1.8%]; P =.02). Patients with cardiac injury had higher mortality than those without cardiac injury (42 of 82 [51.2%] vs 15 of 334 [4.5%]; P <.001).

In a Cox regression model, patients with vs those without cardiac injury were at a higher risk of death, both during the time from symptom onset (hazard ratio, 4.26 [95% CI, 1.92-9.49]) and from admission to end point (hazard ratio, 3.41 [95% CI, 1.62-7.16]). Conclusions and Relevance: Cardiac injury is a common condition among hospitalized patients with COVID-19 in Wuhan, China, and it is associated with higher risk of in-hospital mortality. © 2020 S. Karger AG. All rights reserved.


Abstract:
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. © International & American Associations for Dental Research 2020.
Arabi, Y.M., Murthy, S., Webb, S.  
**COVID-19: a novel coronavirus and a novel challenge for critical care**  
(2020) Intensive Care Medicine

**Passengers' destinations from China: Low risk of Novel Coronavirus (2019-nCoV) transmission into Africa and South America**  
(2020) Epidemiology and Infection, art. no. e41  
**Abstract:**  
Novel Coronavirus (2019-nCoV [SARS-CoV-2]) was detected in humans during the last week of December 2019 at Wuhan city in China, and caused 24,554 cases in 27 countries and territories as of 5 February 2020. The objective of this study was to estimate the risk of transmission of 2019-nCoV through human passenger air flight from four major cities of China (Wuhan, Beijing, Shanghai and Guangzhou) to the passengers' destination countries. We extracted the weekly simulated passengers' end destination data for the period of 1-31 January 2020 from FLIRT, an online air travel dataset that uses information from 800 airlines to show the direct flight and passengers' end destination. We estimated a risk index of 2019-nCoV transmission based on the number of travellers to destination countries, weighted by the number of confirmed cases of the departed city reported by the World Health Organization (WHO). We ranked each country based on the risk index in four quantiles (4th quantile being the highest risk and 1st quantile being the lowest risk). During the period, 388,287 passengers were destined for 1297 airports in 168 countries or territories across the world. The risk index of 2019-nCoV among the countries had a very high correlation with the WHO-reported confirmed cases (0.97). According to our risk score classification, of the countries that reported at least one Coronavirus-infected pneumonia (COVID-19) case as of 5 February 2020, 24 countries were in the 4th quantile of the risk index, two in the 3rd quantile, one in the 2nd quantile and none in the 1st quantile. Outside China, countries with a higher risk of 2019-nCoV transmission are Thailand, Cambodia, Malaysia, Canada and the USA, all of which reported at least one case. In pan-Europe, UK, France, Russia, Germany and Italy; in North America, USA and Canada; in Oceania, Australia had high risk, all of them reported at least one case. In Africa and South America, the risk of transmission is very low with Ethiopia, South Africa, Egypt, Mauritius and Brazil showing a similar risk of transmission compared to the risk of any of the countries where at least one case is detected. The risk of transmission on 31 January 2020 was very high in neighbouring Asian countries, followed by Europe (UK, France, Russia and Germany), Oceania (Australia) and North America (USA and Canada). Increased public health response including early case recognition, isolation of identified case, contract tracing and targeted airport screening, public awareness and vigilance of health workers will help mitigate the force of further spread to naïve countries. © 2020 The Author(s).

Angeletti, S., Benvenuto, D., Bianchi, M., Giovanetti, M., Pascarella, S., Ciccozzi, M.  
**COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis**  
(2020) Journal of Medical Virology  
**Abstract:**  
Last December 2019, a new virus, named novel Coronavirus (COVID-2019) causing many cases of severe pneumonia was reported in Wuhan, China. The virus knowledge is limited and especially about COVID-2019 pathogenesis. The Open Reading Frame 1ab (ORF1ab) of COVID-2019 has been analyzed to evidence the presence of mutation caused by selective pressure on the virus. For selective pressure analysis fast-unconstrained Bayesian approximation (FUBAR) was used.
Homology modelling has been performed by SwissModel and HHpred servers. The presence of transmembrane helical segments in Coronavirus ORF1ab non structural protein 2 (nsp2) and nsp3 was tested by TMHMM, MEMSAT, and MEMPACK tools. Three-dimensional structures have been analyzed and displayed using PyMOL. FUBAR analysis revealed the presence of potential sites under positive selective pressure (P <.05). Position 723 in the COVID-2019 has a serine instead a glycine residue, while at aminoacidic position 1010 a proline instead an isoleucine. Significant (P <.05) pervasive negative selection in 2416 sites (55%) was found. The positive selective pressure could account for some clinical features of this virus compared with severe acute respiratory syndrome (SARS) and Bat SARS-like CoV. The stabilizing mutation falling in the endosome-associated-protein-like domain of the nsp2 protein could account for COVID-2019 high ability of contagious, while the destabilizing mutation in nsp3 proteins could suggest a potential mechanism differentiating COVID-2019 from SARS. These data could be helpful for further investigation aimed to identify potential therapeutic targets or vaccine strategy, especially in the actual moment when the epidemic is ongoing and the scientific community is trying to enrich knowledge about this new viral pathogen. © 2020 Wiley Periodicals, Inc.


2019 novel coronavirus disease (COVID-19) in Taiwan: Reports of two cases from Wuhan, China
(2020) Journal of Microbiology, Immunology and Infection

Abstract:
We reported two cases with community-acquired pneumonia caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) who returned from Wuhan, China in January, 2020. The reported cases highlight non-specific clinical presentations of 2019 novel coronavirus disease (COVID-19) as well as the importance of rapid laboratory-based diagnosis. © 2020

Shanmugaraj, B., Malla, A., Phoolcharoen, W.

Emergence of novel coronavirus 2019-nCoV: Need for rapid vaccine and biologics development
(2020) Pathogens, 9 (2), art. no. 148

Abstract:
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. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.
Abstract:
It has been reported that ACE2 is the main host cell receptor of 2019-nCoV and plays a crucial role in the entry of virus into the cell to cause the final infection. To investigate the potential route of 2019-nCov infection on the mucosa of oral cavity, bulk RNA-seq profiles from two public databases including The Cancer Genome Atlas (TCGA) and Functional Annotation of The Mammalian Genome Cap Analysis of Gene Expression (FANTOM5 CAGE) dataset were collected. RNA-seq profiling data of 13 organ types with para-carcinoma normal tissues from TCGA and 14 organ types with normal tissues from FANTOM5 CAGE were analyzed in order to explore and validate the expression of ACE2 on the mucosa of oral cavity. Further, single-cell transcriptomes from an independent data generated in-house were used to identify and confirm the ACE2-expressing cell composition and proportion in oral cavity. The results demonstrated that the ACE2 expressed on the mucosa of oral cavity. Interestingly, this receptor was highly enriched in epithelial cells of tongue. Preliminarily, those findings have explained the basic mechanism that the oral cavity is a potentially high risk for 2019-nCoV infectious susceptibility and provided a piece of evidence for the future prevention strategy in dental clinical practice as well as daily life. © 2020, The Author(s).

El Zowalaty, M.E., Järhult, J.D.
From SARS to COVID-19: A previously unknown SARS-related coronavirus (SARS-CoV-2) of pandemic potential infecting humans – Call for a One Health approach (2020) One Health, 9, art. no. 100124
Abstract:
Human coronaviruses continue to pose a threat to human health. The emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in December 2019 which causes coronavirus disease-2019 (COVID-19), an acute respiratory disease marked the third introduction of a highly pathogenic coronavirus into the human population in the twenty-first century. This recent emergence of a previously unknown coronavirus in China leads to huge impacts on humans globally. Covid-19 is a challenge to global public health. Here, we discuss the COVID-19 outbreak in a one health context, highlighting the need for the implementation of one health measures and practices to improve human health and reduce the emergence of pandemic viruses. © 2020 The Authors

Abstract:
Background and aims: No drugs are currently approved for Coronavirus Disease-2019 (COVID-19), although some have been tried. In view of recent studies and discussion on chloroquine and hydroxychloroquine (HCQ), we aimed to review existing literature and relevant websites regarding
these drugs and COVID-19, adverse effects related to drugs, and related guidelines. Aims and methods: We systematically searched the PubMed database up till March 21, 2020 and retrieved all the articles published on chloroquine and HCQ and COVID-19. Results: Two small human studies have been conducted with both these drugs in COVID-19, and have shown significant improvement in some parameters in patients with COVID-19. Conclusion: Considering minimal risk upon use, a long experience of use in other diseases, cost-effectiveness and easy availability across India, we propose that both these drugs are worthy of fast track clinical trial for treatment, and may be carefully considered for clinical use as experimental drugs. Since HCQ has been approved for treatment of diabetes in India, it should be further researched in diabetes and COVID-19, a subgroup where significant mortality has been shown. © 2020 Diabetes India

Li, X., Wang, W., Zhao, X., Zai, J., Zhao, Q., Li, Y., Chaillon, A.

Transmission dynamics and evolutionary history of 2019-nCoV

Abstract:
To investigate the time origin, genetic diversity, and transmission dynamics of the recent 2019-nCoV outbreak in China and beyond, a total of 32 genomes of virus strains sampled from China, Thailand, and the USA with sampling dates between 24 December 2019 and 23 January 2020 were analyzed. Phylogenetic, transmission network, and likelihood-mapping analyses of the genome sequences were performed. On the basis of the likelihood-mapping analysis, the increasing tree-like signals (from 0% to 8.2%, 18.2%, and 25.4%) over time may be indicative of increasing genetic diversity of 2019-nCoV in human hosts. We identified three phylogenetic clusters using the Bayesian inference framework and three transmission clusters using transmission network analysis, with only one cluster identified by both methods using the above genome sequences of 2019-nCoV strains. The estimated mean evolutionary rate for 2019-nCoV ranged from 1.7926 × 10−3 to 1.8266 × 10−3 substitutions per site per year. On the basis of our study, undertaking epidemiological investigations and genomic data surveillance could positively impact public health in terms of guiding prevention efforts to reduce 2019-nCoV transmission in real-time. © 2020 Wiley Periodicals, Inc.

Kooraki, S., Hosseiny, M., Myers, L., Gholamrezanezhad, A.

Coronavirus (COVID-19) Outbreak: What the Department of Radiology Should Know

Abstract:
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. © 2020 American College of Radiology

Liang, H., Acharya, G.
Novel corona virus disease (COVID-19) in pregnancy: What clinical recommendations to follow?

Kandel, N., Chungong, S., Omaar, A., Xing, J.
Health security capacities in the context of COVID-19 outbreak: an analysis of International Health Regulations annual report data from 182 countries

Abstract:
Background: Public health measures to prevent, detect, and respond to events are essential to control public health risks, including infectious disease outbreaks, as highlighted in the International Health Regulations (IHR). In light of the outbreak of 2019 novel coronavirus disease (COVID-19), we aimed to review existing health security capacities against public health risks and events. Methods: We used 18 indicators from the IHR State Party Annual Reporting (SPAR) tool and associated data from national SPAR reports to develop five indices: (1) prevent, (2) detect, (3) respond, (4) enabling function, and (5) operational readiness. We used SPAR 2018 data for all of the indicators and categorised countries into five levels across the indices, in which level 1 indicated the lowest level of national capacity and level 5 the highest. We also analysed data at the regional level (using the six geographical WHO regions). Findings: Of 182 countries, 52 (28%) had prevent capacities at levels 1 or 2, and 60 (33%) had response capacities at levels 1 or 2. 81 (45%) countries had prevent capacities and 78 (43%) had response capacities at levels 4 or 5, indicating that these countries were operationally ready. 138 (76%) countries scored more highly in the detect index than in the other indices. 44 (24%) countries did not have an effective enabling function for public health risks and events, including infectious disease outbreaks (7 [4%] at level 1 and 37 [20%] at level 2). 102 (56%) countries had level 4 or level 5 enabling function capacities in place. 32 (18%) countries had low readiness (2 [1%] at level 1 and 30 [17%] at level 2), and 104 (57%) countries were operationally ready to prevent, detect, and control an outbreak of a novel infectious disease (66 [36%] at level 4 and 38 [21%] at level 5). Interpretation: Countries vary widely in terms of their capacity to prevent, detect, and respond to outbreaks. Half of all countries analysed have strong operational readiness capacities in place, which suggests that an effective response to potential health emergencies could be enabled, including to COVID-19. Findings from local risk assessments are needed to fully understand national readiness capacities in relation to COVID-19. Capacity building and collaboration between countries are needed to strengthen global readiness for outbreak control.

Funding: None. © 2020 World Health Organization. Published by Elsevier Ltd. All rights reserved.

Newman, M.
Covid-19: doctors' leaders warn that staff could quit and may die over lack of protective equipment
(2020) BMJ (Clinical research ed.), 368, p. m1257.

Greenhalgh, T., Koh, G.C.H., Car, J.
Covid-19: A remote assessment in primary care
(2020) The BMJ, 368, art. no. m1182

Day, M.
Covid-19: ibuprofen should not be used for managing symptoms, say doctors and scientists
Lessons learned from the 2019-nCoV epidemic on prevention of future infectious diseases

Abstract:
Only a month after the outbreak of pneumonia caused by 2019-nCoV, more than forty-thousand people were infected. This put enormous pressure on the Chinese government, medical healthcare provider, and the general public, but also made the international community deeply nervous. On the 25th day after the outbreak, the Chinese government implemented strict traffic restrictions on the area where the 2019-nCoV had originated—Hubei province, whose capital city is Wuhan. Ten days later, the rate of increase of cases in Hubei showed a significant difference (p = 0.0001) compared with the total rate of increase in other provinces of China. These preliminary data suggest the effectiveness of a traffic restriction policy for this pandemic thus far. At the same time, solid financial support and improved research ability, along with network communication technology, also greatly facilitated the application of epidemic prevention measures. These measures were motivated by the need to provide effective treatment of patients, and involved consultation with three major groups in policy formulation—public health experts, the government, and the general public. It was also aided by media and information technology, as well as international cooperation. This experience will provide China and other countries with valuable lessons for quickly coordinating and coping with future public health emergencies. © 2020 Institut Pasteur

Is COVID-19 receiving ADE from other coronaviruses?

Abstract:
One of the most perplexing questions regarding the current COVID-19 coronavirus epidemic is the discrepancy between the severity of cases observed in the Hubei province of China and those occurring elsewhere in the world. One possible answer is antibody dependent enhancement (ADE) of SARS-CoV-2 due to prior exposure to other coronaviruses. ADE modulates the immune response and can elicit sustained inflammation, lymphopenia, and/or cytokine storm, one or all of which have been documented in severe cases and deaths. ADE also requires prior exposure to similar antigenic epitopes, presumably circulating in local viruses, making it a possible explanation for the observed geographic limitation of severe cases and deaths. © 2020 Institut Pasteur

Covid-19: Italy confirms 11 deaths as cases spread from north
(2020) BMJ (Clinical research ed.), 368, p. m757.

Wuhan: Britons to be evacuated as scientists estimate 44 000 cases of 2019-nCOV in the city
(2020) BMJ (Clinical research ed.), 368, p. m351.

Qiu, H., Wu, J., Hong, L., Luo, Y., Song, Q., Chen, D.

Abstract:
Background: Since December, 2019, an outbreak of coronavirus disease 2019 (COVID-19) has spread globally. Little is known about the epidemiological and clinical features of paediatric patients with COVID-19. Methods: We retrospectively retrieved data for paediatric patients (aged 0–16 years) with confirmed COVID-19 from electronic medical records in three hospitals in Zhejiang, China. We recorded patients' epidemiological and clinical features. Findings: From Jan 17 to March 1, 2020, 36 children (mean age 8·3 [SD 3·5] years) were identified to be infected with severe acute respiratory syndrome coronavirus 2. The route of transmission was by close contact with family members (32 [89%]) or a history of exposure to the epidemic area (12 [33%]); eight (22%) patients had both exposures. 19 (53%) patients had moderate clinical type with pneumonia; 17 (47%) had mild clinical type and either were asymptomatic (ten [28%]) or had acute upper respiratory symptoms (seven [19%]). Common symptoms on admission were fever (13 [36%]) and dry cough (seven [19%]). Of those with fever, four (11%) had a body temperature of 38·5°C or higher, and nine (25%) had a body temperature of 37·5–38·5°C. Typical abnormal laboratory findings were elevated creatine kinase MB (11 [31%]), decreased lymphocytes (11 [31%]), leucopenia (seven [19%]), and elevated procalcitonin (six [17%]). Besides radiographic presentations, variables that were associated significantly with severity of COVID-19 were decreased lymphocytes, elevated body temperature, and high levels of procalcitonin, D-dimer, and creatine kinase MB. All children received interferon alfa by aerosolisation twice a day, 14 (39%) received lopinavir–ritonavir syrup twice a day, and six (17%) needed oxygen inhalation. Mean time in hospital was 14 (SD 3) days. By Feb 28, 2020, all patients were cured. Interpretation: Although all paediatric patients in our cohort had mild or moderate type of COVID-19, the large proportion of asymptomatic children indicates the difficulty in identifying paediatric patients who do not have clear epidemiological information, leading to a dangerous situation in community-acquired infections. Funding: Ningbo Clinical Research Center for Children's Health and Diseases, Ningbo Reproductive Medicine Centre, and Key Scientific and Technological Innovation Projects of Wenzhou.


Coronavirus (COVID-19) outbreak: what the department of endoscopy should know (2020) Gastrointestinal Endoscopy

Abstract:
Italy recorded its first case of confirmed acute respiratory illness because of coronavirus on February 18, 2020, soon after the initial reports in China. Since that time, Italy and nations throughout the world have adopted very stringent and severe measures to protect populations from spread of infection. Despite these measures, the number of infected people is growing exponentially, with a significant number of patients developing acute respiratory insufficiency. Endoscopy departments face significant risk for diffusion of respiratory diseases that can be spread via an airborne route, including aspiration of oral and fecal material via endoscopes. The purpose of this article is to discuss the measures, with specific focus on personal protection equipment and dress code modalities, implemented in our hospital to prevent further dissemination of COVID-19 infection. © 2020 American Society for Gastrointestinal Endoscopy

**Escalating infection control response to the rapidly evolving epidemiology of the Coronavirus disease 2019 (COVID-19) due to SARS-CoV-2 in Hong Kong**
(2020) Infection Control and Hospital Epidemiology

**Abstract:**
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 3.3x10^6 copies/ml (pooled nasopharyngeal/throat swab) and 5.9x10^6 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. © 2020 by The Society for Healthcare Epidemiology of America. All rights reserved.


**Revisiting the one health approach in the context of COVID-19: A look into the ecology of this emerging disease**

Ebrahim, S.H., Memish, Z.A.

**COVID-19 – the role of mass gatherings**
(2020) Travel Medicine and Infectious Disease, art. no. 101617

**Abstract:**
Mass gathering (MG) medicine emerged against the backdrop of the 2009 pandemic H1N1 Public Health Emergency of International Concern (PHEIC) when the Kingdom of Saudi Arabia (KSA) hosted the largest annual mass gathering of over 3 million pilgrims from 180 plus countries. However, the events surrounding the latest threat to global health, the PHEIC COVID-19, may be sufficient to highlight the role of mass gatherings, mass migration, and other forms of dense gatherings of people on the emergence, sustenance, and transmission of novel pathogens. The COVID-19 spread illustrates the role of MGs in exacerbation of the scope of pandemics. Cancellation or suspension of MGs would be critical to pandemic mitigation. It is unlikely that medical countermeasures are available during the early phase of pandemics. Therefore, mitigation of its impact, rather than containment and control becomes a priority during pandemics. As the most systematically studied MG-related respiratory disease data come from KSA, the cancellation of
Umrah by the KSA authorities, prior to emergence of cases, provide the best opportunity to develop mathematical models to quantify event cancellations related mitigation of COVID-19 transmission in KSA and to the home countries of pilgrims. COVID-19 has already provided examples of both clearly planned event cancellations such as the Umrah suspension in KSA, and where outbreaks and events were continued.

Calvo, C., García López-Hortelano, M., de Carlos Vicente, J.C., (...), Jordán García, I., Pilar Orive, J.

**Recommendations on the clinical management of the COVID-19 infection by the «new coronavirus» SARS-CoV2. Spanish Paediatric Association working group**

[Recomendaciones sobre el manejo clínico de la infección por el «nuevo coronavirus» SARS-CoV2. Grupo de trabajo de la Asociación Española de Pediatría (AEP)]

(2020) Anales de Pediatría

**Abstract:**

On 31 December 2019, the Wuhan Municipal Committee of Health and Healthcare (Hubei Province, China) reported that there were 27 cases of pneumonia of unknown origin with symptoms starting on the 8 December. There were 7 serious cases with common exposure in market with shellfish, fish, and live animals, in the city of Wuhan. On 7 January 2020, the Chinese authorities identified that the agent causing the outbreak was a new type of virus of the Coronaviridae family, temporarily called «new coronavirus», 2019-nCoV. On January 30th, 2020, the World Health Organisation (WHO) declared the outbreak an International Emergency. On 11 February 2020 the WHO assigned it the name of SARS-CoV2 and COVID-19 (SARS-CoV2 and COVID-19). The Ministry of Health summoned the Specialties Societies to prepare a clinical protocol for the management of COVID-19. The Spanish Paediatric Association appointed a Working Group of the Societies of Paediatric Infectious Diseases and Paediatric Intensive Care to prepare the present recommendations with the evidence available at the time of preparing them. © 2020 Asociación Española de Pediatría

Han, Y., Yang, H.


(2020) Journal of Medical Virology

**Abstract:**

2019 novel coronavirus (SARS-CoV-2), which originated in Wuhan, China, has attracted the world's attention over the last month. The Chinese government has taken emergency measures to control the outbreak and has undertaken initial steps in the diagnosis and treatment of 2019 novel coronavirus infection disease (COVID-19). However, SARS-CoV-2 possesses powerful pathogenicity as well as transmissibility and still holds many mysteries that are yet to be solved, such as whether the virus can be transmitted by asymptomatic patients or by mothers to their infants. Our research presents selected available cases of COVID-19 in China to better understand the transmission and diagnosis regarding this infectious disease. © 2020 Wiley Periodicals, Inc.

Ahmed, S.F., Quadeer, A.A., McKay, M.R.

**Preliminary identification of potential vaccine targets for the COVID-19 Coronavirus (SARS-CoV-2) Based on SARS-CoV Immunological Studies**

(2020) Viruses, 12 (3), art. no. 254
Abstract:
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. © 2020 by the authors.

Mizumoto, K., Chowell, G.
**Transmission potential of the novel coronavirus (COVID-19) onboard the diamond Princess Cruises Ship, 2020**
(2020) Infectious Disease Modelling, 5, pp. 264-270.

Abstract:
An outbreak of COVID-19 developed aboard the Princess Cruises Ship during January–February 2020. Using mathematical modeling and time-series incidence data describing the trajectory of the outbreak among passengers and crew members, we characterize how the transmission potential varied over the course of the outbreak. Our estimate of the mean reproduction number in the confined setting reached values as high as ~11, which is higher than mean estimates reported from community-level transmission dynamics in China and Singapore (approximate range: 1.1–7). Our findings suggest that Rt decreased substantially compared to values during the early phase after the Japanese government implemented an enhanced quarantine control. Most recent estimates of Rt reached values largely below the epidemic threshold, indicating that a secondary outbreak of the novel coronavirus was unlikely to occur aboard the Diamond Princess Ship. © 2020 The Authors

Ibrahim, I.M., Abdelmalek, D.H., Elshahat, M.E., Elfiky, A.A.
**COVID-19 spike-host cell receptor GRP78 binding site prediction**
(2020) Journal of Infection

Abstract:
Objectives: Understanding the novel coronavirus (COVID-19) mode of host cell recognition may help to fight the disease and save lives. The spike protein of coronaviruses is the main driving force for host cell recognition. Methods: In this study, the COVID-19 spike binding site to the cell-surface receptor (Glucose Regulated Protein 78 (GRP78)) is predicted using combined molecular modeling docking and structural bioinformatics. The COVID-19 spike protein is modeled using its counterpart, the SARS spike. Results: Sequence and structural alignments show that four regions, in addition to its cyclic nature have sequence and physicochemical similarities to the cyclic Pep42. Protein-protein docking was performed to test the four regions of the spike that fit tightly in the GRP78 Substrate Binding Domain β (SBDβ). The docking pose revealed the involvement of the SBDβ of GRP78 and the receptor-binding domain of the coronavirus spike protein in recognition of
the host cell receptor. Conclusions: We reveal that the binding is more favorable between regions III (C391-C525) and IV (C480-C488) of the spike protein model and GRP78. Region IV is the main driving force for GRP78 binding with the predicted binding affinity of -9.8 kcal/mol. These nine residues can be used to develop therapeutics specific against COVID-19. © 2020

Eurosurveillance Editorial Team

Note from the editors: novel coronavirus (2019-nCoV)
(2020) Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 25 (3)

Alijagic, A., Benada, O., Kofroňová, O., Cigna, D., Pinsino, A.
Sea Urchin Extracellular Proteins Design a Complex Protein Corona on Titanium Dioxide Nanoparticle Surface Influencing Immune Cell Behavior
(2019) Frontiers in Immunology, 10, art. no. 2261
Abstract:
Extensive exploitation of titanium dioxide nanoparticles (TiO2NPs) augments rapid release into the marine environment. When in contact with the body fluids of marine invertebrates, TiO2NPs undergo a transformation and adhere various organic molecules that shape a complex protein corona prior to contacting cells and tissues. To elucidate the potential extracellular signals that may be involved in the particle recognition by immune cells of the sea urchin Paracentrotus lividus, we investigated the behavior of TiO2NPs in contact with extracellular proteins in vitro. Our findings indicate that TiO2NPs are able to interact with sea urchin proteins in both cell-free and cell-conditioned media. The two-dimensional proteome analysis of the protein corona bound to TiO2NP revealed that negatively charged proteins bound preferentially to the particles. The main constituents shaping the sea urchin cell-conditioned TiO2NP protein corona were proteins involved in cellular adhesion (Pl-toposome, Pl-galectin-8, Pl-nectin) and cytoskeletal organization (actin and tubulin). Immune cells (phagocytes) aggregated TiO2NPs on the outer cell surface and within well-organized vesicles without eliciting harmful effects on the biological activities of the cells. Cells showed an active metabolism, no oxidative stress or caspase activation. These results provide a new level of understanding of the extracellular proteins involved in the immune-TiO2NP recognition and interaction in vitro, confirming that primary immune cell cultures from P. lividus can be an optional model for swift and efficient immune-toxicological investigations. © Copyright © 2019 Alijagic, Benada, Kofroňová, Cigna and Pinsino.

Asthana, C., Peterson, G.M., Shastri, M., Patel, R.P.
Development and validation of a novel high performance liquid chromatography-coupled with Corona charged aerosol detector method for quantification of glucosamine in dietary supplements
Abstract:
INTRODUCTION: Glucosamine dietary supplements are commonly used for the management of osteoarthritis (OA). However, clinical trials have reported varying outcomes with regard to joint function and disease progression. One of the possible reasons for variability in observed effects of glucosamine could be that, unlike prescription drugs, the quality of manufactured dietary supplements is not closely monitored in many countries. Therefore, there is the possibility that the actual amount of glucosamine present in a dietary supplement is different from that claimed on the label. The quality control of glucosamine supplements is further complicated by the unavailability of a simple and effective analytical method for the analysis of glucosamine. Therefore, the aim of
this study was to develop a simple analytical method that could be easily adapted by the pharmaceutical industry for routine analysis of glucosamine. AIMS: To develop a novel high-performance liquid chromatography (HPLC) method for the quantification of glucosamine, and determine the amount of glucosamine present in a sample of dietary supplements commercially available in Australia and India. METHODS: Chromatographic separation of glucosamine was achieved using a zwitter-ionic hydrophilic interaction liquid chromatography column with a mobile phase consisting of 60% acetonitrile and 40% of 85 mM ammonium acetate, at a flow rate of 0.3 mL/min and column temperature 40°C. The developed method was validated for intra- and inter-day linearity, accuracy, precision, and reproducibility. The newly-developed method was subsequently used to analyse 12 glucosamine supplements. RESULTS: The developed method was selective for glucosamine, which had a retention time of 5.9 min. The standard curve was linear with a correlation coefficient (r2) exceeding 0.99, over the range of 10-200 μg/mL for glucosamine. The relative standard deviations for intra- and inter-day accuracy, precision and reproducibility were all less than 4%. The amount of glucosamine determined in six Australian and six Indian glucosamine supplements ranged between 98.7-101.7% and 85.9-101.8% of the labelled values, respectively. DISCUSSION: Unlike previous HPLC methods, this newly-developed HPLC technique does not require pre-derivatisation and can separate glucosamine from both hydrochloride and sulphate salts, and from other amino sugars, such as chondroitin sulphate present in dietary supplements. This simple and effective technique can be employed by analytical laboratories for the quality control of glucosamine dietary supplements. CONCLUSION: The current study has developed a new analytical technique using HPLC-Corona CAD, which can analyse underivatised glucosamine hydrochloride and sulphate within 6 minutes. Using the novel assay, we confirmed that unlike the tested Australian dietary supplements, only half of the tested Indian products had a glucosamine content within ±10% of what was claimed on the label.

Lippi, G., Plebani, M., Henry, B.M.
Thrombocytopenia is associated with severe coronavirus disease 2019 (COVID-19) infections: A meta-analysis

Abstract:
Background: Coronavirus disease 2019 (COVID-19) is a novel infectious disease with lack of established laboratory markers available to evaluate illness severity. In this study, we investigate whether platelet count could differentiate between COVID-19 patients with or without severe disease. Additionally, we evaluate if thrombocytopenia is associated with severe COVID-19. Methods: An electronic search in Medline, Scopus and Web of Science was performed to identify studies reporting data on platelet count in COVID-19 patients. A meta-analysis was performed, with calculation of weighted mean difference (WMD) of platelet number in COVID-19 patients with or without severe disease and odds ratio (OR) of thrombocytopenia for severe form of COVID-19. Results: Nine studies with 1779 COVID-19 patients, 399 (22.4%) with severe disease, were included in the meta-analysis. The pooled analysis revealed that platelet count was significantly lower in patients with more severe COVID-19 (WMD −31 × 10^9/L; 95% CI, from −35 to −29 × 10^9/L). A subgroup analysis comparing patients by survival, found an even lower platelet count was observed with mortality (WMD, −48 × 10^9/L; 95% CI, −57 to −39 × 10^9/L. In the four studies (n = 1427) which reported data on rate of thrombocytopenia, a low platelet count was associated with over fivefold enhanced risk of severe COVID-19 (OR, 5.1; 95% CI, 1.8–14.6). Conclusions: Low platelet count is associated with increased risk of severe disease and mortality in patients with
COVID-19, and thus should serve as clinical indicator of worsening illness during hospitalization. © 2020 Elsevier B.V.

Cao, W., Fang, Z., Hou, G., Han, M., Xu, X., Dong, J., Zheng, J.

The psychological impact of the COVID-19 epidemic on college students in China
(2020) Psychiatry Research, 287, art. no. 112934

Abstract:
A COVID-19 epidemic has been spreading in China and other parts of the world since December 2019. The epidemic has brought not only the risk of death from infection but also unbearable psychological pressure. We sampled college students from Changzhi medical college by using cluster sampling. They responded to a questionnaire packet that included the 7-item Generalized Anxiety Disorder Scale (GAD-7) and those inquiring the participants’ basic information. We received 7,143 responses. Results indicated that 0.9% of the respondents were experiencing severe anxiety, 2.7% moderate anxiety, and 21.3% mild anxiety. Moreover, living in urban areas (OR = 0.810, 95% CI = 0.709 - 0.925), family income stability (OR = 0.726, 95% CI = 0.645 - 0.817) and living with parents (OR = 0.752, 95% CI = 0.596 - 0.950) were protective factors against anxiety. Moreover, having relatives or acquaintances infected with COVID-19 was a risk factor for increasing the anxiety of college students (OR = 3.007, 95% CI = 2.377 - 3.804). Results of correlation analysis indicated that economic effects, and effects on daily life, as well as delays in academic activities, were positively associated with anxiety symptoms (P <.001). However, social support was negatively correlated with the level of anxiety (P <.001). It is suggested that the mental health of college students should be monitored during epidemics. © 2020 Elsevier B.V.

Liu, K., Chen, Y., Wu, D., Lin, R., Wang, Z., Pan, L.

Effects of progressive muscle relaxation on anxiety and sleep quality in patients with COVID-19
(2020) Complementary Therapies in Clinical Practice, 39, art. no. 101132

Abstract:
Background: Patients with Coronavirus Disease 2019(COVID-19) will experience high levels of anxiety and low sleep quality due to isolation treatment. Some sleep-improving drugs may inhibit the respiratory system and worsen the condition. Prolonged bedside instruction may increase the risk of medical infections. Objective: To investigate the effect of progressive muscle relaxation on anxiety and sleep quality of COVID-19. Methods: In this randomized controlled clinical trial, a total of 51 patients who entered the isolation ward were included in the study and randomly divided into experimental and control groups. The experimental group used progressive muscle relaxation (PMR) technology for 30 min per day for 5 consecutive days. During this period, the control group received only routine care and treatment. Before and after the intervention, the Spielberger State-Trait Anxiety Scale (STAI) and Sleep State Self-Rating Scale (SRSS) were used to measure and record patient anxiety and sleep quality. Finally, data analysis was performed using SPSS 25.0 software. Results: The average anxiety score (STAI) before intervention was not statistically significant (P = 0.730), and the average anxiety score after intervention was statistically significant (P < 0.001). The average sleep quality score (SRSS) of the two groups before intervention was not statistically significant (P = 0.838), and it was statistically significant after intervention (P < 0.001). Conclusion: Progressive muscle relaxation as an auxiliary method can reduce anxiety and improve sleep quality in patients with COVID-19. © 2020 The Authors

Nishiura, H., Linton, N.M., Akhmetzhanov, A.R.
Serial interval of novel coronavirus (COVID-19) infections

Abstract:
Objective: To estimate the serial interval of novel coronavirus (COVID-19) from information on 28 infector-infectee pairs. Methods: We collected dates of illness onset for primary cases (infectors) and secondary cases (infectees) from published research articles and case investigation reports. We subjectively ranked the credibility of the data and performed analyses on both the full dataset (n = 28) and a subset of pairs with highest certainty in reporting (n = 18). In addition, we adjust for right truncation of the data as the epidemic is still in its growth phase. Results: Accounting for right truncation and analyzing all pairs, we estimated the median serial interval at 4.0 days (95% credible interval [CrI]: 3.1, 4.9). Limiting our data to only the most certain pairs, the median serial interval was estimated at 4.6 days (95% CrI: 3.5, 5.9). Conclusions: The serial interval of COVID-19 is close to or shorter than its median incubation period. This suggests that a substantial proportion of secondary transmission may occur prior to illness onset. The COVID-19 serial interval is also shorter than the serial interval of severe acute respiratory syndrome (SARS), indicating that calculations made using the SARS serial interval may introduce bias. © 2020 The Author(s)

Holland, M., Zaloga, D.J., Friderici, C.S.

COVID-19 Personal Protective Equipment (PPE) for the emergency physician
(2020) Visual Journal of Emergency Medicine, 19, art. no. 100740


Drive-through screening center for covid-19: A safe and efficient screening system against massive community outbreak
(2020) Journal of Korean Medical Science, 35 (11), art. no. e123

Abstract:
As the coronavirus disease 2019 (COVID-19) outbreak is ongoing, the number of individuals to be tested for COVID-19 is rapidly increasing. For safe and efficient screening for COVID-19, drive-through (DT) screening centers have been designed and implemented in Korea. Herein, we present the overall concept, advantages, and limitations of the COVID-19 DT screening centers. The steps of the DT centers include registration, examination, specimen collection, and instructions. The entire service takes about 10 minutes for one testee without leaving his or her cars. Increased testing capacity over 100 tests per day and prevention of cross-infection between testees in the waiting space are the major advantages, while protection of staff from the outdoor atmosphere is challenging. It could be implemented in other countries to cope with the global COVID-19 outbreak and transformed according to their own situations. © 2020 The Korean Academy of Medical Sciences.

Garrett, L.

COVID-19: the medium is the message

Ng, Y., Li, Z., Chua, Y.X., Chaw, W.L., Zhao, Z., Er, B., Pung, R., Chiew, C.J., Lye, D.C., Heng, D., Lee, V.J.

Evaluation of the effectiveness of surveillance and containment measures for the first 100 patients with COVID-19 in Singapore - January 2-February 29, 2020
Abstract:
What is already known about this topic? First detected in China in late 2019, coronavirus disease 2019 (COVID-19) transmission has spread globally. What is added by this report? Singapore implemented a multipronged surveillance and containment strategy that contributed to enhanced case ascertainment and slowing of the outbreak. Based on review of the first 100 cases, the mean interval from symptom onset to isolation was 5.6 days and declined after approximately 1 month. What are the implications for public health practice? A multipronged surveillance strategy could lead to enhanced case detection and reduced transmission of highly infectious diseases such as COVID-19. © 2020 Department of Health and Human Services. All rights reserved.

Rimmer, A.  
**Covid-19: GPs can stop health checks for over 75s and routine medicine reviews**  
(2020) BMJ (Clinical research ed.), 368, p. m1157.

Iacobucci, G.  
**Covid-19: all non-urgent elective surgery is suspended for at least three months in England**  
(2020) BMJ (Clinical research ed.), 368, p. m1106.

Mahase, E.  
**Covid-19: outbreak could last until spring 2021 and see 7.9 million hospitalised in the UK**  
(2020) BMJ (Clinical research ed.), 368, p. m1071.

**Active Monitoring of Persons Exposed to Patients with Confirmed COVID-19 - United States, January-February 2020**  

Abstract:
In December 2019, an outbreak of coronavirus disease 2019 (COVID-19), caused by the virus SARS-CoV-2, began in Wuhan, China (1). The disease spread widely in China, and, as of February 26, 2020, COVID-19 cases had been identified in 36 other countries and territories, including the United States. Person-to-person transmission has been widely documented, and a limited number of countries have reported sustained person-to-person spread.* On January 20, state and local health departments in the United States, in collaboration with teams deployed from CDC, began identifying and monitoring all persons considered to have had close contact† with patients with confirmed COVID-19 (2). The aims of these efforts were to ensure rapid evaluation and care of patients, limit further transmission, and better understand risk factors for transmission.

Mahase, E.  
**Covid-19: UK could delay non-urgent care and call doctors back from leave and retirement**  
(2020) BMJ (Clinical research ed.), 368, p. m854.
Eurosurveillance Editorial Team

Abstract: The outbreak of an epidemic disease may pose significant treats to human beings and may further lead to a global crisis. In order to control the spread of an epidemic, the effective management of rapidly increased medical waste through establishing a temporary reverse logistics system is of vital importance. However, no research has been conducted with the focus on the design of an epidemic reverse logistics network for dealing with medical waste during epidemic outbreaks, which, if improperly treated, may accelerate disease spread and pose a significant risk for both medical staffs and patients. Therefore, this paper proposes a novel multi-objective multi-period mixed integer program for reverse logistics network design in epidemic outbreaks, which aims at determining the best locations of temporary facilities and the transportation strategies for effective management of the exponentially increased medical waste within a very short period. The application of the model is illustrated with a case study based on the outbreak of the coronavirus disease 2019 (COVID-19) in Wuhan, China. Even though the uncertainty of the future COVID-19 spread tendency is very high at the time of this research, several general policy recommendations can still be obtained based on computational experiments and quantitative analyses. Among other insights, the results suggest installing temporary incinerators may be an effective solution for managing the tremendous increase of medical waste during the COVID-19 outbreak in Wuhan, but the location selection of these temporary incinerators is of significant importance. Due to the limitation on available data and knowledge at present stage, more real-world information are needed to assess the effectiveness of the current solution. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Abstract: At the end of December 2019, a novel coronavirus, 2019-nCoV, caused an outbreak of pneumonia spreading from Wuhan, Hubei province, to the whole country of China, which has posed great threats to public health and attracted enormous attention around the world. To date, there are no clinically approved vaccines or antiviral drugs available for these human coronavirus infections. Intensive research on the novel emerging human infectious coronaviruses is urgently needed to elucidate their route of transmission and pathogenic mechanisms, and to identify potential drug targets, which would promote the development of effective preventive and therapeutic countermeasures. Herein, we describe the epidemic and etiological characteristics of 2019-nCoV, discuss its essential biological features, including tropism and receptor usage, summarize...
Wang, C., Pan, R., Wan, X., Tan, Y., Xu, L., Ho, C.S., Ho, R.C.

Immediate psychological responses and associated factors during the initial stage of the 2019 coronavirus disease (COVID-19) epidemic among the general population in China


Abstract:
Background: The 2019 coronavirus disease (COVID-19) epidemic is a public health emergency of international concern and poses a challenge to psychological resilience. Research data are needed to develop evidence-driven strategies to reduce adverse psychological impacts and psychiatric symptoms during the epidemic. The aim of this study was to survey the general public in China to better understand their levels of psychological impact, anxiety, depression, and stress during the initial stage of the COVID-19 outbreak. The data will be used for future reference. Methods: From 31 January to 2 February 2020, we conducted an online survey using snowball sampling techniques. The online survey collected information on demographic data, physical symptoms in the past 14 days, contact history with COVID-19, knowledge and concerns about COVID-19, precautionary measures against COVID-19, and additional information required with respect to COVID-19. Psychological impact was assessed by the Impact of Event Scale-Revised (IES-R), and mental health status was assessed by the Depression, Anxiety and Stress Scale (DASS-21). Results: This study included 1210 respondents from 194 cities in China. In total, 53.8% of respondents rated the psychological impact of the outbreak as moderate or severe; 16.5% reported moderate to severe depressive symptoms; 28.8% reported moderate to severe anxiety symptoms; and 8.1% reported moderate to severe stress levels. Most respondents spent 20–24 h per day at home (84.7%); were worried about their family members contracting COVID-19 (75.2%); and were satisfied with the amount of health information available (75.1%). Female gender, student status, specific physical symptoms (e.g., myalgia, dizziness, coryza), and poor self-rated health status were significantly associated with a greater psychological impact of the outbreak and higher levels of stress, anxiety, and depression (p < 0.05). Specific up-to-date and accurate health information (e.g., treatment, local outbreak situation) and particular precautionary measures (e.g., hand hygiene, wearing a mask) were associated with a lower psychological impact of the outbreak and lower levels of stress, anxiety, and depression (p < 0.05). Conclusions: During the initial phase of the COVID-19 outbreak in China, more than half of the respondents rated the psychological impact as moderate-to-severe, and about one-third reported moderate-to-severe anxiety. Our findings identify factors associated with a lower level of psychological impact and better mental health status that can be used to formulate psychological interventions to improve the mental health of vulnerable groups during the COVID-19 epidemic. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Ren, S.-Y., Gao, R.-D., Chen, Y.-L.

Fear can be more harmful than the severe acute respiratory syndrome coronavirus 2 in controlling the coronavirus disease 2019 epidemic


Abstract:
The current coronavirus disease 2019 outbreak caused by severe acute respiratory syndrome coronavirus 2 started in Wuhan, China in December 2019 and has put the world on alert. To safeguard Chinese citizens and to strengthen global health security, China has made great efforts to control the epidemic. Many in the global community have joined China to limit the epidemic.
However, discrimination and prejudice driven by fear or misinformation have been flowing globally, superseding evidence and jeopardizing the anti-severe acute respiratory syndrome coronavirus 2 efforts. We analyze this phenomenon and its underlying causes and suggest practical solutions. © Baishideng Publishing Group Co.

Kmietowicz, Z.
Rules on isolation rooms for suspected covid-19 cases in GP surgeries to be relaxed
(2020) BMJ (Clinical research ed.), 368, p. m707.

Benvenuto, D., Giovanetti, M., Salemi, M., Prosperi, M., De Flora, C., Junior Alcantara, L.C., Angeletti, S., Ciccozzi, M.
The global spread of 2019-nCoV: a molecular evolutionary analysis
Abstract:
The global spread of the 2019-nCoV is continuing and is fast moving, as indicated by the WHO raising the risk assessment to high. In this article, we provide a preliminary phylodynamic and phylogeographic analysis of this new virus. A Maximum Clade Credibility tree has been built using the 29 available whole genome sequences of 2019-nCoV and two whole genome sequences that are highly similar sequences from Bat SARS-like Coronavirus available in GeneBank. We are able to clarify the mechanism of transmission among the countries which have provided the 2019-nCoV sequence isolates from their patients. The Bayesian phylogeographic reconstruction shows that the 2019–2020 nCoV most probably originated from the Bat SARS-like Coronavirus circulating in the Rhinolophus bat family. In agreement with epidemiological observations, the most likely geographic origin of the new outbreak was the city of Wuhan, China, where 2019-nCoV time of the most recent common ancestor emerged, according to molecular clock analysis, around November 25th, 2019. These results, together with previously recorded epidemics, suggest a recurring pattern of periodical epizootic outbreaks due to Betacoronavirus. Moreover, our study describes the same population genetic dynamic underlying the SARS 2003 epidemic, and suggests the urgent need for the development of effective molecular surveillance strategies of Betacoronavirus among animals and Rhinolophus of the bat family. © 2020, © 2020 Informa UK Limited, trading as Taylor & Francis Group.

Clinical features and obstetric and neonatal outcomes of pregnant patients with COVID-19 in Wuhan, China: a retrospective, single-centre, descriptive study
(2020) The Lancet Infectious Diseases
Abstract:
Background: In December, 2019, coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, China. The number of affected pregnant women is increasing, but scarce information is available about the clinical features of COVID-19 in pregnancy. This study aimed to clarify the clinical features and obstetric and neonatal outcomes of pregnant patients with COVID-19. Methods: In this retrospective, single-centre study, we included all pregnant women with COVID-19 who were admitted to Tongji Hospital in Wuhan, China. Clinical features, treatments, and maternal and fetal outcomes were assessed. Findings: Seven patients, admitted to Tongji Hospital from Jan 1, to Feb 8, 2020, were included in our study. The mean age of the patients was 32 years (range 29–34 years) and the mean
gestational age was 39 weeks plus 1 day (range 37 weeks to 41 weeks plus 2 days). Clinical manifestations were fever (six [86%] patients), cough (one [14%] patient), shortness of breath (one [14%] patient), and diarrhoea (one [14%] patient). All the patients had caesarean section within 3 days of clinical presentation with an average gestational age of 39 weeks plus 2 days. The final date of follow-up was Feb 12, 2020. The outcomes of the pregnant women and neonates were good. Three neonates were tested for SARS-CoV-2 and one neonate was infected with SARS-CoV-2 36 h after birth. Interpretation: The maternal, fetal, and neonatal outcomes of patients who were infected in late pregnancy appeared very good, and these outcomes were achieved with intensive, active management that might be the best practice in the absence of more robust data. The clinical characteristics of these patients with COVID-19 during pregnancy were similar to those of non-pregnant adults with COVID-19 that have been reported in the literature. Funding: National Natural Science Foundation of China, Hubei Provincial Natural Science Foundation of China.


The effect of control strategies to reduce social mixing on outcomes of the COVID-19 epidemic in Wuhan, China: a modelling study
(2020) The Lancet Public Health

Abstract:
Background: In December, 2019, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), a novel coronavirus, emerged in Wuhan, China. Since then, the city of Wuhan has taken unprecedented measures in response to the outbreak, including extended school and workplace closures. We aimed to estimate the effects of physical distancing measures on the progression of the COVID-19 epidemic, hoping to provide some insights for the rest of the world. Methods: To examine how changes in population mixing have affected outbreak progression in Wuhan, we used synthetic location-specific contact patterns in Wuhan and adapted these in the presence of school closures, extended workplace closures, and a reduction in mixing in the general community. Using these matrices and the latest estimates of the epidemiological parameters of the Wuhan outbreak, we simulated the ongoing trajectory of an outbreak in Wuhan using an age-structured susceptible-exposed-infected-removed (SEIR) model for several physical distancing measures. We fitted the latest estimates of epidemic parameters from a transmission model to data on local and internationally exported cases from Wuhan in an age-structured epidemic framework and investigated the age distribution of cases. We also simulated lifting of the control measures by allowing people to return to work in a phased-in way and looked at the effects of returning to work at different stages of the underlying outbreak (at the beginning of March or April). Findings: Our projections show that physical distancing measures were most effective if the staggered return to work was at the beginning of April; this reduced the median number of infections by more than 92% (IQR 66–97) and 24% (13–90) in mid-2020 and end-2020, respectively. There are benefits to sustaining these measures until April in terms of delaying and reducing the height of the peak, median epidemic size at end-2020, and affording health-care systems more time to expand and respond. However, the modelled effects of physical distancing measures vary by the duration of infectiousness and the role school children have in the epidemic. Interpretation: Restrictions on activities in Wuhan, if maintained until April, would probably help to delay the epidemic peak. Our projections suggest that premature and sudden lifting of interventions could lead to an earlier secondary peak, which could be flattened by relaxing the interventions gradually. However, there

Rapid viral diagnosis and ambulatory management of suspected COVID-19 cases presenting at the infectious diseases referral hospital in Marseille, France, - January 31st to March 1st, 2020: A respiratory virus snapshot

Abstract:

Background: Rapid virological diagnosis is needed to limit the length of isolation for suspected COVID-19 cases. Method: We managed the first 280 patients suspected to have COVID-19 through a rapid care circuit and virological diagnosis in our infectious disease reference hospital in Marseille, France. Rapid viral detection was performed on sputum and nasopharyngeal samples. Results: Over our study period, no SARS-CoV-2 was detected. Results were obtained within approximately 3 h of the arrival of patient samples at the laboratory. Other viral infections were identified in 49% of the patients, with most common pathogens being influenza A and B viruses, rhinovirus, metapneumovirus and common coronaviruses, notably HKU1 and NL63. Conclusion: Early recognition of COVID-19 is critical to isolate confirmed cases and prevent further transmission. Early rule-out of COVID-19 allows public health containment measures to be adjusted by reducing the time spent in isolation.

Yang, C.-J., Chen, T.-C., Chen, Y.-H.

The preventive strategies of community hospital in the battle of fighting pandemic COVID-19 in Taiwan

Ahorsu, D.K., Lin, C.-Y., Imani, V., Saffari, M., Griffiths, M.D., Pakpour, A.H.

The Fear of COVID-19 Scale: Development and Initial Validation

Abstract:

Background: The emergence of the COVID-19 and its consequences has led to fears, worries, and anxiety among individuals worldwide. The present study developed the Fear of COVID-19 Scale (FCV-19S) to complement the clinical efforts in preventing the spread and treating of COVID-19 cases. Methods: The sample comprised 717 Iranian participants. The items of the FCV-19S were constructed based on extensive review of existing scales on fears, expert evaluations, and participant interviews. Several psychometric tests were conducted to ascertain its reliability and validity properties. Results: After panel review and corrected item-total correlation testing, seven items with acceptable corrected item-total correlation (0.47 to 0.56) were retained and further confirmed by significant and strong factor loadings (0.66 to 0.74). Also, other properties evaluated using both classical test theory and Rasch model were satisfactory on the seven-item scale. More specifically, reliability values such as internal consistency (α =.82) and test–retest reliability (ICC =.72) were acceptable. Concurrent validity was supported by the Hospital Anxiety and Depression Scale (with depression, r = 0.425 and anxiety, r = 0.511) and the Perceived Vulnerability to Disease Scale (with perceived infectability, r = 0.483 and germ aversion, r = 0.459). Conclusion: The Fear of COVID-19 Scale provides a useful tool to assess individual fear of contracting COVID-19 within a community.
19 Scale, a seven-item scale, has robust psychometric properties. It is reliable and valid in assessing fear of COVID-19 among the general population and will also be useful in allaying COVID-19 fears among individuals. © 2020, Springer Science+Business Media, LLC, part of Springer Nature.

Combination of western medicine and Chinese traditional patent medicine in treating a family case of COVID-19 in Wuhan
(2020) Frontiers of Medicine
Abstract:
In December 2019, an outbreak of novel Coronavirus (2019-nCoV) occurred in Wuhan, Hubei Province, China. By February 14, 2020, it has led to 66,492 confirmed patients in China and high mortality up to ∼2.96% (1123/37,914) in Wuhan. Here we report the first family case of coronavirus disease 2019 (COVID-19) confirmed in Wuhan and treated using the combination of western medicine and Chinese traditional patent medicine Shuanghuanglian oral liquid (SHL). This report describes the identification, diagnosis, clinical course, and management of three cases from a family, suggests the expected therapeutic effects of SHL on COVID-19, and warrants further clinical trials. © 2020, Higher Education Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Ji, L.-N., Chao, S., Wang, Y.-J., Li, X.-J., Mu, X.-D., Lin, M.-G., Jiang, R.-M.
Clinical features of pediatric patients with COVID-19: a report of two family cluster cases
Abstract:
Background: Coronavirus disease 2019 (COVID-19) has spread rapidly across the globe. People of all ages are susceptible to COVID-19. However, literature reports on pediatric patients are limited.
Methods: To improve the recognition of COVID-19 infection in children, we retrospectively reviewed two confirmed pediatric cases from two family clusters. Both clinical features and laboratory examination results of the children and their family members were described.
Results: The two confirmed children only presented with mild respiratory or gastrointestinal symptoms. Both of them had normal chest CT images. After general and symptomatic treatments, both children recovered quickly. Both families had travel histories to Hubei Province.
Conclusions: Pediatric patients with COVID-19 are mostly owing to family cluster or with a close contact history. Infected children have relatively milder clinical symptoms than infected adults. We should attach importance to early recognition, early diagnosis, and early treatment of infected children. © 2020, Children's Hospital, Zhejiang University School of Medicine.

Nakajima, K., Kato, H., Yamashiro, T., Izumi, T., Takeuchi, I., Nakajima, H., Utsunomiya, D.
COVID-19 pneumonia: infection control protocol inside computed tomography suites
Abstract:
A novel coronavirus (severe acute respiratory syndrome coronavirus 2) causes a cluster of pneumonia cases in Wuhan, China. It spread rapidly and globally. CT imaging is helpful for the evaluation of the novel coronavirus disease 2019 (COVID-19) pneumonia. Infection control inside the CT suites is also important to prevent hospital-related transmission of COVID-19. We present our experience with infection control protocol for COVID-19 inside the CT suites. © 2020, Japan Radiological Society.

**Treatment of 5 Critically Ill Patients with COVID-19 with Convalescent Plasma** (2020) JAMA - Journal of the American Medical Association

**Abstract:**
Importance: Coronavirus disease 2019 (COVID-19) is a pandemic with no specific therapeutic agents and substantial mortality. It is critical to find new treatments. Objective: To determine whether convalescent plasma transfusion may be beneficial in the treatment of critically ill patients with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. Design, Setting, and Participants: Case series of 5 critically ill patients with laboratory-confirmed COVID-19 and acute respiratory distress syndrome (ARDS) who met the following criteria: severe pneumonia with rapid progression and continuously high viral load despite antiviral treatment; Pao2/Fio2 <300; and mechanical ventilation. All 5 were treated with convalescent plasma transfusion. The study was conducted at the infectious disease department, Shenzhen Third People's Hospital in Shenzhen, China, from January 20, 2020, to March 25, 2020; final date of follow-up was March 25, 2020. Clinical outcomes were compared before and after convalescent plasma transfusion. Exposures: Patients received transfusion with convalescent plasma with a SARS-CoV-2-specific antibody (IgG) binding titer greater than 1:1000 (end point dilution titer, by enzyme-linked immunosorbent assay [ELISA]) and a neutralization titer greater than 40 (end point dilution titer) that had been obtained from 5 patients who recovered from COVID-19. Convalescent plasma was administered between 10 and 22 days after admission. Main Outcomes and Measures: Changes of body temperature, Sequential Organ Failure Assessment (SOFA) score (range 0-24, with higher scores indicating more severe illness), Pao2/Fio2, viral load, serum antibody titer, routine blood biochemical index, ARDS, and ventilatory and extracorporeal membrane oxygenation (ECMO) supports before and after convalescent plasma transfusion. Results: All 5 patients (age range, 36-65 years; 2 women) were receiving mechanical ventilation at the time of treatment and all had received antiviral agents and methylprednisolone. Following plasma transfusion, body temperature normalized within 3 days in 4 of 5 patients, the SOFA score decreased, and Pao2/Fio2 increased within 12 days (range, 172-276 before and 284-366 after). Viral loads also decreased and became negative within 12 days after the transfusion, and SARS-CoV-2-specific ELISA and neutralizing antibody titers increased following the transfusion (range, 40-60 before and 80-320 on day 7). ARDS resolved in 4 patients at 12 days after transfusion, and 3 patients were weaned from mechanical ventilation within 2 weeks of treatment. Of the 5 patients, 3 have been discharged from the hospital (length of stay: 53, 51, and 55 days), and 2 are in stable condition at 37 days after transfusion. Conclusions and Relevance: In this preliminary uncontrolled case series of 5 critically ill patients with COVID-19 and ARDS, administration of convalescent plasma containing neutralizing antibody was followed by improvement in their clinical status. The limited sample size and study design preclude a definitive statement about the potential effectiveness of this treatment, and these observations require evaluation in clinical trials.. © 2020 American Medical Association.


Abstract:
This study aims to analyze the different clinical characteristics between children and their families infected with severe acute respiratory syndrome coronavirus 2. Clinical data from nine children and their 14 families were collected, including general status, clinical, laboratory test, and imaging characteristics. All the children were detected positive result after their families onset. Three children had fever (22.2%) or cough (11.2%) symptoms and six (66.7%) children had no symptom. Among the 14 adult patients, the major symptoms included fever (57.1%), cough (35.7%), chest tightness/pain (21.4%), fatigue (21.4%) and sore throat (7.1%). Nearly 70% of the patients had normal (71.4%) or decreased (28.6%) white blood cell counts, and 50% (7/14) had lymphocytopenia. There were 10 adults (71.4%) showed abnormal imaging. The main manifestations were pulmonary consolidation (70%), nodular shadow (50%), and ground glass opacity (50%). Five discharged children were admitted again because their stool showed positive result in SARS-CoV-2 PCR. COVID-19 in children is mainly caused by family transmission, and their symptoms are mild and prognosis is better than adult. However, their PCR result in stool showed longer time than their families. Because of the mild or asymptomatic clinical process, it is difficult to recognize early for pediatrician and public health staff. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.

Chan, K.W., Wong, V.T., Tang, S.C.W.
Abstract:
As of 22 February 2020, more than 77662 cases of confirmed COVID-19 have been documented globally with over 2360 deaths. Common presentations of confirmed cases include fever, fatigue, dry cough, upper airway congestion, sputum production, shortness of breath, myalgia/arthritis with lymphopenia, prolonged prothrombin time, elevated C-reactive protein, and elevated lactate dehydrogenase. The reported severe/critical case ratio is approximately 7-10% and median time to intensive care admission is 9.5-10.5 days with mortality of around 1-2% varied geographically. Similar to outbreaks of other newly identified virus, there is no proven regimen from conventional medicine and most reports managed the patients with lopinavir/ritonavir, ribavirin, beta-interferon, glucocorticoid and supportive treatment with remdesivir undergoing clinical trial. In China, Chinese medicine is proposed as a treatment option by national and provincial guidelines with substantial utilization. We reviewed the latest national and provincial clinical guidelines, retrospective cohort studies, and case series regarding the treatment of COVID-19 by add-on Chinese medicine. We have also reviewed the clinical evidence generated from SARS and H1N1 management with hypothesized mechanisms and latest in silico findings to identify candidate Chinese medicines for the consideration of possible trials and management. Given the paucity of strongly evidence-based regimens, the available data suggest that Chinese medicine could be considered as an adjunctive therapeutic option in the management of COVID-19. © 2020 World Scientific Publishing Company. Institute for Advanced Research in Asian Science and Medicine.

Tilocca, B., Soggiu, A., Musella, V., Britti, D., Sanguinetti, M., Urbani, A., Roncada, P.
Molecular basis of COVID-19 relationships in different species: a one health perspective (2020) Microbes and Infection
Abstract:
Outside the Hubei province, China, the mild form of infection and the progressive recover of the COVID-19 patients suggest the intervention of “unconventional” biological mechanisms worthy of attention. Based on the high-homology between the Spike protein epitopes of taxonomically-related coronaviruses, we hypothesized that past contact with infected dogs shield humans against the circulating SARS-CoV-2. Elseways, the recurrent virus exposure over a short time-lapse might result in the Antibody Dependent Enhancement, triggering the violent immune reaction responsible for the severe clinical outcomes observed in the Hubei province. Nevertheless, further experimental studies are desired for a confidential evaluation of the postulated hypotheses. © 2020 Institut Pasteur

Ki, M., Task Force for 2019-nCoV

Epidemiologic characteristics of early cases with 2019 novel coronavirus (2019-nCoV) disease in Korea
(2020) Epidemiology and health, 42, p. e2020007.

Abstract:
In about 20 days since the diagnosis of the first case of the 2019 novel coronavirus (2019-nCoV) in Korea on January 20, 2020, 28 cases have been confirmed. Fifteen patients (53.6%) of them were male and median age of was 42 years (range, 20-73). Of the confirmed cases, 16, 9, and 3 were index (57.2%), first-generation (32.1%), and second-generation (10.7%) cases, respectively. All first-generation and second-generation patients were family members or intimate acquaintances of the index cases with close contacts. Fifteen among 16 index patients had entered Korea from January 19 to 24, 2020 while 1 patient had entered Korea on January 31, 2020. The average incubation period was 3.9 days (median, 3.0), and the reproduction number was estimated as 0.48. Three of the confirmed patients were asymptomatic when they were diagnosed. Epidemiological indicators will be revised with the availability of additional data in the future. Sharing epidemiological information among researchers worldwide is essential for efficient preparation and response in tackling this new infectious disease.

Koenig, K.L., Beý, C.K., McDonald, E.C.

2019-nCoV: The identify-isolate-inform (3I) Tool applied to a novel emerging coronavirus

Abstract:
2019 Novel Coronavirus (2019-nCoV) is an emerging infectious disease closely related to MERS-CoV and SARS-CoV that was first reported in Wuhan City, Hubei Province, China in December 2019. As of January 2020, cases of 2019-nCoV are continuing to be reported in other Eastern Asian countries as well as in the United States, Europe, Australia, and numerous other countries. An unusually high volume of domestic and international travel corresponding to the beginning of the 2020 Chinese New Year complicated initial identification and containment of infected persons. Due to the rapidly rising number of cases and reported deaths, all countries should be considered at risk of imported 2019-nCoV. Therefore, it is essential for prehospital, clinic, and emergency department personnel to be able to rapidly assess 2019-nCoV risk and take immediate actions if indicated. The Identify-Isolate-Inform (3I) Tool, originally conceived for the initial detection and management of Ebola virus and later adjusted for other infectious agents, can be adapted for any emerging infectious disease. This paper reports a modification of the 3I Tool for use in the initial detection and management of patients under investigation for 2019-nCoV. After initial assessment for symptoms and epidemiological risk factors, including travel to affected areas and exposure to confirmed 2019-
nCoV patients within 14 days, patients are classified in a risk-stratified system. Upon confirmation of a suspected 2019-nCoV case, affected persons must immediately be placed in airborne infection isolation and the appropriate public health agencies notified. This modified 3I Tool will assist emergency and primary care clinicians, as well as out-of-hospital providers, in effectively managing persons with suspected or confirmed 2019-nCoV. © 2020 eScholarship. All rights reserved.

Li, Y., Guo, F., Cao, Y., Li, L., Guo, Y.

**Insight into COVID-2019 for pediatricians**

(2020) Pediatric Pulmonology

**Abstract:**

Since December 2019, patients with unexplained pneumonia have been found in Wuhan City, Hubei Province, China. The pathogen in these cases is a new type of coronavirus. The World Health Organization confirmed this diagnosis and named the pathogen SARSCoV-2. The disease caused by SARSCoV-2 is called Corona Virus Disease (COVID-2019). The virus is highly infectious and pathogenic, causing human-to-human transmission. At present, SARSCoV-2 is still rampant in the world. Zhengzhou City in Henan Province serves as an example, 102 people have been confirmed to be infected with SARSCoV-2 (at 24:00 on February 5th, 2020), including three children, the youngest is 4 years old. From the perspective of clinical pediatricians as the first line fighting the epidemic, this paper will discuss the clinical characteristics, prevention and control measures, outcomes, diagnosis, and treatment of pediatric cases. © 2020 Wiley Periodicals, Inc.

Yen, M.-Y., Schwartz, J., Chen, S.-Y., King, C.-C., Yang, G.-Y., Hsueh, P.-R.

**Interrupting COVID-19 transmission by implementing enhanced traffic control bundling: Implications for global prevention and control efforts**

(2020) Journal of Microbiology, Immunology and Infection

**Abstract:**

We argue that enhanced Traffic Control Bundling (eTCB) can interrupt the community-hospital-community transmission cycle, thereby limiting COVID-19’s impact. Enhanced TCB is an expansion of the traditional TCB that proved highly effective during Taiwan’s 2003 SARS outbreak. TCB’s success derived from ensuring that Health Care Workers (HCWs) and patients were protected from fomite, contact and droplet transmission within hospitals. Although TCB proved successful during SARS, achieving a similar level of success with the COVID-19 outbreak requires adapting TCB to the unique manifestations of this new disease. These manifestations include asymptomatic infection, a hyper-affinity to ACE2 receptors resulting in high transmissibility, false negatives, and an incubation period of up to 22 days. Enhanced TCB incorporates the necessary adaptations. In particular, eTCB includes expanding the TCB transition zone to incorporate a new sector – the quarantine ward. This ward houses patients exhibiting atypical manifestations or awaiting definitive diagnosis. A second adaptation involves enhancing the checkpoint hand disinfection and gowning up with Personal Protective Equipment deployed in traditional TCB. Under eTCB, checkpoint hand disinfection and donning of face masks are now required of all visitors who seek to enter hospitals. These enhancements ensure that transmissions by droplets, fomites and contact are disrupted both within hospitals and between hospitals and the broader community. Evidencing eTCB effectiveness is Taiwan’s success to date in containing and controlling the community-hospital-community transmission cycle. © 2020

Wu, D., Yang, X.O.

**TH17 responses in cytokine storm of COVID-19: An emerging target of JAK2 inhibitor Fedratinib**
Abstract:
COVID-19 emerges as a pandemic disease with high mortality. Development of effective prevention and treatment is an urgent need. We reviewed TH17 responses in patients with SARS-CoV-2 and proposed an FDA approved JAK2 inhibitor Fedratinib for reducing mortality of patients with TH17 type immune profiles. © 2020

Rao, A.S.R.S., Vazquez, J.A.
Identification of COVID-19 Can be Quicker through Artificial Intelligence framework using a Mobile Phone-Based Survey in the Populations when Cities/Towns Are under Quarantine
(2020) Infection Control and Hospital Epidemiology

Abstract:
We are proposing to use machine learning algorithms to be able to improve possible case identifications of COVID-19 more quicker when we use a mobile phone-based web survey. This will also reduce the spread in the susceptible populations. © 2020 by The Society for Healthcare Epidemiology of America. All rights reserved.

Analyzing the epidemiological outbreak of COVID-19: A visual exploratory data analysis approach
(2020) Journal of Medical Virology

Abstract:
There is an obvious concern globally regarding the fact about the emerging coronavirus 2019 novel coronavirus (2019-nCoV) as a worldwide public health threat. As the outbreak of COVID-19 causes by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) progresses within China and beyond, rapidly available epidemiological data are needed to guide strategies for situational awareness and intervention. The recent outbreak of pneumonia in Wuhan, China, caused by the SARS-CoV-2 emphasizes the importance of analyzing the epidemiological data of this novel virus and predicting their risks of infecting people all around the globe. In this study, we present an effort to compile and analyze epidemiological outbreak information on COVID-19 based on the several open datasets on 2019-nCoV provided by the Johns Hopkins University, World Health Organization, Chinese Center for Disease Control and Prevention, National Health Commission, and DXY. An exploratory data analysis with visualizations has been made to understand the number of different cases reported (confirmed, death, and recovered) in different provinces of China and outside of China. Overall, at the outset of an outbreak like this, it is highly important to readily provide information to begin the evaluation necessary to understand the risks and begin containment activities. © 2020 Wiley Periodicals, Inc.

Sayed, A.S.M., Malek, S.S., Abushahba, M.F.N.
Seroprevalence of Middle East Respiratory Syndrome Corona Virus in dromedaries and their traders in upper Egypt

Abstract:
Introduction: Camel trade in Egypt depends mainly on importation. Seemingly healthy imported camels are responsible for the ingress of serious diseases into Egypt. A striking example of this concerning public health globally is the Middle East respiratory coronavirus (MERS-CoV) which
causes case fatalities of over 34%. Here, we determined the seroepidemiological situation of the MERS-CoV in imported camels and their traders in Upper Egypt. Methodology: Sera of sixty-three dromedaries and twenty-eight camel traders were recruited (January 2015-December 2016). The age, gender, and sampling locality of each sampled camel and human were obtained. Semiquantitative anti-MERS-CoV IgG ELISAs which utilize the purified spike protein domain S1 antigen of MERS coronavirus (MERS-CoV S1) were used to detect specific IgG antibodies against the virus. Results: The data showed that 58.73% of imported camels and 25% of traders had antibodies specific to MERS-CoV. Interestingly, like seroreactive camels, all seropositive humans were apparently healthy without any history of developing severe respiratory disease in the 14 days prior to sampling. Having specific antibodies among the examined camel sera was significantly different (P < 0.0001) in relation to various sampling localities, gender and age groups. In contrast, the seropositivity rate of MERS-CoV IgG in humans did not differ significantly by any of the studied factors. Conclusions: The current study provides the first serological evidence of occupational exposure of humans to MERS-CoV in Africa. Additionally, it reports that imported camels could be implicated in introducing MERS-CoV into Egypt. Accordingly, application of strict control measures to camel importation is a priority. © 2020 Sayed et al.

Lee, N.-Y., Li, C.-W., Tsai, H.-P., Chen, P.-L., Syue, L.-S., Li, M.-C., Tsai, C.-S., Lo, C.-L., Hsueh, P.-R., Ko, W.-C.

A case of COVID-19 and pneumonia returning from Macau in Taiwan: Clinical course and anti-SARS-CoV-2 IgG dynamic
(2020) Journal of Microbiology, Immunology and Infection

Abstract:
A 46-year-old woman presented to the emergency department with 2-day fever and cough at seven days after returning from Macau. COVID-19 and pneumonia was diagnosed based on the positive real-time RT-PCR tests for oropharyngeal swab samples and the presence of anti-SARS-COV-2 IgG starting from the illness day 11 and post-exposure 18–21 days. © 2020 Guo, H., Zhou, Y., Liu, X., Tan, J.

The impact of the COVID-19 epidemic on the utilization of emergency dental services
(2020) Journal of Dental Sciences

Abstract:
Background/Purpose: To assess how the current COVID-19 epidemic influenced peoples' utilization of emergency dental services in Beijing, China. Methods: The first-visit patients seeking emergency dental services before or at the beginning of the COVID-19 epidemic were retrieved. Their demographic characteristics and the reasons for visiting were recorded and analyzed. Results: There were 2,537 patients involved in this study. Thirty-eight percent fewer patients visited the dental urgency at the beginning of the COVID-19 epidemic than before. The distribution of dental problems has changed significantly. The proportion of dental and oral infection raised from 51.0% of pre-COVID-19 to 71.9% during COVID-19, and dental trauma decreased from 14.2% to 10.5%. Meanwhile, the non-urgency cases reduced to three-tenths of pre-COVID-19. Conclusion: Within the limitation of this study, the COVID-19 epidemic had a strong influence on the utilization of emergency dental services. © 2020 Association for Dental Sciences of the Republic of China


Identification of coronavirus isolated from a patient in Korea with covid-19
Abstract:
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. © 2020 Korea Centers for Disease Control and Prevention.

Abstract:
The initial cluster of severe pneumonia cases that triggered the COVID-19 epidemic was identified in Wuhan, China in December 2019. While early cases of the disease were linked to a wet market, human-to-human transmission has driven the rapid spread of the virus throughout China. The Chinese government has implemented containment strategies of city-wide lockdowns, screening at airports and train stations, and isolation of suspected patients; however, the cumulative case count keeps growing every day. The ongoing outbreak presents a challenge for modelers, as limited data are available on the early growth trajectory, and the epidemiological characteristics of the novel coronavirus are yet to be fully elucidated. We use phenomenological models that have been validated during previous outbreaks to generate and assess short-term forecasts of the cumulative number of confirmed reported cases in Hubei province, the epicenter of the epidemic, and for the overall trajectory in China, excluding the province of Hubei. We collect daily reported cumulative confirmed cases for the 2019-nCoV outbreak for each Chinese province from the National Health Commission of China. Here, we provide 5, 10, and 15 day forecasts for five consecutive days, February 5th through February 9th, with quantified uncertainty based on a generalized logistic growth model, the Richards growth model, and a sub-epidemic wave model. Our most recent forecasts reported here, based on data up until February 9, 2020, largely agree across the three models presented and suggest an average range of 7409–7496 additional confirmed cases in Hubei and 1128–1929 additional cases in other provinces within the next five days. Models also predict an average total cumulative case count between 37,415 and 38,028 in Hubei and 11,588–13,499 in other provinces by February 24, 2020. Mean estimates and uncertainty bounds for both Hubei and other provinces have remained relatively stable in the last three reporting dates (February 7th – 9th). We also observe that each of the models predicts that the epidemic has reached saturation in both Hubei and other provinces. Our findings suggest that the containment strategies implemented in China are successfully reducing transmission and that the epidemic growth has slowed in recent days. © 2020 The Authors

Shell disorder analysis predicts greater resilience of the SARS-CoV-2 (COVID-19) outside the body and in body fluids
(2020) Microbial Pathogenesis, 144, art. no. 104177

Abstract:
The coronavirus (CoV) family consists of viruses that infects a variety of animals including humans with various levels of respiratory and fecal-oral transmission levels depending on the behavior of the viruses' natural hosts and optimal viral fitness. A model to classify and predict the levels of respective respiratory and fecal-oral transmission potentials of the various viruses was built before the outbreak of MERS-CoV using AI and empirically-based molecular tools to predict the disorder level of proteins. Using the percentages of intrinsic disorder (PID) of the nucleocapsid (N) and membrane (M) proteins of CoV, the model easily clustered the viruses into three groups with the SARS-CoV (M PID = 8%, N PID = 50%) falling into Category B, in which viruses have intermediate levels of both respiratory and fecal-oral transmission potentials. Later, MERS-CoV (M PID = 9%, N PID = 44%) was found to be in Category C, which consists of viruses with lower respiratory transmission potential but with higher fecal-oral transmission capabilities. Based on the peculiarities of disorder distribution, the SARS-CoV-2 (M PID = 6%, N PID = 48%) has to be placed in Category B. Our data show however, that the SARS-CoV-2 is very strange with one of the hardest protective outer shell, (M PID = 6%) among coronaviruses. This means that it might be expected to be highly resilient in saliva or other body fluids and outside the body. An infected body is likelier to shed greater numbers of viral particles since the latter is more resistant to antimicrobial enzymes in body fluids. These particles are also likelier to remain active longer. These factors could account for the greater contagiousness of the SARS-CoV-2 and have implications for efforts to prevent its spread.

Jansen, J.H., Day, R.L.

A novel presentation of COVID-19 via community acquired infection
(2020) Visual Journal of Emergency Medicine, 20, art. no. 100760

Fahmi, M., Kubota, Y., Ito, M.

Nonstructural proteins NS7b and NS8 are likely to be phylogenetically associated with evolution of 2019-nCoV
(2020) Infection, Genetics and Evolution, 81, art. no. 104272

Abstract:
The seventh novel human infecting Betacoronavirus that causes pneumonia (2019 novel coronavirus, 2019-nCoV) originated in Wuhan, China. The evolutionary relationship between 2019-nCoV and the other human respiratory illness-causing coronavirus is not closely related. We sought to characterize the relationship of the translated proteins of 2019-nCoV with other species of Orthocoronavirinae. A phylogenetic tree was constructed from the genome sequences. A cluster tree was developed from the profiles retrieved from the presence and absence of homologs of ten 2019-nCoV proteins. The combined data were used to characterize the relationship of the translated proteins of 2019-nCoV to other species of Orthocoronavirinae. Our analysis reliably suggests that 2019-nCoV is most closely related to BatCoV RaTG13 and belongs to subgenus Sarbecovirus of Betacoronavirus, together with SARS coronavirus and Bat-SARS-like coronavirus. The
phylogenetic profiling cluster of homolog proteins of one annotated 2019-nCoV protein against other genome sequences revealed two clades of ten 2019-nCoV proteins. Clade 1 consisted of a group of conserved proteins in Orthocoronavirinae comprising Orf1ab polyprotein, Nucleocapsid protein, Spike glycoprotein, and Membrane protein. Clade 2 comprised six proteins exclusive to Sarbecovirus and Hibecovirus. Two of six Clade 2 nonstructural proteins, NS7b and NS8, were exclusively conserved among 2019-nCoV, BetaCoV_RaTG, and BatSARS-like Cov. NS7b and NS8 have previously been shown to affect immune response signaling in the SARS-CoV experimental model. Thus, we speculated that knowledge of the functional changes in the NS7b and NS8 proteins during evolution may provide important information to explore the human infective property of 2019-nCoV. © 2020 The Authors


Abstract: Novel Corona Virus Disease (COVID-19) originating from China has rapidly crossed borders, infecting people throughout the whole world. This phenomenon has led to a massive public reaction; the media has been reporting continuously across borders to keep all informed about the pandemic situation. All these things are creating a lot of concern for people leading to heightened levels of anxiety. Pandemics can lead to heightened levels of stress; Anxiety is a common response to any stressful situation. This study attempted to assess the knowledge, attitude, anxiety experience, and perceived mental healthcare need among adult Indian population during the COVID-19 pandemic. An online survey was conducted using a semi-structured questionnaire using a non-probability snowball sampling technique. A total of 662 responses were received. The responders had a moderate level of knowledge about the COVID-19 infection and adequate knowledge about its preventive aspects. The attitude towards COVID-19 showed peoples' willingness to follow government guidelines on quarantine and social distancing. The anxiety levels identified in the study were high. More than 80 % of the people were preoccupied with the thoughts of COVID-19 and 72 % reported the need to use gloves, and sanitizers. In this study, sleep difficulties, paranoia about acquiring COVID-19 infection and distress related social media were reported in 12.5 %, 37.8 %, and 36.4 % participants respectively. The perceived mental healthcare need was seen in more than 80 % of participants. There is a need to intensify the awareness and address the mental health issues of people during this COVID-19 pandemic. © 2020 Elsevier B.V.


Abstract: Objectives: Following the public-health emergency of international concern (PHEIC) declared by the World Health Organization (WHO) on 30 January 2020 and the recent outbreak caused by 2019 novel coronavirus (2019-nCoV) [officially renamed severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)] in China and 29 other countries, we aimed to summarise the clinical aspects of
the novel Betacoronavirus disease (COVID-19) and its possible clinical presentations together with suggested therapeutic algorithms for patients who may require antimicrobial treatment. Methods: The currently available literature was reviewed for microbiologically confirmed infections by 2019-nCoV or COVID-19 at the time of writing (13 February 2020). A literature search was performed using the PubMed database and Cochrane Library. Search terms included ‘novel coronavirus’ or ‘2019-nCoV’ or ‘COVID-19’. Results: Published cases occurred mostly in males (age range, 8–92 years). Cardiovascular, digestive and endocrine system diseases were commonly reported, except previous chronic pulmonary diseases [e.g. chronic obstructive pulmonary disease (COPD), asthma, bronchiectasis] that were surprisingly underreported. Fever was present in all of the case series available, flanked by cough, dyspnoea, myalgia and fatigue. Multiple bilateral lobular and subsegmental areas of consolidation or bilateral ground-glass opacities were the main reported radiological features of 2019-nCoV infection, at least in the early phases of the disease. Conclusion: The new 2019-nCoV epidemic is mainly associated with respiratory disease and few extrapulmonary signs. However, there is a low rate of associated pre-existing respiratory co-morbidities. © 2020

Zhuang, Z., Zhao, S., Lin, Q., Cao, P., Lou, Y., Yang, L., He, D.


Abstract:
As of March 1, 2020, Iran had reported 987 novel coronavirus disease (COVID-19) cases, including 54 associated deaths. At least six neighboring countries (Bahrain, Iraq, Kuwait, Oman, Afghanistan, and Pakistan) had reported imported COVID-19 cases from Iran. In this study, air travel data and the numbers of cases from Iran imported into other Middle Eastern countries were used to estimate the number of COVID-19 cases in Iran. It was estimated that the total number of cases in Iran was 16 533 (95% confidence interval: 5925–35 538) by February 25, 2020, before the UAE and other Gulf Cooperation Council countries suspended inbound and outbound flights from Iran. © 2020 The Author(s)

Han, Y., Jiang, M., Xia, D., He, L., Lv, X., Liao, X., Meng, J.

COVID-19 in a patient with long-term use of glucocorticoids: A study of a familial cluster (2020) Clinical Immunology, 214, art. no. 108413

Abstract:
Clusters of patients with novel coronavirus disease 2019 (COVID-19) have been successively reported globally. Studies show clear person-to-person transmission. The average incubation period is 2–14 days, and mostly 3–7 days. However, in some patients, this period may be longer. Here, we report a familial cluster of COVID-19 where a 47-year-old woman with long-term use of glucocorticoids did not develop any symptoms within the 14-day quarantine period but was confirmed with COVID-19 by tested positive of antibody on day 40 after she left Wuhan. Almost at the same time, her father and sister were diagnosed with COVID-19. The results suggest that the long-term use of glucocorticoids might cause atypical infections, a long incubation period, and extra transmission of COVID-19. © 2020 Elsevier Inc.

Esler, M., Esler, D.

Can angiotensin receptor-blocking drugs perhaps be harmful in the COVID-19 pandemic?

COVID-19: Global radiation oncology's targeted response for pandemic preparedness

Abstract:
As the global COVID-19 pandemic escalates there is a need within radiation oncology to work to support our patients in the best way possible. Measures are required to reduce infection spread between patients and within the workforce. Departments need contingency planning to create capacity and continue essential treatments despite a reduced workforce. The #radonc community held an urgent online journal club on Twitter in March 2020 to discuss these issues and create some consensus on crucial next steps. There were 121 global contributors. This document summarises these discussions around themes of infection prevention, rationalisation of workload and working practice in the presence of infection. © 2020 The Authors

Moazzami, B., Razavi-Khorasani, N., Dooghaie Moghadam, A., Farokhi, E., Rezaei, N.
COVID-19 and telemedicine: Immediate action required for maintaining healthcare providers well-being
(2020) Journal of Clinical Virology, 126, art. no. 104345

Abstract:
The well-being of the health care workforce is the cornerstone of every well-functioning health system. As a result of the pandemic, medical healthcare providers are under an enormous amount of workload pressure along with increased total health expenditures. The overwhelming burden of COVID-19 illness could lead to caregiver burnout. Direct-to-consumer telemedicine can enable patients to connect with their healthcare provider at a distance. This virtual platform could be used by smartphones or webcam-enabled computers and allows physicians to effectively screen patients with early signs of COVID-19 before they reach to hospital. © 2020 Elsevier B.V.

Grech, V.
Unknown unknowns – COVID-19 and potential global mortality
(2020) Early Human Development, 144, art. no. 105026

Abstract:
COVID-19 (SARS-CoV-2) is currently a global pandemic. This paper will attempt to estimate global infection rates and potential resultant mortality in the absence of effective treatment and/or vaccination. Calculations are based on World Health Organisation data from Wuhan in China: 14% of infected cases are severe, 5% require intensive care and 4% die. Estimated infection rates and mortality rates at the level of continents and some individual countries (when these are of sufficient size) are tabulated. This pandemic may cause close to half a billion deaths, i.e. 6% of the global population – and potentially more. At the risk of sounding sensational, but with a sober sense of realism, healthcare risks being plunged into the Middle-Ages if the public do not do their part. Infection cannot occur in the absence of contact. The only way to mitigate these numbers is to apply social distancing and take the standard precautions so frequently reiterated by Public Health: hand washing, avoid touching the face and so on. These measures are crucial as the human cost is going to be unthinkable even in the best-case scenarios that epidemiologists are modelling. © 2020 Elsevier B.V.

Misra, A.
Doctors and healthcare workers at frontline of COVID 19 epidemic: Admiration, a pat on the back, and need for extreme caution

Liu, K., Zhang, W., Yang, Y., Zhang, J., Li, Y., Chen, Y.
Respiratory rehabilitation in elderly patients with COVID-19: A randomized controlled study
(2020) Complementary Therapies in Clinical Practice, 39, art. no. 101166
Abstract:
Background: Different degrees of disorders are reported in respiratory function, physical function and psychological function in patients with corona virus disease 2019 (COVID-19), especially in elderly patients. With the experience of improved and discharged COVID-19 patients, timely respiratory rehabilitation intervention may improve prognosis, maximize functional preservation and improve quality of life (QoL), but there lacks of studies worldwide exploring the outcome of this intervention. Objective: To investigate the effects of 6-week respiratory rehabilitation training on respiratory function, QoL, mobility and psychological function in elderly patients with COVID-19. Methods: This paper reported the findings of an observational, prospective, quasi-experimental study, which totally recruited 72 participants, of which 36 patients underwent respiratory rehabilitation and the rest without any rehabilitation intervention. The following outcomes were measured: pulmonary function tests including plethysmography and diffusing lung capacity for carbon monoxide (DLCO), functional tests (6-min walk distance test), Quality of life (QoL) assessments (SF-36 scores), activities of daily living (Functional Independence Measure, FIM scores), and mental status tests (SAS anxiety and SDS depression scores). Results: After 6 weeks of respiratory rehabilitation in the intervention group, there disclosed significant differences in FEV1(L), FVC(L), FEV1/FVC%, DLCO% and 6-min walk test. The SF-36 scores, in 8 dimensions, were statistically significant within the intervention group and between the two groups. SAS and SDS scores in the intervention group decreased after the intervention, but only anxiety had significant statistical significance within and between the two groups. Conclusions: Six-week respiratory rehabilitation can improve respiratory function, QoL and anxiety of elderly patients with COVID-19, but it has little significant improvement on depression in the elderly. © 2020

Zumla, A., Niederman, M.S.
Editorial: The explosive epidemic outbreak of novel coronavirus disease 2019 (COVID-19) and the persistent threat of respiratory tract infectious diseases to global health security

Chen, D., Yang, H., Cao, Y., (...), Zhang, Y., Guan, X.
Expert consensus for managing pregnant women and neonates born to mothers with suspected or confirmed novel coronavirus (COVID-19) infection
Abstract:
Objective: To provide clinical management guidelines for novel coronavirus (COVID-19) in pregnancy. Methods: On February 5, 2020, a multidisciplinary teleconference comprising Chinese physicians and researchers was held and medical management strategies of COVID-19 infection in pregnancy were discussed. Results: Ten key recommendations were provided for the management of COVID-19 infections in pregnancy. Conclusion: Currently, there is no clear evidence regarding
optimal delivery timing, the safety of vaginal delivery, or whether cesarean delivery prevents vertical transmission at the time of delivery; therefore, route of delivery and delivery timing should be individualized based on obstetrical indications and maternal–fetal status. © 2020 International Federation of Gynecology and Obstetrics


Prevalence and predictors of PTSS during COVID-19 outbreak in China hardest-hit areas: Gender differences matter
(2020) Psychiatry Research, 287, art. no. 112921

Abstract:
The outbreak of COVID-19 in China in December 2019 has been identified as a pandemic and a health emergency of global concern. Our objective was to investigate the prevalence and predictors of posttraumatic stress symptoms (PTSS) in China hardest-hit areas during COVID-19 outbreak, especially exploring the gender difference existing in PTSS. One month after the December 2019 COVID-19 outbreak in Wuhan China, we surveyed PTSS and sleep qualities among 285 residents in Wuhan and surrounding cities using the PTSD Checklist for DSM-5 (PCL-5) and 4 items from the Pittsburgh Sleep Quality Index (PSQI). Hierarchical regression analysis and non-parametric test were used to analyze the data. Results indicated that the prevalence of PTSS in China hardest-hit areas a month after the COVID-19 outbreak was 7%. Women reported significant higher PTSS in the domains of re-experiencing, negative alterations in cognition or mood, and hyper-arousal. Participants with better sleep quality or less frequency of early awakenings reported lower PTSS. Professional and effective mental health services should be designed in order to aid the psychological wellbeing of the population in affected areas, especially those living in hardest-hit areas, females and people with poor sleep quality. © 2020 Elsevier B.V.


High-resolution computed tomography manifestations of COVID-19 infections in patients of different ages
(2020) European Journal of Radiology, 126, art. no. 108972

Abstract:
Purpose: We aimed to compare chest HRCT lung signs identified in scans of differently aged patients with COVID-19 infections. Methods: Case data of patients diagnosed with COVID-19 infection in Hangzhou City, Zhejiang Province in China were collected, and chest HRCT signs of infected patients in four age groups (<18 years, 18–44 years, 45–59 years, ≥60 years) were compared. Results: Small patchy, ground-glass opacity (GGO), and consolidations were the main HRCT signs in 98 patients with confirmed COVID-19 infections. Patients aged 45–59 years and aged ≥60 years had more bilateral lung, lung lobe, and lung field involvement, and greater lesion numbers than patients <18 years. GGO accompanied with the interlobular septa thickening or a crazy-paving pattern, consolidation, and air bronchogram sign were more common in patients aged 45–59 years, and ≥60 years, than in those aged <18 years, and aged 18–44 years. Conclusions: Chest HRCT manifestations in patients with COVID-19 are related to patient's age, and HRCT signs may be milder in younger patients. © 2020 Elsevier B.V.

Wang, K., Kang, S., Tian, R., Zhang, X., Wang, Y.

Imaging manifestations and diagnostic value of chest CT of coronavirus disease 2019 (COVID-19) in the Xiaogan area

...
Abstract:
AIM: To report the epidemiological, clinical, and radiological characteristics of patients with COVID-19 in Xiaogan, Hubei, China. MATERIALS AND METHODS: The complete clinical and imaging data of 114 confirmed COVID-19 patients treated in Xiaogan Hospital were analysed retrospectively. Data were gathered regarding the presence of chest computed tomography (CT) abnormalities; the distribution, morphology, density, location, and stage of abnormal shadows on chest CT; and observing the correlation between the severity of chest infection and lymphocyte ratio and blood oxygen saturation (SPO2) in patients. RESULTS: Chest CT revealed abnormal lung shadows in 110 patients. Regarding lesion distribution, multi-lobe lesions in both lungs were present in most patients (80 cases; 72.7%). Lesions most frequently involved both the peripheral zone and the central zone (62 cases; 56.4%). Regarding lesion morphology, 56 cases (50.1%) demonstrated patchy shadows that were partially fused into large areas. Thirty cases showed ground-glass opacity (27.3%), 30 cases showed the consolidation change (27.3%), and the remaining 50 cases showed both types of changes (45.4%). The progressing stage was the most common stage (54 cases; 49.1%). CT results showed a negative correlation with SPO2 and lymphocyte numbers (p<0.05), with r-values of −0.446 and −0.780, respectively. CONCLUSION: Spiral CT is a sensitive examination method, which can be applied to make an early diagnosis and for evaluation of progression, with a diagnostic sensitivity and accuracy better than that of nucleic acid detection. © 2020 The Royal College of Radiologists

Abstract:
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. © 2020 Elsevier Inc.
Touyz, R.M., Li, H., Delles, C.
ACE2 the Janus-faced protein - from cardiovascular protection to severe acute respiratory syndrome-coronavirus and COVID-19

Abstract:
Angiotensin converting enzyme 2 (ACE2) is the major enzyme responsible for conversion of Ang II into Ang-(1-7). It also acts as the receptor for severe acute respiratory syndrome (SARS)-coronavirus (CoV)-2, which causes Coronavirus Disease (COVID)-19. In recognition of the importance of ACE2 and to celebrate 20 years since its discovery, the journal will publish a focused issue on the basic science and (patho)physiological role of this multifunctional protein. © 2020 The Author(s). Published by Portland Press Limited on behalf of the Biochemical Society.

Changoiwala, P.
The doctors navigating covid-19 with no internet
(2020) BMJ (Clinical research ed.), 369, p. m1417.

Prediction models for diagnosis and prognosis of covid-19 infection: systematic review and critical appraisal
(2020) BMJ (Clinical research ed.), 369, p. m1328.

Abstract:
OBJECTIVE: To review and critically appraise published and preprint reports of prediction models for diagnosing coronavirus disease 2019 (covid-19) in patients with suspected infection, for prognosis of patients with covid-19, and for detecting people in the general population at risk of being admitted to hospital for covid-19 pneumonia. DESIGN: Rapid systematic review and critical appraisal. DATA SOURCES: PubMed and Embase through Ovid, Arxiv, medRxiv, and bioRxiv up to 24 March 2020. STUDY SELECTION: Studies that developed or validated a multivariable covid-19 related prediction model. DATA EXTRACTION: At least two authors independently extracted data using the CHARMS (critical appraisal and data extraction for systematic reviews of prediction modelling studies) checklist; risk of bias was assessed using PROBAST (prediction model risk of bias assessment tool). RESULTS: 2696 titles were screened, and 27 studies describing 31 prediction models were included. Three models were identified for predicting hospital admission from pneumonia and other events (as proxy outcomes for covid-19 pneumonia) in the general population; 18 diagnostic models for detecting covid-19 infection (13 were machine learning based on computed tomography scans); and 10 prognostic models for predicting mortality risk, progression to severe disease, or length of hospital stay. Only one study used patient data from outside of China. The most reported predictors of presence of covid-19 in patients with suspected disease included age, body temperature, and signs and symptoms. The most reported predictors of severe prognosis in patients with covid-19 included age, sex, features derived from computed tomography scans, C reactive protein, lactic dehydrogenase, and lymphocyte count. C index estimates ranged from 0.73 to 0.81 in prediction models for the general population (reported for all three models), from 0.81 to more than 0.99 in diagnostic models (reported for 13 of the 18 models), and from 0.85 to 0.98 in prognostic models (reported for six of the 10 models). All studies were rated at high risk of bias, mostly because of non-representative selection of control patients, exclusion of patients who had not experienced the event of interest by the end of the study, and high risk of model overfitting.
Reporting quality varied substantially between studies. Most reports did not include a description of the study population or intended use of the models, and calibration of predictions was rarely assessed. CONCLUSION: Prediction models for covid-19 are quickly entering the academic literature to support medical decision making at a time when they are urgently needed. This review indicates that proposed models are poorly reported, at high risk of bias, and their reported performance is probably optimistic. Immediate sharing of well documented individual participant data from covid-19 studies is needed for collaborative efforts to develop more rigorous prediction models and validate existing ones. The predictors identified in included studies could be considered as candidate predictors for new models. Methodological guidance should be followed because unreliable predictions could cause more harm than benefit in guiding clinical decisions. Finally, studies should adhere to the TRIPOD (transparent reporting of a multivariable prediction model for individual prognosis or diagnosis) reporting guideline. SYSTEMATIC REVIEW REGISTRATION: Protocol https://osf.io/ehc47/, registration https://osf.io/wy245. © Author(s) (or their employer(s)) 2019. Re-use permitted under CC BY. No commercial re-use. See rights and permissions. Published by BMJ.


Nelson, B. Seattle's covid-19 lessons are yielding hope (2020) BMJ (Clinical research ed.), 369, p. m1389.


Iacobucci, G.
**Covid-19: government promises 100 000 tests per day in England by end of April**
(2020) BMJ (Clinical research ed.), 369, p. m1392.

Sayburn, A.
**Covid-19: PHE upgrades PPE advice for all patient contacts with risk of infection**
(2020) BMJ (Clinical research ed.), 369, p. m1391.

Kamerow, D.
**Covid-19: The crisis of personal protective equipment in the US**
(2020) The BMJ, 369, art. no. m1367

Sjödin, H., Wilder-Smith, A., Osman, S., Farooq, Z., Rocklöv, J.
**Only strict quarantine measures can curb the coronavirus disease (COVID-19) outbreak in Italy, 2020**
(2020) Eurosurveillance, 25 (13)
**Abstract:**
Several Italian towns are under lockdown to contain the COVID-19 outbreak. The level of transmission reduction required for physical distancing interventions to mitigate the epidemic is a crucial question. We show that very high adherence to community quarantine (total stay-home policy) and a small household size is necessary for curbing the outbreak in a locked-down town. The larger the household size and amount of time in the public, the longer the lockdown period needed. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Verelst, F., Kuylen, E., Beutels, P.
**Indications for healthcare surge capacity in European countries facing an exponential increase in coronavirus disease (COVID-19) cases, March 2020**
(2020) Eurosurveillance, 25 (13)
**Abstract:**
European healthcare systems face extreme pressure from coronavirus disease (COVID-19). We relate country-specific accumulated COVID-19 deaths (intensity approach) and active COVID-19 cases (magnitude approach) to measures of healthcare system capacity: hospital beds, healthcare workers and healthcare expenditure. Modelled by the intensity approach with a composite measure for healthcare capacity, the countries experiencing the highest pressure on 25 March 2020 - relative to Italy on 11 March - were Italy, Spain, the Netherlands and France (www.covid-hcpressure.org). © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Dyer, C.
**Covid-19: Rules on sharing confidential patient information are relaxed in England**
(2020) BMJ (Clinical research ed.), 369, p. m1378.

Arie, S.
**Covid-19: Can France's ethical support units help doctors make challenging decisions?**
(2020) BMJ (Clinical research ed.), 369, p. m1291.
Abstract:
The outbreak of coronavirus disease 2019 (COVID-19) in Wuhan has aroused widespread concern and attention from all over the world. Many articles have predicted the development of the epidemic. Most of them only use very basic SEIR model without considering the real situation. In this paper, we build a model called e-ISHR model based on SEIR model. Then we add hospital system and time delay system into the original model to simulate the spread of COVID-19 better. Besides, in order to take the government’s control and people’s awareness into consideration, we change our e-ISHR model into a 3-staged model which effectively shows the impact of these factors on the spread of the disease. By using this e-ISHR model, we fit and predict the number of confirmed cases in Wuhan and China except Hubei. We also change some of parameters in our model. The results indicate the importance of isolation and increasing the number of beds in hospital. © 2020, Shanghai Jiao Tong University and Springer-Verlag GmbH Germany, part of Springer Nature.

Sarkodie, S.A., Owusu, P.A.
Investigating the cases of novel coronavirus disease (COVID-19) in China using dynamic statistical techniques
(2020) Heliyon, 6 (4), art. no. e03747

Abstract:
The initial investigation by local hospital attributed the outbreak of the novel coronavirus disease (COVID-19) to pneumonia with unknown cause that appeared like the 2003 severe acute respiratory syndrome (SARS). The World Health Organization declared COVID-19 as public health emergency
after it spread outside China to several countries. Thus, an assessment of the novel coronavirus disease (COVID-19) with novel estimation approaches is essential to the global debate. This study is the first to develop both time series and panel data models to construct conceptual tools that examine the nexus between death from COVID-19 and confirmed cases. We collected daily data on four health indicators namely deaths, confirmed cases, suspected cases, and recovered cases across 31 Provinces/States in China. Due to the complexities of the COVID-19, we investigated the unobserved factors including environmental exposures accounting for the spread of the disease through human-to-human transmission. We used estimation methods capable of controlling for cross-sectional dependence, endogeneity, and unobserved heterogeneity. We predicted the impulse-response between confirmed cases of COVID-19 and COVID-19-attributable deaths. Our study revealed that the effect of confirmed cases on the novel coronavirus attributable deaths is heterogeneous across Provinces/States in China. We found a linear relationship between COVID-19 attributable deaths and confirmed cases whereas a nonlinear relationship was confirmed for the nexus between recovery cases and confirmed cases. The empirical evidence revealed that an increase in confirmed cases by 1% increases coronavirus attributable deaths by \( \approx 0.10\%\)–\(\approx 1.71\%\) (95% CI). Our empirical results confirmed the presence of unobserved heterogeneity and common factors that facilitates the novel coronavirus attributable deaths caused by increased levels of confirmed cases. Yet, the role of such a medium that facilitates the transmission of COVID-19 remains unclear. We highlight safety precaution and preventive measures to circumvent the human-to-human transmission. © 2020 The Author(s)

Lenzer, J.  
Covid-19: US gives emergency approval to hydroxychloroquine despite lack of evidence  
(2020) BMJ (Clinical research ed.), 369, p. m1335.

Tanne, J.H.  
Covid-19: New York City deaths pass 1000 as Trump tells Americans to distance for 30 days  
(2020) BMJ (Clinical research ed.), 369, p. m1333.

Iacobucci, G.  
Covid-19: UK deaths are higher than previously reported, new data suggest  
(2020) BMJ (Clinical research ed.), 369, p. m1330.

Mahase, E.  
Covid-19: Use radiotherapy only if "unavoidable," says NICE  
(2020) BMJ (Clinical research ed.), 369, p. m1338.

Iacobucci, G.  
Covid-19: Hospitals can remove 15% cap on testing of NHS staff  
(2020) BMJ (Clinical research ed.), 369, p. m1339.
Shim, E., Tariq, A., Choi, W., Lee, Y., Chowell, G.

**Transmission potential and severity of COVID-19 in South Korea**

**Abstract:**
Objectives: Since the first case of 2019 novel coronavirus (COVID-19) identified on Jan 20, 2020, in South Korea, the number of cases rapidly increased, resulting in 6284 cases including 42 deaths as of Mar 6, 2020. To examine the growth rate of the outbreak, we present the first study to report the reproduction number of COVID-19 in South Korea. Methods: The daily confirmed cases of COVID-19 in South Korea were extracted from publicly available sources. By using the empirical reporting delay distribution and simulating the generalized growth model, we estimated the effective reproduction number based on the discretized probability distribution of the generation interval. Results: We identified four major clusters and estimated the reproduction number at 1.5 (95% CI: 1.4–1.6). In addition, the intrinsic growth rate was estimated at 0.6 (95% CI: 0.6, 0.7), and the scaling of growth parameter was estimated at 0.8 (95% CI: 0.7, 0.8), indicating sub-exponential growth dynamics of COVID-19. The crude case fatality rate is higher among males (1.1%) compared to females (0.4%) and increases with older age. Conclusions: Our results indicate an early sustained transmission of COVID-19 in South Korea and support the implementation of social distancing measures to rapidly control the outbreak. © 2020 The Author(s)


**Proposal of a low-dose, long-pitch, dual-source chest CT protocol on third-generation dual-source CT using a tin filter for spectral shaping at 100 kVp for CoronaVirus Disease 2019 (COVID-19) patients: a feasibility study**

**Abstract:**
Aim: To subjectively and objectively evaluate the feasibility and diagnostic reliability of a low-dose, long-pitch dual-source chest CT protocol on third-generation dual-source CT (DSCT) with spectral shaping at 100Sn kVp for COVID-19 patients. Materials and methods: Patients with COVID-19 and positive swab-test undergoing to a chest CT on third-generation DSCT were included. The imaging protocol included a dual-energy acquisition (HD-DECT, 90/150Sn kVp) and fast, low-dose, long-pitch CT, dual-source scan at 100Sn kVp (LDCT). Subjective (Likert Scales) and objective (signal-to-noise and contrast-to-noise ratios, SNR and CNR) analyses were performed; radiation dose and acquisition times were recorded. Nonparametric tests were used. Results: The median radiation dose was lower for LDCT than HD-DECT (Effective dose, ED: 0.28 mSv vs. 3.28 mSv, p = 0.016). LDCT had median acquisition time of 0.62 s (vs 2.02 s, p = 0.016). SNR and CNR were significantly different in several thoracic structures between HD-DECT and LDCT, with exception of lung parenchyma. Qualitative analysis demonstrated significant reduction in motion artifacts (p = 0.031) with comparable diagnostic reliability between HD-DECT and LDCT. Conclusions: Ultra-low-dose, dual-source, fast CT protocol provides highly diagnostic images for COVID-19 with potential for reduction in dose and motion artifacts. © 2020, Italian Society of Medical Radiology.

Hua, J., Shaw, R.

**Corona virus (Covid-19) “infodemic” and emerging issues through a data lens: The case of china**
(2020) International Journal of Environmental Research and Public Health, 17 (7), art. no. 2309

**Abstract:**
Coronavirus (COVID-19) is a humanitarian emergency, which started in Wuhan in China in early December 2019, brought into the notice of the authorities in late December, early January 2020, and, after investigation, was declared as an emergency in the third week of January 2020. The WHO declared this as Public Health Emergency of International Concern (PHEIC) on 31th of January 2020, and finally a pandemic on 11th March 2020. As of March 24th, 2020, the virus has caused a casualty of over 16,600 people worldwide with more than 380,000 people confirmed as infected by it, of which more than 10,000 cases are serious. Mainly based on Chinese newspapers, social media and other digital platform data, this paper analyzes the timeline of the key actions taken by the government and people over three months in five different phases. It found that although there was an initial delay in responding, a unique combination of strong governance, strict regulation, strong community vigilance and citizen participation, and wise use of big data and digital technologies, were some of the key factors in China’s efforts to combat this virus. Being inviable and non-measurable (unlike radioactive exposure), appropriate and timely information is very important to form the basic foundation of mitigation and curative measures. Infodemic, as it is termed by WHO, is a key word, where different stakeholder’s participation, along with stricter regulation, is required to reduce the impact of fake news in this information age and social media. Although different countries will need different approaches, focusing on its humanitarian nature and addressing infodemic issues are the two critical factors for future global mitigation efforts. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Kim, H.J., Ko, J.S., Kim, T.-Y.
Recommendations for anesthesia in patients suspected of COVID-19 Coronavirus infection

Khurshid, Z., Asiri, F.Y.I., Al Wadaani, H.
Human saliva: Non-invasive fluid for detecting novel coronavirus (2019-nCoV)
(2020) International Journal of Environmental Research and Public Health, 17 (7), art. no. 2225
Abstract:
The breakthrough of novel coronavirus (2019-nCoV) in Wuhan, a city of China, has damaged the status of health and quality of life. In the sequel of this epidemic or contagious disease, the patient experiences fever, chest paint, chills, a rapid heartbeat, breathing difficulties, pneumonia, and kidney failure. It has been suggested that this disease can spread through human-to-human transmission or by super spreading. By the help of the non-invasive fluid “saliva”, it is easy to detect the virus. This can help with the comfort of the patient as well as healthcare personnel. Under this perspective, we discuss the epidemic situation of 2019-nCOV and its relationship with human saliva. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

As We Went to Press: COVID-19 Continues to Spread
Abstract:
Updates on the coronavirus.

The outbreak of Coronavirus Disease 2019 (COVID-19)—An emerging global health threat
Abstract:
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.

Chen, D., Xu, W., Lei, Z., Huang, Z., Liu, J., Gao, Z., Peng, L.
**Recurrence of positive SARS-CoV-2 RNA in COVID-19: A case report**

**Abstract:**
The ongoing outbreak of COVID-19 that began in Wuhan, China, has constituted a Public Health Emergency of International Concern, with cases confirmed in multiple countries. Currently, patients are the primary source of infection. We report a confirmed case of COVID-19 whose oropharyngeal swab test of SARS-CoV-2 RNA turned positive in convalescence. This case highlights the importance of active surveillance of SARS-CoV-2 RNA for infectivity assessment. © 2020 The Author(s)

Yang, R., Gui, X., Xiong, Y.
**Patients with respiratory symptoms are at greater risk of COVID-19 transmission**
(2020) Respiratory Medicine, 165, art. no. 105935

Lin, Q., Zhao, S., Gao, D., Lou, Y., Yang, S., Musa, S.S., Wang, M.H., Cai, Y., Wang, W., Yang, L., He, D.
**A conceptual model for the coronavirus disease 2019 (COVID-19) outbreak in Wuhan, China with individual reaction and governmental action**

**Abstract:**
The ongoing coronavirus disease 2019 (COVID-19) outbreak, emerged in Wuhan, China in the end of 2019, has claimed more than 2600 lives as of 24 February 2020 and posed a huge threat to global public health. The Chinese government has implemented control measures including setting up special hospitals and travel restriction to mitigate the spread. We propose conceptual models for the COVID-19 outbreak in Wuhan with the consideration of individual behavioural reaction and governmental actions, e.g., holiday extension, travel restriction, hospitalisation and quarantine. We employ the estimates of these two key components from the 1918 influenza pandemic in London, United Kingdom, incorporated zoonotic introductions and the emigration, and then compute future trends and the reporting ratio. The model is concise in structure, and it successfully captures the course of the COVID-19 outbreak, and thus sheds light on understanding the trends of the outbreak. © 2020

Robson, B.
Computers and viral diseases. Preliminary bioinformatics studies on the design of a **synthetic vaccine and a preventative peptidomimetic antagonist against the SARS-CoV-2 (2019-nCoV, COVID-19) coronavirus**
Abstract:
This paper concerns study of the genome of the Wuhan Seafood Market isolate believed to represent the causative agent of the disease COVID-19. This is to find a short section or sections of viral protein sequence suitable for preliminary design proposal for a peptide synthetic vaccine and a peptidomimetic therapeutic, and to explore some design possibilities. The project was originally directed towards a use case for the Q-UEL language and its implementation in a knowledge management and automated inference system for medicine called the BioIngine, but focus here remains mostly on the virus itself. However, using Q-UEL systems to access relevant and emerging literature, and to interact with standard publically available bioinformatics tools on the Internet, did help quickly identify sequences of amino acids that are well conserved across many coronaviruses including 2019-nCoV. KRSFIEDDLLFNKV was found to be particularly well conserved in this study and corresponds to the region around one of the known cleavage sites of the SARS virus that are believed to be required for virus activation for cell entry. This sequence motif and surrounding variations formed the basis for proposing a specific synthetic vaccine epitope and peptidomimetic agent. The work can, nonetheless, be described in traditional bioinformatics terms, and readily reproduced by others, albeit with the caveat that new data and research into 2019-nCoV is emerging and evolving at an explosive pace. Preliminary studies using molecular modeling and docking, and in that context the potential value of certain known herbal extracts, are also described.

Zhang, Y., Ma, Z.F.
Impact of the COVID-19 Pandemic on Mental Health and Quality of Life among Local Residents in Liaoning Province, China: A Cross-Sectional Study
(2020) International journal of environmental research and public health, 17 (7)
Abstract:
Our study aimed to investigate the immediate impact of the COVID-19 pandemic on mental health and quality of life among local Chinese residents aged ≥18 years in Liaoning Province, mainland China. An online survey was distributed through a social media platform between January and February 2020. Participants completed a modified validated questionnaire that assessed the Impact of Event Scale (IES), indicators of negative mental health impacts, social and family support, and mental health-related lifestyle changes. A total of 263 participants (106 males and 157 females) completed the study. The mean age of the participants was 37.7 ± 14.0 years, and 74.9% had a high level of education. The mean IES score in the participants was 13.6 ± 7.7, reflecting a mild stressful impact. Only 7.6% of participants had an IES score ≥26. The majority of participants (53.3%) did not feel helpless due to the pandemic. On the other hand, 52.1% of participants felt horrified and apprehensive due to the pandemic. Additionally, the majority of participants (57.8-77.9%) received increased support from friends and family members, increased shared feeling and caring with family members and others. In conclusion, the COVID-19 pandemic was associated with mild stressful impact in our sample, even though the COVID-19 pandemic is still ongoing. These findings would need to be verified in larger population studies.

Qin, L., Sun, Q., Wang, Y., Wu, K.-F., Chen, M., Shia, B.-C., Wu, S.-Y.
Prediction of Number of Cases of 2019 Novel Coronavirus (COVID-19) Using Social Media Search Index
(2020) International journal of environmental research and public health, 17 (7)
Abstract:
Predicting the number of new suspected or confirmed cases of novel coronavirus disease 2019 (COVID-19) is crucial in the prevention and control of the COVID-19 outbreak. Social media search
indexes (SMSI) for dry cough, fever, chest distress, coronavirus, and pneumonia were collected from 31 December 2019 to 9 February 2020. The new suspected cases of COVID-19 data were collected from 20 January 2020 to 9 February 2020. We used the lagged series of SMSI to predict new suspected COVID-19 case numbers during this period. To avoid overfitting, five methods, namely subset selection, forward selection, lasso regression, ridge regression, and elastic net, were used to estimate coefficients. We selected the optimal method to predict new suspected COVID-19 case numbers from 20 January 2020 to 9 February 2020. We further validated the optimal method for new confirmed cases of COVID-19 from 31 December 2019 to 17 February 2020. The new suspected COVID-19 case numbers correlated significantly with the lagged series of SMSI. SMSI could be detected 6-9 days earlier than new suspected cases of COVID-19. The optimal method was the subset selection method, which had the lowest estimation error and a moderate number of predictors. The subset selection method also significantly correlated with the new confirmed COVID-19 cases after validation. SMSI findings on lag day 10 were significantly correlated with new confirmed COVID-19 cases. SMSI could be a significant predictor of the number of COVID-19 infections. SMSI could be an effective early predictor, which would enable governments' health departments to locate potential and high-risk outbreak areas.

Corruble, E.
**A Viewpoint From Paris on the COVID-19 Pandemic: A Necessary Turn to Telepsychiatry**
(2020) The Journal of clinical psychiatry, 81 (3)

Iacobucci, G.
**Covid-19: Doctors still at "considerable risk" from lack of PPE, BMA warns**
(2020) BMJ (Clinical research ed.), 368, p. m1316.

Fagiolini, A., Cuomo, A., Frank, E.
**COVID-19 Diary From a Psychiatry Department in Italy**
(2020) The Journal of clinical psychiatry, 81 (3)

Iacobucci, G.
**Covid-19: healthcare staff in hotspot areas are prioritised as testing expands**
(2020) BMJ (Clinical research ed.), 368, p. m1318.

**Urgent need for individual mobile phone and institutional reporting of at home, hospitalized, and intensive care unit cases of SARS-CoV-2 (COVID-19) infection**

**Abstract:**
Approximately 90 days of the SARS-CoV-2 (COVID-19) spreading originally from Wuhan, China, and across the globe has led to a widespread chain of events with imminent threats to the fragile relationship between community health and economic health. Despite near hourly reporting on this crisis, there has been no regular, updated, or accurate reporting of hospitalizations for COVID-19. It is known that many test-positive individuals may not develop symptoms or have a mild self-limited viral syndrome consisting of fever, malaise, dry cough, and constitutional symptoms.
However some individuals develop a more fulminant syndrome including viral pneumonia, respiratory failure requiring oxygen, acute respiratory distress syndrome requiring mechanical ventilation, and in substantial fractions leading to death attributable to COVID-19. The pandemic is evolving in a clustered, non-inform fashion resulting in many hospitals with preparedness but few or no cases, and others that are completely overwhelmed. Thus, a considerable risk of spread when personal protection equipment becomes exhausted and a large fraction of mortality in those not offered mechanical ventilation are both attributable to a crisis due to maldistribution of resources. The pandemic is amenable to self-reporting through a mobile phone application that could obtain critical information on suspected cases and report on the results of self testing and actions taken. The only method to understand the clustering and the immediate hospital resource needs is mandatory, uniform, daily reporting of hospital censuses of COVID-19 cases admitted to hospital wards and intensive care units. Current reports of hospitalizations are delayed, uncertain, and wholly inadequate. This paper urges all the relevant stakeholders to take up self-reporting and reporting of hospitalizations of COVID-19 as an urgent task in combating this devastating pandemic. © 2020 McCullough et al. Published by IMR press.

Mahase, E.
**Covid-19: Mercedes F1 to provide breathing aid as alternative to ventilator** (2020) BMJ (Clinical research ed.), 368, p. m1294.

Tanne, J.H.
**Covid-19: Trump extends physical distancing to 30 April, as cases climb in New York** (2020) BMJ (Clinical research ed.), 368, p. m1289.

**Cancer care during the spread of coronavirus disease 2019 (COVID-19) in Italy: Young oncologists' perspective** (2020) ESMO Open, 5 (2), art. no. e000759

Mahase, E., Kmietowicz, Z.
**Covid-19: Doctors are told not to perform CPR on patients in cardiac arrest** (2020) BMJ (Clinical research ed.), 368, p. m1282.

**In other Covid-19 news**

Daniels, J.P.

Córdova-Lepe, F., Gutiérrez-Aguilar, R., Gutiérrez-Jara, J.P.
**Number of COVID-19 cases in Chile at 120 days with data at 21/03/2020 and threshold of daily effort to flatten the epi-curve [Número de casos COVID-19 en Chile a 120 días con datos al 21/03/2020 y umbral del esfuerzo diario para aplanar la epi-curva]**
Abstract:
We present a straightforward projection with data up to 21/03/2020 of the evolution of the number of COVID-19 cases per day in Chile using data from the Ministry of Health. Assuming an arithmetical growth in the second variation of the data, we present a cubic adjustment model in which we estimate over 100 000 cases at 120 days consistent with the data recorded to date. Furthermore, we use an exponential total case model to represent (using a parameter) the daily effort to reduce a high initial daily growth rate. We simulate this model with different numerical scenarios of feasibility and desired future prevalence.

Realizamos una prospectiva básica, con datos al 21/03/2020 de la evolución del número de casos COVID-19 diarios en Chile con datos del Ministerio de Salud. Asumiendo un crecimiento aritmético en la segunda variación de los datos, se presenta un modelo de ajuste cúbico que estima en más de 100 mil casos a 120 días y que es consistente con los datos registrados a la fecha. Además, se interviene un modelo de casos totales exponencial, para representar en él (mediante un parámetro) el esfuerzo diario por rebajar una elevada primera tasa de crecimiento diario. Este modelo se simula con distinto escenarios numéricos de factibilidad y prevalencia futura deseada.

Tolia, V.M., Chan, T.C., Castillo, E.M.
Preliminary Results of Initial Testing for Coronavirus (COVID-19) in the Emergency Department
(2020) The western journal of emergency medicine, 21 (3)

Abstract:
INTRODUCTION: On March 10, 2020, the World Health Organization declared a global pandemic due to widespread infection of the novel coronavirus 2019 (COVID-19). We report the preliminary results of a targeted program of COVID-19 infection testing in the ED in the first 10 days of its initiation at our institution. METHODS: We conducted a review of prospectively collected data on all ED patients who had targeted testing for acute COVID-19 infection at two EDs during the initial 10 days of testing (March 10-19, 2020). During this initial period with limited resources, testing was targeted toward high-risk patients per Centers for Disease Control and Prevention guidelines. Data collected from patients who were tested included demographics, clinical characteristics, and test qualifying criteria. We present the data overall and by test results with descriptive statistics. RESULTS: During the 10-day study period, the combined census of the study EDs was 2157 patient encounters. A total of 283 tests were ordered in the ED. The majority of patients were 18-64 years of age, male, non-Hispanic white, had an Emergency Severity Index score of three, did not have a fever, and were discharged from the ED. A total of 29 (10.2%) tested positive. Symptoms-based criteria most associated with COVID-19 were the most common criteria identified for testing (90.6%). All other criteria were reported in 5.51-43.0% of persons being tested. Having contact with a person under investigation was significantly more common in those who tested positive compared to those who tested negative (63% vs 24.5%, respectively). The majority of patients in both results groups had at least two qualifying criteria for testing (75.2%). CONCLUSION: In this review of prospectively collected data on all ED patients who had targeted testing for acute COVID-19 infection at two EDs in the first 10 days of testing, we found that 10.2% of those tested were identified as positive. The continued monitoring of testing and results will help providers understand how COVID-19 is progressing in the community.

Iacobucci, G.
Covid-19: "Illogical" lack of testing is causing healthy staff to self-isolate, BMA chief warns
Iacobucci, G.  
**Covid-19: diabetes clinicians set up social media account to help alleviate patients' fears**  
(2020) BMJ (Clinical research ed.), 368, p. m1262.

Mayor, S.  
**Covid-19: Researchers launch app to track spread of symptoms in the UK**  
(2020) BMJ (Clinical research ed.), 368, p. m1263.

Paterlini, M.  
**Covid-19: Over 300 Italian doctors and scientists call for more testing**  
(2020) BMJ (Clinical research ed.), 368, p. m1274.

Harvey, A.  
**Covid-19: medical students and FY1 doctors to be given early registration to help combat covid-19**  
(2020) BMJ (Clinical research ed.), 368, p. m1268.

Dyer, O.  
**Covid-19: hospitals brace for disaster as US surpasses China in number of cases**  
(2020) BMJ (Clinical research ed.), 368, p. m1278.

Iacobucci, G.  
**Covid-19: Lack of PPE in care homes is risking spread of virus, leaders warn**  
(2020) BMJ (Clinical research ed.), 368, p. m1280.

O'Dowd, A.  
**Guidance needed for singlehanded GPs to deal with covid-19 pandemic**  
(2020) BMJ (Clinical research ed.), 368, p. m1261.

**Public Health Responses to COVID-19 Outbreaks on Cruise Ships - Worldwide, February-March 2020**  
**Abstract:**  
An estimated 30 million passengers are transported on 272 cruise ships worldwide each year* (1). Cruise ships bring diverse populations into proximity for many days, facilitating transmission of respiratory illness (2). SARS-CoV-2, the virus that causes coronavirus disease (COVID-19) was...
first identified in Wuhan, China, in December 2019 and has since spread worldwide to at least 187 countries and territories. Widespread COVID-19 transmission on cruise ships has been reported as well (3). Passengers on certain cruise ship voyages might be aged ≥65 years, which places them at greater risk for severe consequences of SARS-CoV-2 infection (4). During February-March 2020, COVID-19 outbreaks associated with three cruise ship voyages have caused more than 800 laboratory-confirmed cases among passengers and crew, including 10 deaths. Transmission occurred across multiple voyages of several ships. This report describes public health responses to COVID-19 outbreaks on these ships. COVID-19 on cruise ships poses a risk for rapid spread of disease, causing outbreaks in a vulnerable population, and aggressive efforts are required to contain spread. All persons should defer all cruise travel worldwide during the COVID-19 pandemic.

Vince, G.
**The world's largest refugee camp prepares for covid-19**
(2020) BMJ (Clinical research ed.), 368, p. m1205.

Harvey, A.
**Covid-19: medical schools given powers to graduate final year students early to help NHS**
(2020) BMJ (Clinical research ed.), 368, p. m1227.

Kamerow, D.
**Covid-19: Don't forget the impact on US family physicians**
(2020) BMJ (Clinical research ed.), 368, p. m1260.

Pulla, P.
**Covid-19: India imposes lockdown for 21 days and cases rise**
(2020) BMJ (Clinical research ed.), 368, p. m1251.

Iacobucci, G.
**Covid-19: What is the UK's testing strategy?**
(2020) BMJ (Clinical research ed.), 368, p. m1222.

Greenberg, N., Docherty, M., Gnanapragasam, S., Wessely, S.
**Managing mental health challenges faced by healthcare workers during covid-19 pandemic**
(2020) BMJ (Clinical research ed.), 368, p. m1211.

Mahase, E.
**Covid-19: Gilead withdraws orphan drug designation from potential treatment after criticism**
(2020) BMJ (Clinical research ed.), 368, p. m1259.

Mahase, E.
**Covid-19: what treatments are being investigated?**
(2020) BMJ (Clinical research ed.), 368, p. m1252.

Tanne, J.H.
Covid-19: FDA approves use of convalescent plasma to treat critically ill patients
(2020) BMJ (Clinical research ed.), 368, p. m1256.

Extance, A.
Covid-19 and long term conditions: what if you have cancer, diabetes, or chronic kidney disease?
(2020) BMJ (Clinical research ed.), 368, p. m1174.

Dyer, O.
Covid-19: Trump declares intention to "re-open economy" within weeks against experts' advice
(2020) BMJ (Clinical research ed.), 368, p. m1217.

Sayburn, A.
Covid-19: experts question analysis suggesting half UK population has been infected
(2020) BMJ (Clinical research ed.), 368, p. m1216.

Iacobucci, G.
Covid-19: doctors are given new guidelines on when to admit patients to critical care
(2020) BMJ (Clinical research ed.), 368, p. m1189.

Harvey, A.
Covid-19: medical students should not work outside their competency, says BMA
(2020) BMJ (Clinical research ed.), 368, p. m1197.

Thornton, J.
Don't forget chronic lung and immune conditions during covid-19, says WHO
(2020) BMJ (Clinical research ed.), 368, p. m1192.

Mahase, E.
Covid-19: most patients require mechanical ventilation in first 24 hours of critical care
(2020) BMJ (Clinical research ed.), 368, p. m1201.

Sayburn, A.
Covid-19: trials of four potential treatments to generate "robust data" of what works
(2020) BMJ (Clinical research ed.), 368, p. m1206.

Iacobucci, G.
Covid-19: UK lockdown is "crucial" to saving lives, say doctors and scientists
(2020) BMJ (Clinical research ed.), 368, p. m1204.
Thornton, J.
**Clinical trials suspended in UK to prioritise covid-19 studies and free up staff**
(2020) BMJ (Clinical research ed.), 368, p. m1172.

Day, M.
**Covid-19: identifying and isolating asymptomatic people helped eliminate virus in Italian village**
(2020) BMJ (Clinical research ed.), 368, p. m1165.

Rimmer, A.
**Covid-19: doctors in final trimester of pregnancy should avoid direct patient contact**
(2020) BMJ (Clinical research ed.), 368, p. m1173.

Nickel Christian, H., Bingisser, R.
**Mimics and chameleons of COVID-19**
(2020) Swiss Medical Weekly, 150 (13-14), art. no. 20231

Mahase, E.
**Covid-19: six million doses of hydroxychloroquine donated to US despite lack of evidence**
(2020) BMJ (Clinical research ed.), 368, p. m1166.

Swiss Society Of Intensive Care Medicine
**Recommendations for the admission of patients with COVID-19 to intensive care and intermediate care units (ICUs and IMCUs)**
(2020) Swiss medical weekly, 150, p. w20227.

Dyer, O.
**Covid-19: US testing ramps up as early response draws harsh criticism**
(2020) BMJ (Clinical research ed.), 368, p. m1167.

Kmietowicz, Z.
**Covid-19: Highest risk patients are asked to stay at home for 12 weeks**
(2020) BMJ (Clinical research ed.), 368, p. m1170.

Swiss Academy Of Medical Sciences
**COVID-19 pandemic: triage for intensive-care treatment under resource scarcity**
(2020) Swiss medical weekly, 150, p. w20229.

Day, M.
**Covid-19: European drugs agency to review safety of ibuprofen**
(2020) BMJ (Clinical research ed.), 368, p. m1168.
Rimmer, A.
Covid-19: give NHS staff rest spaces and free parking not thank yous, says doctor
(2020) BMJ (Clinical research ed.), 368, p. m1171.

Roland, K., Markus, M.
COVID-19 pandemic: Palliative care for elderly and frail patients at home and in residential and nursing homes
(2020) Swiss Medical Weekly, 150 (13-14), art. no. 20235

Rimmer, A.
Sixty seconds on . . . covid kindness
(2020) BMJ (Clinical research ed.), 368, p. m1169.

Borasio, G.D., Gamondi, C., Obrist, M., Jox, R., For The Covid-Task Force Of Palliative Ch
COVID-19: decision making and palliative care
(2020) Swiss medical weekly, 150, p. w20233.
Abstract:
Due to the current development around the COVID-19 pandemic, palliative ch has created a Task Force to provide recommendations for health professionals on the treatment of palliative care patients in the various settings – inpatient and outpatient.

Coombes, R.
Covid-19: experts question the evidence behind closing London Underground and city metros during the pandemic
(2020) BMJ (Clinical research ed.), 368, p. m1154.

Tanne, J.H.
Covid-19: cases grow in US as Trump pushes promise of a malaria drug
(2020) BMJ (Clinical research ed.), 368, p. m1155.

Dyer, C.
Covid-19: 15 000 deregistered doctors are told, "Your NHS needs you"
(2020) BMJ (Clinical research ed.), 368, p. m1152.

Tolksdorf, K., Buda, S., Schuler, E., Wieler, L.H., Haas, W.
Influenza-associated pneumonia as reference to assess seriousness of coronavirus disease (COVID-19)
(2020) Eurosurveillance, 25 (11), art. no. 2000258
Abstract:
Information on severity of coronavirus disease (COVID-19) (transmissibility, disease seriousness, impact) is crucial for preparation of healthcare sectors. We present a simple approach to assess disease seriousness, creating a reference cohort of pneumonia patients from sentinel hospitals. First comparisons exposed a higher rate of COVID-19 patients requiring ventilation. There were more case fatalities among COVID-19 patients without comorbidities than in the reference cohort.
Hospitals should prepare for high utilisation of ventilation and intensive care resources. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Nicastri, E., D’Abramo, A., Faggioni, G., (...), Lista, F., Ippolito, G.  
Coronavirus disease (COVID-19) in a paucisymptomatic patient: Epidemiological and clinical challenge in settings with limited community transmission, Italy, February 2020  
(2020) Eurosurveillance, 25 (11), art. no. 2000230  
Abstract:  
Data concerning the transmission of the novel severe acute respiratory syndrome coronavirus (SARS-CoV-2) in paucisymptomatic patients are lacking. We report an Italian paucisymptomatic case of coronavirus disease 2019 with multiple biological samples positive for SARS-CoV-2. This case was detected using the World Health Organization protocol on cases and contact investigation. Current discharge criteria and the impact of extra-pulmonary SARS-CoV-2 samples are discussed. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

COVID-19 epidemic in Switzerland: On the importance of testing, contact tracing and isolation  
(2020) Swiss Medical Weekly, 150 (11-12), art. no. e20225  
Abstract:  
Switzerland is among the countries with the highest number of coronavirus disease-2019 (COVID-19) cases per capita in the world. There are likely many people with undetected SARS-CoV-2 infection because testing efforts are currently not detecting all infected people, including some with clinical disease compatible with COVID-19. Testing on its own will not stop the spread of SARS-CoV-2. Testing is part of a strategy. The World Health Organization recommends a combination of measures: rapid diagnosis and immediate isolation of cases, rigorous tracking and precautionary self-isolation of close contacts. In this article, we explain why the testing strategy in Switzerland should be strengthened urgently, as a core component of a combination approach to control COVID-19. © 2020 EMH Swiss Medical Publishers Ltd.. All rights reserved.

Mahase, E.  
Covid-19: schools set to close across UK except for children of health and social care workers  
(2020) BMJ (Clinical research ed.), 368, p. m1140.

Iacobucci, G.  
Covid-19: UK government calls on industry to help boost testing capacity to 25 000 people a day  
(2020) BMJ (Clinical research ed.), 368, p. m1118.

Rimmer, A.  
Covid-19: pregnant doctors should speak to occupational health, say experts  
(2020) BMJ (Clinical research ed.), 368, p. m1104.

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Covid-19: Trump sought to buy vaccine developer exclusively for US, say German officials
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Covid-19: Doctors warn of humanitarian catastrophe at Europe's largest refugee camp
(2020) BMJ (Clinical research ed.), 368, p. m1097.

Rimmer, A.
Covid-19: trainees will not move jobs in April
(2020) BMJ (Clinical research ed.), 368, p. m1088.

Rimmer, A.
Covid-19: BMA calls for rapid testing and appropriate protective equipment for doctors
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Covid-19: UK starts social distancing after new model points to 260 000 potential deaths
(2020) BMJ (Clinical research ed.), 368, p. m1089.

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Covid-19: medical schools are urged to fast-track final year students
(2020) BMJ (Clinical research ed.), 368, p. m1064.

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Covid-19: junior doctor calls on colleagues to gather supplies for staff working long hours
(2020) BMJ (Clinical research ed.), 368, p. m1072.

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Keeping the Fire House Running: A Proposed Approach to Mitigate Spread of COVID-19 Among Public Safety Personnel
(2020) The western journal of emergency medicine, 21 (3)

Quantifying the association between domestic travel and the exportation of novel coronavirus (2019-nCoV) cases from Wuhan, China in 2020: a correlational analysis
(2020) Journal of travel medicine, 27 (2)

Rimmer, A.
Trainees and covid-19: your questions answered
Mahase, E.  
**Covid-19: UK holds off closing schools and restricts testing to people in hospital**  
(2020) BMJ (Clinical research ed.), 368, p. m1060.

Rimmer, A.  
**Covid-19: Medical conferences around the world are cancelled after US cases are linked to Massachusetts meeting**  
(2020) BMJ (Clinical research ed.), 368, p. m1054.

Rimmer, A.  
**Covid-19: GPs call for same personal protective equipment as hospital doctors**  
(2020) BMJ (Clinical research ed.), 368, p. m1055.

Trilla, A.  
**One world, one health: The novel coronavirus COVID-19 epidemic [Un mundo, una salud: la epidemia por el nuevo coronavirus COVID-19]**  

Mahase, E.  
**Covid-19: WHO declares pandemic because of "alarming levels" of spread, severity, and inaction**  
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**Covid-19: GPs call for appraisals and CQC inspections to be suspended**  
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**Covid-19: Trump cancels all flights from Europe, apart from the UK**  
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**Covid-19: UK budget gives £94 a week statutory sick pay to self-isolators and their carers**  
(2020) BMJ (Clinical research ed.), 368, p. m1001.

Dyer, O.  
**Covid-19: China's president Xi visits Wuhan amid confidence that virus is under control**  
(2020) BMJ (Clinical research ed.), 368, p. m995.

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**Covid-19: Trump proposes tax cuts and improved health insurance, but millions are not covered**
Iacobucci, G.  
**Covid-19: roundup of latest news**  
(2020) BMJ (Clinical research ed.), 368, p. m969.

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**Covid-19: UK trade talks with EU must not hinder cooperation in tackling threat, BMA warns**  
(2020) BMJ (Clinical research ed.), 368, p. m988.

Mahase, E.  
**Covid-19: out-of-hours providers are drafted in to manage non-urgent patients in community**  
(2020) BMJ (Clinical research ed.), 368, p. m959.

Iacobucci, G.  
Covid-19: emergency departments lack proper isolation facilities, senior medic warns  
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Glauser, W.  
Proposed protocol to keep COVID-19 out of hospitals  

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**Covid-19: UK records first death, as world's cases exceed 100 000**  
(2020) BMJ (Clinical research ed.), 368, p. m943.

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**Trump claims public health warnings on covid-19 are a conspiracy against him**  
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Iacobucci, G.  
**Covid-19: GP surgeries close for two weeks after staff test positive**  
(2020) BMJ (Clinical research ed.), 368, p. m936.

Mahase, E.  
**Covid-19: 90% of cases will hit NHS over nine week period, chief medical officer warns**  
(2020) BMJ (Clinical research ed.), 368, p. m918.

Mahase, E.  
**Covid-19: hoarding and misuse of protective gear is jeopardising the response, WHO warns**  
(2020) BMJ (Clinical research ed.), 368, p. m869.
Li, S., Wang, Y., Xue, J., Zhao, N., Zhu, T.
The impact of covid-19 epidemic declaration on psychological consequences: A study on active weibo users
(2020) International Journal of Environmental Research and Public Health, 17 (6), art. no. 2032
Abstract:
COVID-19 (Corona Virus Disease 2019) has significantly resulted in a large number of psychological consequences. The aim of this study is to explore the impacts of COVID-19 on people’s mental health, to assist policy makers to develop actionable policies, and help clinical practitioners (e.g., social workers, psychiatrists, and psychologists) provide timely services to affected populations. We sample and analyze the Weibo posts from 17,865 active Weibo users using the approach of Online Ecological Recognition (OER) based on several machine-learning predictive models. We calculated word frequency, scores of emotional indicators (e.g., anxiety, depression, indignation, and Oxford happiness) and cognitive indicators (e.g., social risk judgment and life satisfaction) from the collected data. The sentiment analysis and the paired sample t-test were performed to examine the differences in the same group before and after the declaration of COVID-19 on 20 January, 2020. The results showed that negative emotions (e.g., anxiety, depression and indignation) and sensitivity to social risks increased, while the scores of positive emotions (e.g., Oxford happiness) and life satisfaction decreased. People were concerned more about their health and family, while less about leisure and friends. The results contribute to the knowledge gaps of short-term individual changes in psychological conditions after the outbreak. It may provide references for policy makers to plan and fight against COVID-19 effectively by improving stability of popular feelings and urgently prepare clinical practitioners to deliver corresponding therapy foundations for the risk groups and affected people. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Mahase, E.
Covid-19: retired doctors could be asked to return to work, says Hancock
(2020) BMJ (Clinical research ed.), 368, p. m831.

Dyer, O.
Covid-19: US health department staff sent to meet citizens returning from China weren’t protected, claims whistleblower
(2020) BMJ (Clinical research ed.), 368, p. m833.

Yu, S., Wang, J., Shen, H.
Network pharmacology-based analysis of the role of traditional Chinese herbal medicines in the treatment of COVID-19
Abstract:
Background: The novel coronavirus named COVID-19, which originated in Wuhan, China, has spread to many countries around the world. Currently, no effective medical treatment exists to combat this disease. Traditional Chinese herbal medicines (CHM) have unique roles in the treatment of viral infections. In this article we analyzed the effectiveness and possible molecular mechanisms of CHM formulas for the prevention of COVID-19. Methods: The active ingredients and action
targets of CHM formulas were obtained from the TCMSP database. Genes related to severe acute respiratory syndromes (SARS) and Middle East respiratory syndrome (MERS) were queried on the GeneCards database. The action mechanisms of these genes were predicted using a Gene Ontology (GO)-based functional enrichment and annotation tool and the Kyoto Encyclopedia of Genes and Genomes (KEGG). Results: CHM formulas played a positive role in preventing COVID-19 and warrant further application. Conclusions: Our research provides new evidence to support the possible value of CHM formulas for the prevention of COVID-19. However, further clinical studies with large sample sizes are required to verify their effectiveness. © 2020, Annals of Palliative Medicine.

MacKenzie, J.S., Smith, D.W.
COVID-19: A novel zoonotic disease caused by a coronavirus from China: What we know and what we don't
Abstract:
At the end of December, 2019, a new disease of unknown aetiology appeared in Wuhan, China. It was quickly identified as an novel betacoronavirus, and related to SARS-CoV and a number of other bat-borne SARS-like coronaviruses. The virus rapidly spread to all provinces in China, as well as a number of countries overseas, and was declared a Public Health Emergency of International Concern by the Director General of the World Health Organization on 30 January 2020. This paper describes the evolution of the outbreak, and the known properties of the novel virus, SARS-CoV-2 and the clinical disease it causes, COVID-19, and comments on some of the important gaps in our knowledge of the virus and the disease it causes. The virus is the third zoonotic coronavirus, after SARS-CoV and MERS-CoV, but appears to be the only one with pandemic potential. © 2020 CSIRO. All rights reserved.

Yu, S., Wang, J., Shen, H.
Network pharmacology-based analysis of the role of traditional chinese herbal medicines in the treatment of covid-19
Abstract:
Background: The novel coronavirus named COVID-19, which originated in Wuhan, China, has spread to many countries around the world. Currently, no effective medical treatment exists to combat this disease. Traditional Chinese herbal medicines (CHM) have unique roles in the treatment of viral infections. In this article we analyzed the effectiveness and possible molecular mechanisms of CHM formulas for the prevention of COVID-19. Methods: The active ingredients and action targets of CHM formulas were obtained from the TCMSP database. Genes related to severe acute respiratory syndromes (SARS) and Middle East respiratory syndrome (MERS) were queried on the GeneCards database. The action mechanisms of these genes were predicted using a Gene Ontology (GO)-based functional enrichment and annotation tool and the Kyoto Encyclopedia of Genes and Genomes (KEGG). Results: CHM formulas played a positive role in preventing COVID-19 and warrant further application. Conclusions: Our research provides new evidence to support the possible value of CHM formulas for the prevention of COVID-19. However, further clinical studies with large sample sizes are required to verify their effectiveness. © Annals of Palliative Medicine. All rights reserved.

Cancer care delivery challenges amidst coronavirus disease -19 (covid-19) outbreak: Specific precautions for cancer patients and cancer care providers to prevent spread

Abstract:
Coronavirus outbreak has affected thousands of people in at least 186 countries which has affected the cancer care delivery system apart from affecting the overall health system. Cancer patients are more susceptible to coronavirus infection than individuals without cancer as they are in an immunosuppressive state because of the malignancy and anticancer treatment. Oncologists should be more attentive to detect coronavirus infection early, as any type of advanced cancer is at much higher risk for unfavorable outcomes. Oncology communities must ensure that cancer patients should spend more time at home and less time out in the community. Oncologists and other health care professionals involved in cancer care have a critical opportunity to communicate to their patients to pass on right information regarding practice modifications in view of COVID-19 outbreaks. Countries must isolate, test, treat and trace to control the coronavirus pandemic. There is a paucity of information on novel coronavirus infection and its impact on cancer patients and cancer care providers. To date, there is no scientific guideline regarding management of cancer patients in a background of coronavirus outbreak. © 2020, Asian Pacific Organization for Cancer Prevention.


Tabletop exercise to prepare institutions of higher education for an outbreak of COVID-19

Abstract:
Preparing for public health emergencies is an ongoing process and involves a variety of approaches and tools. Tabletop exercises are one of the tools designed to simulate the emergence of a public health emergency and address some or all of the phases of emergency management: mitigation, preparedness, response, and recovery.1 They typically are designed to include participation of stakeholders from diverse and complementary backgrounds, including command, operations, logistics, planning, and finance.2 Effective tabletop exercises provide a plausible scenario that require cooperation and communication from these functional areas. Tabletops also require forward thinking and planning in a variety of scenarios. When a public health emergency occurs, decision makers may be overwhelmed with decisions that need their immediate attention. Tabletop exercises can provide a framework to help decision makers anticipate future challenges, which may provide the mental model encompassing knowledge and insights that inform both current and future decisions.

Eurosurveillance Editorial Team

Updated rapid risk assessment from ECDC on the outbreak of COVID-19: increased transmission globally
(2020) Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 25 (9)

Kumar, S., Maurya, V.K., Prasad, A.K., Bhatt, M.L.B., Saxena, S.K.

Structural, glycosylation and antigenic variation between 2019 novel coronavirus (2019-nCoV) and SARS coronavirus (SARS-CoV)
Abstract:
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. © 2020, Indian Virological Society.

Chatterjee, P.
Indian pharma threatened by COVID-19 shutdowns in China

Moberly, T.
Covid-19: school closures and bans on mass gatherings will need to be considered, says England's CMO
(2020) BMJ (Clinical research ed.), 368, p. m806.

Tanne, J.H.
Covid-19: Trump says risk to Americans is "very low"
(2020) BMJ (Clinical research ed.), 368, p. m793.

Bischof, E., Chen, G., Ferretti, M.T.
Understanding COVID-19 new diagnostic guidelines - a message of reassurance from an internal medicine doctor in Shanghai
(2020) Swiss medical weekly, 150, p. w20216.

**2019-Novel Coronavirus (2019-NCOV): Estimating the case fatality rate – A word of caution**  
(2020) Swiss Medical Weekly, 150 (5-6), art. no. w20203

Eurosurveillance Editorial Team  
**Latest assessment on COVID-19 from the European Centre for Disease Prevention and Control (ECDC)**  

Eurosurveillance Editorial Team  
**Latest updates on COVID-19 from the European Centre for Disease Prevention and Control**  

Moreira, B.L., Brotto, M.P.D., Marchiori, E.  
*Chest radiography and computed tomography findings from a Brazilian patient with COVID-19 pneumonia*  

Helmich, R.C., Bloem, B.R.  
**The Impact of the COVID-19 Pandemic on Parkinson's Disease: Hidden Sorrows and Emerging Opportunities**  

Salomé, B., Magen, A.  
**Dysregulation of lung myeloid cells in COVID-19**  
(2020) Nature Reviews Immunology

Marinelli, K.A.  
**International Perspectives Concerning Donor Milk Banking During the SARS-CoV-2 (COVID-19) Pandemic**  
(2020) Journal of Human Lactation

**Assessing Viral Shedding and Infectivity of Tears in Coronavirus Disease 2019 (COVID-19) Patients**  
(2020) Ophthalmology

Mitra, R.L., Greenstein, S.A., Epstein, L.M.
An algorithm for managing QT prolongation in coronavirus disease 2019 (COVID-19) patients treated with either chloroquine or hydroxychloroquine in conjunction with azithromycin: Possible benefits of intravenous lidocaine
(2020) HeartRhythm Case Reports

Nasir, M.U., Roberts, J., Muller, N.L., Macri, F., Mohammed, M.F., Akhlaghpoor, S., Parker, W., Eftekhar, A., Rezaei, S., Mayo, J., Nicolaou, S.

The Role of Emergency Radiology in COVID-19: From Preparedness to Diagnosis
(2020) Canadian Association of Radiologists Journal

Abstract:
Emergency trauma radiology, although a relatively new subspecialty of radiology, plays a critical role in both the diagnosis/triage of acutely ill patients, but even more important in providing leadership and taking the lead in the preparedness of imaging departments in dealing with novel highly infectious communicable diseases and mass casualties. This has become even more apparent in dealing with COVID-19, the disease caused by the novel coronavirus SARS-CoV-2, first emerged in late 2019. We review the symptoms, epidemiology, and testing for this disease. We discuss characteristic imaging findings of COVID-19 in relation to other modern coronavirus diseases including SARS and MERS. We discuss roles that community radiology clinics, outpatient radiology departments, and emergency radiology departments can play in the diagnosis of this disease. We review practical methods to reduce spread of infections within radiology departments.
© The Author(s) 2020.

Gabriels, J., Saleh, M., Chang, D., Epstein, L.M.

Inpatient use of mobile continuous telemetry for COVID-19 patients treated with hydroxychloroquine and azithromycin
(2020) HeartRhythm Case Reports


Case report of COVID-19 in a kidney transplant recipient: Does immunosuppression alter the clinical presentation?
(2020) American Journal of Transplantation

Abstract:
COVID-19 is novel infectious disease with an evolving understanding of its epidemiology and clinical manifestations. Immunocompromised patients often present atypical presentations of viral diseases. Herein we report a case of a COVID-19 infection in a solid organ transplant recipient, in which the first clinical symptoms were of gastrointestinal viral disease and fever, which further progressed to respiratory symptoms in 48 hours. In these high risk populations, protocols for screening for SARS-Cov2 may be needed to be re-evaluated. © 2020 The American Society of Transplantation and the American Society of Transplant Surgeons

Zha, L., Li, S., Pan, L., Tefsen, B., Li, Y., French, N., Chen, L., Yang, G., Villanueva, E.V.

Corticosteroid treatment of patients with coronavirus disease 2019 (COVID-19)
(2020) Medical Journal of Australia

Abstract:
Objectives: To assess the efficacy of corticosteroid treatment of patients with coronavirus disease 2019 (COVID-19). Design, setting: Observational study in the two COVID-19-designated hospitals in Wuhu, Anhui province, China, 24 January – 24 February 2020. Participants: Thirty-one patients infected with the severe acute respiratory coronavirus 2 (SARS-CoV-2) treated at the two designated hospitals. Main outcome measures: Virus clearance time, length of hospital stay, and duration of symptoms, by treatment type (including or not including corticosteroid therapy). Results: Eleven of 31 patients with COVID-19 received corticosteroid treatment. Cox proportional hazards regression analysis indicated no association between corticosteroid treatment and virus clearance time (hazard ratio [HR], 1.26; 95% CI, 0.58–2.74), hospital length of stay (HR, 0.77; 95% CI, 0.33–1.78), or duration of symptoms (HR, 0.86; 95% CI, 0.40–1.83). Univariate analysis indicated that virus clearance was slower in two patients with chronic hepatitis B infections (mean difference, 10.6 days; 95% CI, 6.2–15.1 days). Conclusions: Corticosteroids are widely used when treating patients with COVID-19, but we found no association between therapy and outcomes in patients without acute respiratory distress syndrome. An existing HBV infection may delay SARS-CoV-2 clearance, and this association should be further investigated. © 2020 AMPCo Pty Ltd


Clinical features of the first cases and a cluster of Coronavirus Disease 2019 (COVID-19) in Bolivia imported from Italy and Spain (2020) Travel Medicine and Infectious Disease, art. no. 101653

Abstract:
Introduction: In March 2020, Coronavirus Disease 2019 (COVID-19) arrived in Bolivia. Here, we report the main clinical findings, and epidemiological features of the first series of cases, and a cluster, confirmed in Bolivia. Methods: For this observational, retrospective and cross-sectional study, information was obtained from the Hospitals and the Ministry of Health for the cases that were laboratory-diagnosed and related, during March 2020. rRT-PCR was used for the detection of the RNA of SARS-CoV-2 following the protocol Charité, Berlin, Germany, from nasopharyngeal swabs. Results: Among 152 suspected cases investigated, 12 (7.9%) were confirmed with SARS-CoV-2 infected by rRT-PCR. The median age was 39 years (IQR 25–43), six of them male. Two cases proceed from Italy and three from Spain. Nine patients presented fever, and cough, five sore throat, and myalgia, among other symptoms. Only a 60 y-old woman with hypertension was hospitalized. None of the patients required ICU nor fatalities occurred in this group. Conclusions: This is the first report of surveillance of COVID-19 in Bolivia, with patients managed mainly with home isolation. Preparedness for a significant epidemic, as is going on in other countries, and the deployment of response plans for it, in the country is now taking place to mitigate the impact of the COVID-19 pandemic in the population.


Abstract:
Introduction: In the context of the COVID-19 pandemic, specific recommendations are required for the management of patients with gynecologic cancer. Materials and method: The FRANCOGYN group of the National College of French Gynecologists and Obstetricians (CNGOF) convened to develop recommendations based on the consensus conference model. Results: If a patient with a gynecologic cancer presents with COVID-19, surgical management should be postponed for at least 15 days. For cervical cancer, radiotherapy and concomitant radiochemotherapy could replace surgery as first-line treatment and the value of lymph node staging should be reviewed on a case-by-case basis. For advanced ovarian cancers, neoadjuvant chemotherapy should be preferred over primary cytoreduction surgery. It is legitimate not to perform hyperthermic intraperitoneal chemotherapy during the COVID-19 pandemic. For patients who are scheduled to undergo interval surgery, chemotherapy can be continued and surgery performed after 6 cycles. For patients with early stage endometrial cancer of low and intermediate preoperative ESMO risk, hysterectomy with bilateral adnexectomy combined with a sentinel lymph node procedure is recommended. Surgery can be postponed for 1–2 months in low-risk endometrial cancers (FIGO Ia stage on MRI and grade 1–2 endometrioid cancer on endometrial biopsy). For patients of high ESMO risk, the MSKCC algorithm (combining PET-CT and sentinel lymph node biopsy) should be applied to avoid pelvic and lumbar-aortic lymphadenectomy. Conclusion: During the COVID-19 pandemic, management of a patient with cancer should be adapted to limit the risks associated with the virus without incurring loss of chance. © 2020 The Author(s)

Wang, L.

C-reactive protein levels in the early stage of COVID-19
(2020) Medecine et Maladies Infectieuses

Abstract:
Background: COVID-19 is a new infectious disease, for which there is currently no treatment. It is therefore necessary to explore biomarkers to determine the extent of lung lesions and disease severity. Objective: We aimed to assess the usefulness of CRP levels in the early stage of COVID-19 and to correlate them with lung lesions and severe presentation. Methods: Confirmed cases of COVID-19 were selected at the Fever Unit in two regions of Guizhou, China. On admission CRP levels were collected, and the diameter of the largest lung lesion was measured in the most severe lung lesion by lung CT scan. Differences in the diameter and CRP levels were compared in the following groups of patients: mild group, moderate group, severe group, and critical group. Result: CRP levels and the diameter of the largest lung lesion in the moderate group were higher than those in the mild group (Mann-Whitney test = −2.647, −2.171, P < 0.05), those in the severe group were higher than those in the moderate group (Mann-Whitney test = 0.693, −2.177, P < 0.05), and those in the critical group were higher than those in the severe group (Mann-Whitney test = −0.068, −1.549, P < 0.05). The difference was statistically significant. CRP levels were positively correlated with the diameter of lung lesion and severe presentation (correlation coefficient = 0.873, 0.734, P < 0.001). Conclusion: In the early stage of COVID-19 CRP levels were positively correlated with lung lesions and could reflect disease severity. © 2020 The Author

Sifuentes-Rodriguez, E., Palacios-Reyes, D.


Abstract:
Before the severe acute respiratory syndrome outbreak in 2003, coronaviruses (CoVs) were not considered to be highly pathogenic to humans. However, it was this epidemic that highlighted this
group of viruses and included them among the causative agents of emerging epidemic diseases. In addition, in 2012, another new CoV responsible for the Middle East respiratory syndrome was identified. Both infections were considered a threat to global health security. At present, the third epidemic caused by a CoV is being faced. This new CoV, called 2019-nCoV, was originated in the city of Wuhan, China, and has been linked to severe respiratory infections in humans. Thanks to the collaboration of experts worldwide, more information about this virus and its infection is reported each day, which allows modifying the recommendations for its prevention and treatment, without forgetting that the ultimate goal is to control this epidemic. In this review, the important aspects of this new coronavirus, 2019-nCoV, and its disease, COVID-19, have been summarized with the information available up to February 2020. © 2020 Hospital Infantil de México Federico Gómez. Published by Permanyer.

Gracia-Ramos, A.E.

Is the ACE2 Overexpression a Risk Factor for COVID-19 Infection?
(2020) Archives of Medical Research

Abstract:
In the recent coronavirus disease (COVID-19) outbreak, a higher proportion of patients with severe disease were found in older persons with comorbidities. This observation has been related to the use of drugs that can increase the cellular expression of angiotensin-converting enzyme 2 (ACE2) that has been recognized as target to which the virus bind to cells. Although this hypothesis is possible, it may also have other explanations which are discussed. © 2020 IMSS

Raurell-Torredà, M., Martínez-Estalella, G., Frade-Mera, M.J., Carrasco Rodríguez-Rey, L.F., Romero de San Pío, E.

Reflections arising from the COVID-19 pandemic [Reflexiones derivadas de la pandemia COVID-19]
(2020) Enfermería Intensiva

Abstract:
While we were drafting the recommendations for the joint contingency plan between the Spanish Society of Intensive Care and Coronary Unit Nursing (SEEIUC) and the Spanish Society of Intensive and Critical Care Medicine and Coronary Units (SEMICYUC), predictions were overtaken by events with regard to the magnitude of the COVID-19 pandemic. Members informed us of the lack of personal protection equipment (PPE), the rapid provision of improvised ICUs in various hospital areas and the recruitment of nurses to cover shifts. The failure to recognise the specialty of critical care nursing, included in the macro-specialty of medical-surgical nursing and not yet developed, has highlighted the urgent need to learn from our mistakes: specialisation, increase the number of nurses in teams and protect the public health system. © 2020 Sociedad Española de Enfermería Intensiva y Unidades Coronarias (SEEIUC)

Mash, B.

Primary care management of the coronavirus (Covid-19)
(2020) South African Family Practice, 62 (1), art. no. a5115

Abstract:
South Africa is in the grip of a novel coronavirus pandemic (COVID-19). Primary care providers are in the frontline. COVID-19 is spread primarily by respiratory droplets contaminating surfaces and hands that then transmit the virus to another person’s respiratory system. The incubation period is 2–9 days and the majority of cases are mild. The most common symptoms are fever, cough and
shortness of breath. Older people and those with cardiopulmonary comorbidities or immunological deficiency will be more at risk of severe disease. If people meet the case definition, the primary care provider should immediately adopt infection prevention and control measures. Diagnosis is made by a RT-PCR test using respiratory secretions, usually nasopharyngeal and oropharyngeal swabs. Mild cases can be managed at home with self-isolation, symptomatic treatment and follow-up if the disease worsens. Contact tracing is very important. Observed case fatality is between 0.5% and 4%, but may be overestimated as mild cases are not always counted. Primary care providers must give clear, accurate and consistent messages on infection prevention and control in communities and homes. © 2020, AOSIS (pty) Ltd. All rights reserved.

Moon, C.
**Fighting COVID-19 exhausts T cells**  
(2020) Nature Reviews Immunology

**Sixty-eight consecutive patients assessed for COVID-19 infection: Experience from a UK Regional infectious diseases Unit**  
(2020) Influenza and other Respiratory Viruses

**Abstract:**  
Background: Assessment of possible infection with SARS-CoV-2, the novel coronavirus responsible for COVID-19 illness, has been a major activity of infection services since the first reports of cases in December 2019. Objectives: We report a series of 68 patients assessed at a Regional Infection Unit in the UK. Methods: Between 29 January 2020 and 24 February 2020, demographic, clinical, epidemiological and laboratory data were collected. We compared clinical features between patients not requiring admission for clinical reasons or antimicrobials with those assessed as needing either admission or antimicrobial treatment. Results: Patients assessed were aged from 0 to 76 years; 36/68 were female. Peaks of clinical assessments coincided with updates to the case definition for suspected COVID-19. Microbiological diagnoses included SARS-CoV-2, mycoplasma pneumonia, influenza A, non-SARS/MERS coronaviruses and rhinovirus/enterovirus. Nine of sixty-eight received antimicrobials, 15/68 were admitted, 5 due to inability to self-isolate. Patients requiring admission on clinical grounds or antimicrobials (14/68) were more likely to have fever or raised respiratory rate compared to those not requiring admission or antimicrobials. Conclusions: The majority of patients had mild illness, which did not require clinical intervention. This finding supports a community testing approach, supported by clinicians able to review more unwell patients. Extensions of the epidemiological criteria for the case definition of suspected COVID-19 lead to increased screening intensity; strategies must be in place to accommodate this in time for forthcoming changes as the epidemic develops. © 2020 The Authors. Influenza and Other Respiratory Viruses Published by John Wiley & Sons Ltd.

Li, Y., Yao, L., Li, J., Chen, L., Song, Y., Cai, Z., Yang, C.
**Stability issues of RT-PCR testing of SARS-CoV-2 for hospitalized patients clinically diagnosed with COVID-19**  
(2020) Journal of Medical Virology

**Abstract:**  
In this study, we collected a total of 610 hospitalized patients from Wuhan between February 2, 2020, and February 17, 2020. We reported a potentially high false negative rate of real-time reverse-transcriptase polymerase chain reaction (RT-PCR) testing for SARS-CoV-2 in the 610 hospitalized
patients clinically diagnosed with COVID-19 during the 2019 outbreak. We also found that the RT-PCR results from several tests at different points were variable from the same patients during the course of diagnosis and treatment of these patients. Our results indicate that in addition to the emphasis on RT-PCR testing, clinical indicators such as computed tomography images should also be used not only for diagnosis and treatment but also for isolation, recovery/discharge, and transferring for hospitalized patients clinically diagnosed with COVID-19 during the current epidemic. These results suggested the urgent needs for the standard of procedures of sampling from different anatomic sites, sample transportation, optimization of RT-PCR, serology diagnosis/screening for SARS-CoV-2 infection, and distinct diagnosis from other respiratory diseases such as influenza infections as well. © 2020 Wiley Periodicals, Inc.

Gostin, L.O., Friedman, E.A., Wetter, S.A.
**Responding to COVID-19: How to Navigate a Public Health Emergency Legally and Ethically**
(2020) Hastings Center Report

**Abstract:**
Few novel or emerging infectious diseases have posed such vital ethical challenges so quickly and dramatically as the novel coronavirus SARS-CoV-2. The World Health Organization declared a public health emergency of international concern and recently classified COVID-19 as a worldwide pandemic. As of this writing, the epidemic has not yet peaked in the United States, but community transmission is widespread. President Trump declared a national emergency as fifty governors declared state emergencies. In the coming weeks, hospitals will become overrun, stretched to their capacities. When the health system becomes stretched beyond capacity, how can we ethically allocate scarce health goods and services? How can we ensure that marginalized populations can access the care they need? What ethical duties do we owe to vulnerable people separated from their families and communities? And how do we ethically and legally balance public health with civil liberties?. © 2020 The Hastings Center

Paganini, M., Conti, A., Weinstein, E., Della Corte, F., Ragazzoni, L.
**Translating COVID-19 Pandemic Surge Theory to Practice in the Emergency Department: How to Expand Structure**
(2020) Disaster Medicine and Public Health Preparedness

**Abstract:**
Multiple professional societies, nongovernment and government agencies have studied the science of sudden onset disaster mass casualty incidents to create and promote surge response guidelines. The COVID-19 pandemic has presented the health care system with challenges that have limited science to guide the staff, stuff and structure surge response. This study reviewed the available surge science literature specifically to guide an Emergency Department's surge structural response using a translational science approach to answer the question: How does the concept of sudden onset mass casualty incident (MCI) surge capability apply to the process to expand COVID-19 Pandemic surge structure response? The available surge structural science literature was reviewed to determine the application to a pandemic response. The on-line ahead of print and print COVID-19 scientific publications, as well as grey, literature were studied to learn the best available COVID-19 surge structural response science. A checklist was created to guide the Emergency Department team's COVID-19 surge structural response. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.
Szperka, C.L., Ailani, J., Barmherzig, R., Klein, B.C., Minen, M.T., Halker Singh, R.B., Shapiro, R.E.

**Migraine Care in the Era of COVID-19: Clinical Pearls and Plea to Insurers**
(2020) Headache

**Abstract:**
Objective: To outline strategies for the treatment of migraine which do not require in-person visits to clinic or the emergency department, and to describe ways that health insurance companies can remove barriers to quality care for migraine. Background: COVID-19 is a global pandemic causing widespread infections and death. To control the spread of infection we are called to observe “social distancing” and we have been asked to postpone any procedures which are not essential. Since procedural therapies are a mainstay of headache care, the inability to do procedures could negatively affect our patients with migraine. In this manuscript we review alternative therapies, with particular attention to those which may be contra-indicated in the setting of COVID-19 infection.

Design/Results: The manuscript reviews the use of telemedicine visits and acute, bridge, and preventive therapies for migraine. We focus on evidence-based treatment where possible, but also describe “real world” strategies which may be tried. In each section we call out areas where changes to rules from commercial health insurance companies would facilitate better migraine care.

Conclusions: Our common goal as health care providers is to maximize the health and safety of our patients. Successful management of migraine with avoidance of in-person clinic and emergency department visits further benefits the current urgent societal goal of maintaining social distance to contain the COVID-19 pandemic.

© 2020 American Headache Society


**Diabetes is a risk factor for the progression and prognosis of COVID-19**
(2020) Diabetes/Metabolism Research and Reviews

**Abstract:**
Background: To figure out whether diabetes is a risk factor influencing the progression and prognosis of 2019 novel coronavirus disease (COVID-19). Methods: A total of 174 consecutive patients confirmed with COVID-19 were studied. Demographic data, medical history, symptoms and signs, laboratory findings, chest computed tomography (CT) as well the treatment measures were collected and analysed. Results: We found that COVID-19 patients without other comorbidities but with diabetes (n = 24) were at higher risk of severe pneumonia, release of tissue injury-related enzymes, excessive uncontrolled inflammation responses and hypercoagulable state associated with dysregulation of glucose metabolism. Furthermore, serum levels of inflammation-related biomarkers such as IL-6, C-reactive protein, serum ferritin and coagulation index, D-dimer, were significantly higher (P <.01) in diabetic patients compared with those without, suggesting that patients with diabetes are more susceptible to an inflammatory storm eventually leading to rapid deterioration of COVID-19. Conclusions: Our data support the notion that diabetes should be considered as a risk factor for a rapid progression and bad prognosis of COVID-19. More intensive attention should be paid to patients with diabetes, in case of rapid deterioration. © 2020 The Authors. Diabetes/Metabolism Research and Reviews published by John Wiley & Sons Ltd.

Dong, S., Sun, J., Mao, Z., Wang, L., Lu, Y.-L., Li, J.

**A guideline for homology modeling of the proteins from newly discovered betacoronavirus, 2019 novel coronavirus (2019-nCoV)**
(2020) Journal of Medical Virology

**Abstract:**
During an outbreak of respiratory diseases including atypical pneumonia in Wuhan, a previously unknown β-coronavirus was detected in patients. The newly discovered coronavirus is similar to some β-coronaviruses found in bats but different from previously known SARS-CoV and MERS-CoV. High sequence identities and similarities between 2019-nCoV and SARS-CoV were found. In this study, we searched the homologous templates of all nonstructural and structural proteins of 2019-nCoV. Among the nonstructural proteins, the leader protein (nsp1), the papain-like protease (nsp3), the nsp4, the 3C-like protease (nsp5), the nsp7, the nsp8, the nsp9, the nsp10, the RNA-directed RNA polymerase (nsp12), the helicase (nsp13), the guanine-N7 methyltransferase (nsp14), the uridylate-specific endoribonuclease (nsp15), the 2’-O-methyltransferase (nsp16), and the ORF7a protein could be built on the basis of homology templates. Among the structural proteins, the spike protein (S-protein), the envelope protein (E-protein), and the nucleocapsid protein (N-protein) can be constructed based on the crystal structures of the proteins from SARS-CoV. It is known that PL-Pro, 3CL-Pro, and RdRp are important targets for design antiviral drugs against 2019-nCoV. And S protein is a critical target candidate for inhibitor screening or vaccine design against 2019-nCoV because coronavirus replication is initiated by the binding of S protein to cell surface receptors. It is believed that these proteins should be useful for further structure-based virtual screening and related computer-aided drug development and vaccine design. © 2020 Wiley Periodicals, Inc.


Abstract:

Objectives: To explore the relationship between the imaging manifestations and clinical classification of COVID-19. Methods: We conducted a retrospective single-center study on patients with COVID-19 from Jan. 18, 2020 to Feb. 7, 2020 in Zhuhai, China. Patients were divided into 3 types based on Chinese guideline: mild (patients with minimal symptoms and negative CT findings), common, and severe-critical (patients with positive CT findings and different extent of clinical manifestations). CT visual quantitative evaluation was based on summing up the acute lung inflammatory lesions involving each lobe, which was scored as 0 (0%), 1 (1–25%), 2 (26–50%), 3 (51–75%), or 4 (76–100%), respectively. The total severity score (TSS) was reached by summing the five lobe scores. The consistency of two observers was evaluated. The TSS was compared with the clinical classification. ROC was used to test the diagnosis ability of TSS for severe-critical type. Results: This study included 78 patients, 38 males and 40 females. There were 24 mild (30.8%), 46 common (59.0%), and 8 severe-critical (10.2%) cases, respectively. The median TSS of severe-critical type group was significantly higher than common type (p < 0.001). The ICC value of the two observers was 0.976 (95% CI 0.962–0.985). ROC analysis showed the area under the curve (AUC) of TSS for diagnosing severe-critical type was 0.918. The TSS cutoff of 7.5 had 82.6% sensitivity and 100% specificity. Conclusions: The proportion of mild-type patients with COVID-19 was relatively high; CT was not suitable for independent screening tool. The CT visual quantitative analysis has high consistency and can reflect the clinical classification of COVID-19. Key Points: • CT visual quantitative evaluation has high consistency (ICC value of 0.976) among the observers. The median TSS of severe-critical type group was significantly higher than common type (p < 0.001). • ROC analysis showed the area under the curve (AUC) of TSS for diagnosing severe-critical type was 0.918 (95% CI 0.843–0.994). The TSS cutoff of 7.5 had 82.6% sensitivity and 100% specificity. • The proportion of confirmed COVID-19 patients with normal chest CT was relatively high (30.8%); CT was not a suitable screening modality © 2020, European Society of Radiology.
Vaninov, N.
In the eye of the COVID-19 cytokine storm
(2020) Nature Reviews Immunology

Zhao, G.
Taking preventive measures immediately: evidence from China on COVID-19
[Tomar medidas preventivas inmediatamente: evidencia de China sobre el COVID-19]
(2020) Gaceta Sanitaria

Amariles, P., Granados, J., Ceballos, M., Montoya, C.J.
COVID-19 in Colombia endpoints. Are we different, like Europe?
(2020) Research in Social and Administrative Pharmacy

Abstract:
The infection by the new coronavirus (SARS-CoV-2) has taken the dimension of a pandemic, affecting more than 160 countries in a few weeks. In Colombia, despite the implementation of the rules established by the national government, exists an elevate concern both for mortality and for the limited capacity of the health system to respond effectively to the needs of patients infected. For Colombia, assuming a case fatality rate among people infected with SARS-CoV-2 of 0.6% (average data from the information reported for Latin American countries for March 18) (Table 1), the number of deaths, in one or two weeks, could be 16 and 243, respectively. These estimates differ markedly from those documented in countries such as Spain and Italy, in which COVID-19 case fatality rates exceed 8% (case of Italy) and from the percentage of patients who have required intensive care, which has ranged from 9% to 11% of patients in Mediterranean European countries. These differences could be explained due to: a) the percentage of the population at risk (individuals older than 60 years); b) a higher epidemiological exposure to viral respiratory infections associated with more frequent exposure to them, due to geographic and climatic conditions; c) less spread of the virus by location in the tropical zone; and d) earlier preventive measures to contain the spread of SARS-CoV-2 infection. Therefore, it is possible to establish that the situation in this country will be different from in European Mediterranean and that Colombia could have different endpoints from Spain and Italy. © 2020

COVID-19 and people followed for breast cancer: French guidelines for clinical practice of Nice-St Paul de Vence In collaboration with the Collège Nationale des Gynécologues et Obstétriciens Français (CNGOF), the Société d’Imagerie de la FEMme (SIFEM), the Société Française de Chirurgie Oncologique (SFCO), the Société Française de Sénologie et Pathologie Mammaire (SFSPM) and the French Breast Cancer Intergroup-UNICANCER (UCBG) [COVID-19 et personnes suivies pour un cancer du sein: recommandations françaises pour la
Cao, C., Li, Y., Liu, S., Fan, H., Hao, L.
Epidemiological Features of 135 Patients with Coronavirus Disease (COVID-19) in Tianjin, China
(2020) Disaster Medicine and Public Health Preparedness

Abstract:
ObjectiveTo describe the epidemiologic features of an outbreak of coronavirus disease (COVID-19) in Tianjin caused by a novel coronavirus (2019-nCoV) and to provide scientific basis for prevention and control measures.
MethodsData from COVID-19 cases were collected from daily notifications given to the National Health Commission of the People's Republic of China and Tianjin Health Committee. All of the data were analyzed with SPSS version 24.0 software.
ResultsAs of February 24, 2020, there have been 135 confirmed cases, 3 deaths, and 87 recoveries in Tianjin, China. The incidence of COVID-19 was 8.65/1,000,000 with a 2.22% case fatality rate. Regarding geographic distribution, the incidence was 8.82 per 1,000,000 in urban areas and 8.00 per 1,000,000 in suburbs. During the early stage of the epidemic, most cases came from urban areas and in patients with a history of sojourning in Hubei Province. The majority of patients were 31-70 years old (75.97%). A familial cluster was the most important characteristic of COVID-19 (accounting for 74.81%).
ConclusionsCurrent information suggests that people are generally susceptible to COVID-19, which has shown a familial cluster in Tianjin. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.

Rey Galán, C., Manrique de Lara, L.A., Antón Gamero, M., Cano Garcinuño, A., Solís Sánchez, G.
Coronavirus infection (COVID-19) in Anales de Pediatría [Infección por coronavirus (COVID-19) en Anales de Pediatría]
(2020) Anales de Pediatría

Schwartz, S.A.
Climate Change, Covid-19, Preparedness, and Consciousness
(2020) Explore

Cook, T.M., El-Boghdadly, K., McGuire, B., McNarry, A.F., Patel, A., Higgs, A.
Consensus guidelines for managing the airway in patients with COVID-19: Guidelines from the Difficult Airway Society, the Association of Anaesthetists the Intensive Care Society, the Faculty of Intensive Care Medicine and the Royal College of Anaesthetists
(2020) Anaesthesia

Abstract:
Severe acute respiratory syndrome-corona virus-2, which causes coronavirus disease 2019 (COVID-19), is highly contagious. Airway management of patients with COVID-19 is high risk to staff and patients. We aimed to develop principles for airway management of patients with COVID-
to encourage safe, accurate and swift performance. This consensus statement has been brought together at short notice to advise on airway management for patients with COVID-19, drawing on published literature and immediately available information from clinicians and experts. Recommendations on the prevention of contamination of healthcare workers, the choice of staff involved in airway management, the training required and the selection of equipment are discussed. The fundamental principles of airway management in these settings are described for: emergency tracheal intubation; predicted or unexpected difficult tracheal intubation; cardiac arrest; anaesthetic care; and tracheal extubation. We provide figures to support clinicians in safe airway management of patients with COVID-19. The advice in this document is designed to be adapted in line with local workplace policies. © 2020 The Authors. Anaesthesia published by John Wiley & Sons Ltd on behalf of Association of Anaesthetists


Infection Control against COVID-19 in Departments of Radiology (2020) Academic Radiology

Abstract:
The COVID-19 epidemic, which is caused by the novel coronavirus SARS-CoV-2, has spread rapidly to become a world-wide pandemic. Chest radiography and chest CT are frequently used to support the diagnosis of COVID-19 infection. However, multiple cases of COVID-19 transmission in radiology department have been reported. Here we summarize the lessons we learned and provide suggestions to improve the infection control and prevention practices of healthcare workers in departments of radiology. © 2020 The Association of University Radiologists


COVID-19 pneumonia manifestations at the admission on chest ultrasound, radiographs, and CT: single-center study and comprehensive radiologic literature review (2020) European Journal of Radiology Open, 7, art. no. 100231

Abstract:
Purpose: To investigate the imaging features of emerging COVID-19 pneumonia on chest ultrasound (US), radiographs (CXR) and computed tomography (CT) examinations performed at admission and to provide a comprehensive radiological literature review on ongoing radiological data from recent publications. Materials and methods: In this retrospective single-center study, we enrolled consecutive patients from February 15, 2020, to March 15, 2020, with laboratory-confirmed SARS-CoV-2 hospitalized in Valduce Hospital (Como, Italy). Multi-modality imaging findings were evaluated and compared. Literature research was conducted through a methodical search on Pubmed and Embase databases. Results: Fifty-eight patients (36 men, 22 women; age range, 18–98 years) were included in the study. Among these, chest US, CXR, and CT were performed respectively in twenty-two, thirty-two and forty-two patients. Lung US findings were consistent with diffuse B lines (100%) and subpleural consolidations (27.3%). CXR showed prevalent manifestations of consolidations (46.9%) and hazy increased opacities (37.5%). Typical CT features included bilateral and multilobar ground-glass opacities (GGO) with (59.5%) and without (35.7%) consolidations having a predominantly peripheral distribution (64.3%). Other imaging features included crazy paving pattern (57.1%), fibrous stripes (50%), subpleural lines (35.7%), architectural distortion (28.6%), air bronchogram sign (26.2%), vascular thickening (23.8%) and nodules (2.4%). Also, enlarged lymph nodes (14.3 %) and pleural effusion (7.1%) were
observed. The literature review identified twenty-six original studies supporting our imaging chest findings. Conclusion: The spectrum of chest imaging manifestations of COVID-19 pneumonia upon admission includes B-lines and consolidations on US, consolidations and hazy increased opacities on CXR, and multifocal GGO with consolidations on CT. © 2020 The Author(s)

Wu, H.-L., Huang, J., Zhang, C.J.P., He, Z., Ming, W.-K.
Facemask shortage and the novel coronavirus disease (COVID-19) outbreak: Reflections on public health measures (2020) EClinicalMedicine, art. no. 100329

Abstract:
Background: A novel coronavirus disease (COVID-19) outbreak due to the severe respiratory syndrome coronavirus (SARS-CoV-2) infection occurred in China in late December 2019. Facemask wearing with proper hand hygiene is considered an effective measure to prevent SARS-CoV-2 transmission, but facemask wearing has become a social concern due to the global facemask shortage. China is the major facemask producer in the world, contributing to 50% of global production. However, a universal facemask wearing policy would put an enormous burden on the facemask supply. Methods: We performed a policy review concerning facemasks using government websites and mathematical modelling shortage analyses based on data obtained from the National Health Commission (NHC), the Ministry of Industry and Information Technology (MIIT), the Centre for Disease Control and Prevention (CDC), and General Administration of Customs (GAC) of the People's Republic of China. Three scenarios with respect to wearing facemasks were considered: (1) a universal facemask wearing policy implementation in all regions of mainland China; (2) a universal facemask wearing policy implementation only in the epicentre (Hubei province, China); and (3) no implementation of a universal facemask wearing policy. Findings: Regardless of different universal facemask wearing policy scenarios, facemask shortage would occur but eventually end during our prediction period (from 20 Jan 2020 to 30 Jun 2020). The duration of the facemask shortage described in the scenarios of a country-wide universal facemask wearing policy, a universal facemask wearing policy in the epicentre, and no universal facemask wearing policy were 132, seven, and four days, respectively. During the prediction period, the largest daily facemask shortages were predicted to be 589·5, 49·3, and 37·5 million in each of the three scenarios, respectively. In any scenario, an N95 mask shortage was predicted to occur on 24 January 2020 with a daily facemask shortage of 2·2 million. Interpretation: Implementing a universal facemask wearing policy in the whole of China could lead to severe facemask shortage. Without effective public communication, a universal facemask wearing policy could result in societal panic and subsequently, increase the nationwide and worldwide demand for facemasks. These increased demands could cause a facemask shortage for healthcare workers and reduce the effectiveness of outbreak control in the affected regions, eventually leading to a pandemic. To fight novel infectious disease outbreaks, such as COVID-19, governments should monitor domestic facemask supplies and give priority to healthcare workers. The risk of asymptomatic transmission and facemask shortages should be carefully evaluated before introducing a universal facemask wearing policy in high-risk regions. Public health measures aimed at improving hand hygiene and effective public communication should be considered along with the facemask policy. © 2020 The Author(s)

Clinical characteristics and outcomes of patients undergoing surgeries during the incubation period of COVID-19 infection
Abstract:
Background: The outbreak of 2019 novel coronavirus disease (COVID-19) in Wuhan, China, has spread rapidly worldwide. In the early stage, we encountered a small but meaningful number of patients who were unintentionally scheduled for elective surgeries during the incubation period of COVID-19. We intended to describe their clinical characteristics and outcomes. Methods: We retrospectively analyzed the clinical data of 34 patients underwent elective surgeries during the incubation period of COVID-19 at Renmin Hospital, Zhongnan Hospital, Tongji Hospital and Central Hospital in Wuhan, from January 1 to February 5, 2020. Findings: Of the 34 operative patients, the median age was 55 years (IQR, 43–63), and 20 (58·8%) patients were women. All patients developed COVID-19 pneumonia shortly after surgery with abnormal findings on chest computed tomographic scans. Common symptoms included fever (31 [91·2%]), fatigue (25 [73·5%]) and dry cough (18 [52·9%]). 15 (44·1%) patients required admission to intensive care unit (ICU) during disease progression, and 7 patients (20·5%) died after admission to ICU. Compared with non-ICU patients, ICU patients were older, were more likely to have underlying comorbidities, underwent more difficult surgeries, as well as more severe laboratory abnormalities (eg, hyperleukocytemia, lymphopenia). The most common complications in non-survivors included ARDS, shock, arrhythmia and acute cardiac injury. Interpretation: In this retrospective cohort study of 34 operative patients with confirmed COVID-19, 15 (44·1%) patients needed ICU care, and the mortality rate was 20·5%. Funding: National Natural Science Foundation of China. © 2020 The Author(s)


Abstract:
The Covid-19 pandemic is changing the organization of healthcare and has a direct impact on digestive surgery. Healthcare priorities and circuits are being modified. Emergency surgery is still a priority. Functional surgery is to be deferred. Laparoscopic surgery must follow strict rules so as not to expose healthcare professionals (HCPs) to added risk. The question looms large in cancer surgery—go ahead or defer? There is probably an added risk due to the pandemic that must be balanced against the risk incurred by deferring surgery. For each type of cancer—colon, pancreas, oesogastric, hepatocellular carcinoma—morbidity and mortality rates are stated and compared with the oncological risk incurred by deferring surgery and/or the tumour doubling time. Strategies can be proposed based on this comparison. For colonic cancers T1-2, N0, it is advisable to defer surgery. For advanced colonic lesions, it seems judicious to undertake neoadjuvant chemotherapy and then wait. For rectal cancers T3-4 and/or N+, chemoradiotherapy is indicated, short radiotherapy must be discussed (followed by a waiting period) to reduce time of exposure in the hospital and to prevent infections. Most complex surgery with high morbidity and mortality—oesogastric, hepatic or pancreatic—is most often best deferred. © 2020 Elsevier Masson SAS

Krishnakumar, B., Rana, S. COVID 19 in INDIA: Strategies to combat from combination threat of life and livelihood (2020) Journal of Microbiology, Immunology and Infection

Abstract:
INDIA- As for reported in 360 COVID-19 cases (till March 22, 2020), seven people were died, and 23 people were treated successfully. This virus can easily affect who having respiratory problem and especially who all have been aged older than sixty. Most of the affected peoples had reached India from different part of the world, as like of carrier. Owing to this, India made several precautionary measures to mitigate/neglect the disease in beginning stage, however, the denser population of country will not be simple to control the same for long time (community spread), if government will not incorporate the visionary strategies. Since attacked several nations have been worried mostly for their people life (health), despite that developing country like India with huge population should consider about the livelihood (for Below Poverty Line (BPL) people), equally with the life. This article will give insights to make effective strategy to culminate the world threat COVID-19 in India. © 2020


**Abstract:**
What will be the global impact of the novel coronavirus (COVID-19)? Answering this question requires accurate forecasting the spread of confirmed cases as well as analysis of the number of deaths and recoveries. Forecasting, however, requires ample historical data. At the same time, no prediction is certain as the future rarely repeats itself in the same way as the past. Moreover, forecasts are influenced by the reliability of the data, vested interests, and what variables are being predicted. Also, psychological factors play a significant role in how people perceive and react to the danger from the disease and the fear that it may affect them personally. This paper introduces an objective approach to predicting the continuation of the COVID-19 using a simple, but powerful method to do so. Assuming that the data used is reliable and that the future will continue to follow the past pattern of the disease, our forecasts suggest a continuing increase in the confirmed COVID-19 cases with sizable associated uncertainty. The risks are far from symmetric as underestimating its spread like a pandemic and not doing enough to contain it is much more severe than overspending and being over careful when it will not be needed. This paper describes the timeline of a live forecasting exercise with massive potential implications for planning and decision making and provides objective forecasts for the confirmed cases of COVID-19. © 2020 Petropoulos, Makridakis. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

The surgeons and the covid-19 pandemic [Os cirurgiões e a pandemia do covid-19]
(2020) Revista do Colegio Brasileiro de Cirurgiões, 47 (1), art. no. e20202536
Abstract:
The current world Covid-19 pandemic has been the most discussed topic in the media and scientific journals. Fear, uncertainty, and lack of knowledge about the disease may be the significant factors that justify such reality. It has been known that the disease presents with a rapidly spreading, it is significantly more severe among the elderly, and it has a substantial global socioeconomic impact. Besides the challenges associated with the unknown, there are other factors, such as the deluge of information. In this regard, the high number of scientific publications, encompassing in vitro, case studies, observational and randomized clinical studies, and even systematic reviews add up to the uncertainty. Such a situation is even worse when considering that most healthcare professionals lack adequate knowledge to critically appraise the scientific method, something that has been previously addressed by some authors. Therefore, it is of utmost importance that expert societies supported by data provided by the World Health Organization and the National Health Department take the lead in spreading trustworthy and reliable information. The Brazilian College of Surgeons suggests in this document various initiatives that may help surgeons, healthcare providers, and patients who will have to face a surgical event under the pandemic. © 2020, Colegio Brasileiro de Cirurgiões.

Hindson, J.
COVID-19: faecal–oral transmission?
(2020) Nature Reviews Gastroenterology and Hepatology

Akladios, C., Azais, H., Ballester, M., (...), Raimond, E., Touboul, C.
(2020) Gynecologie Obstetrique Fertilite et Senologie
Abstract:
Introduction: Recommendations for the management of patients with gynecological cancer during the COVID-19 pandemic period. Material and method: Recommendations based on the consensus conference model. Results: In the case of a COVID-19 positive patient, surgical management should be postponed for at least 15 days. For cervical cancer, the place of surgery must be re-evaluated in relation to radiotherapy and Radio-Chemotherapy-Concomitant and the value of lymph node staging surgeries must be reviewed on a case-by-case basis. For advanced ovarian cancers, neo-adjuvant chemotherapy should be favored even if primary cytoreduction surgery could be envisaged. It is lawful not to offer hyperthermic intraperitoneal chemotherapy during a COVID-19 pandemic. In the case of patients who must undergo interval surgery, it is possible to continue the chemotherapy and to offer surgery after 6 cycles of chemotherapy. For early stage endometrial cancer, in case of low and intermediate preoperative ESMO risk, hysterectomy with bilateral annexectomy associated with a sentinel lymph node procedure should be favored. It is possible to consider postponing surgery for 1 to 2 months in low-risk endometrial cancers (FIGO Ia stage on MRI and grade 1-2 endometrioid cancer on endometrial biopsy). For high ESMO risk, it is possible to favor the MSKCC algorithm (combining PET-CT and sentinel lymph node biopsy) in order to omit pelvic and lumbar-aortic lymphadenectomies. Conclusion: During COVID-19 pandemic, patients suffering from...
cancer should not lose life chance, while limiting the risks associated with the virus. © 2020 Elsevier Masson SAS

Chang, D., Saleh, M., Garcia-Bengo, Y., Choi, E., Epstein, L., Willner, J.  
COVID-19 Infection Unmasking Brugada Syndrome  
(2020) HeartRhythm Case Reports

Anastassopoulou, C., Russo, L., Tsakris, A., Siettos, C.  
Data-based analysis, modelling and forecasting of the COVID-19 outbreak  
(2020) PLoS ONE, 15 (3), art. no. e0230405  
Abstract:
Since the first suspected case of coronavirus disease-2019 (COVID-19) on December 1st, 2019, in Wuhan, Hubei Province, China, a total of 40,235 confirmed cases and 909 deaths have been reported in China up to February 10, 2020, evoking fear locally and internationally. Here, based on the publicly available epidemiological data for Hubei, China from January 11 to February 10, 2020, we provide estimates of the main epidemiological parameters. In particular, we provide an estimation of the case fatality and case recovery ratios, along with their 90% confidence intervals as the outbreak evolves. On the basis of a Susceptible-Infectious-Recovered-Dead (SIRD) model, we provide estimations of the basic reproduction number (R0), and the per day infection mortality and recovery rates. By calibrating the parameters of the SIRD model to the reported data, we also attempt to forecast the evolution of the outbreak at the epicenter three weeks ahead, i.e. until February 29. As the number of infected individuals, especially of those with asymptomatic or mild courses, is suspected to be much higher than the official numbers, which can be considered only as a subset of the actual numbers of infected and recovered cases in the total population, we have repeated the calculations under a second scenario that considers twenty times the number of confirmed infected cases and forty times the number of recovered, leaving the number of deaths unchanged. Based on the reported data, the expected value of R0 as computed considering the period from the 11th of January until the 18th of January, using the official counts of confirmed cases was found to be ~4.6, while the one computed under the second scenario was found to be ~3.2. Thus, based on the SIRD simulations, the estimated average value of R0 was found to be ~2.6 based on confirmed cases and ~2 based on the second scenario. Our forecasting flashes a note of caution for the presently unfolding outbreak in China. Based on the official counts for confirmed cases, the simulations suggest that the cumulative number of infected could reach 180,000 (with a lower bound of 45,000) by February 29. Regarding the number of deaths, simulations forecast that on the basis of the up to the 10th of February reported data, the death toll might exceed 2,700 (as a lower bound) by February 29. Our analysis further reveals a significant decline of the case fatality ratio from January 26 to which various factors may have contributed, such as the severe control measures taken in Hubei, China (e.g. quarantine and hospitalization of infected individuals), but mainly because of the fact that the actual cumulative numbers of infected and recovered cases in the population most likely are much higher than the reported ones. Thus, in a scenario where we have taken twenty times the confirmed number of infected and forty times the confirmed number of recovered cases, the case fatality ratio is around ~0.15% in the total population. Importantly, based on this scenario, simulations suggest a slow down of the outbreak in Hubei at the end of February. Copyright: © 2020 Anastassopoulou et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Ehrlich, H., McKenney, M., Elkbuli, A.
Strategic planning and recommendations for healthcare workers during the COVID-19 pandemic
(2020) American Journal of Emergency Medicine

Functional exhaustion of antiviral lymphocytes in COVID-19 patients
(2020) Cellular and Molecular Immunology
Contini, C., Nuzzo, M.D., Barp, N., Bonazza, A., de Giorgio, R., Tognon, M., Rubino, S.

The novel zoonotic COVID-19 pandemic: An expected global health concern

Abstract:
18 years ago, in 2002, the world was astonished by the appearance of Severe Acute Respiratory Syndrome (SARS), supported by a zoonotic coronavirus, called SARS-CoV, from the Guangdong Province of southern China. After about 10 years, in 2012, another similar coronavirus triggered the Middle East Respiratory Syndrome (MERS-CoV) in Saudi Arabia. Both caused severe pneumonia killing 774 and 858 people with 8700 cases of confirmed infection for the former, and 2494 for the latter, causing significant economic losses. 8 years later, despite the MERS outbreak remaining in certain parts of the world, at the end of 2019, a new zoonotic coronavirus (SARS-CoV-2) and responsible of coronavirus Disease (COVID-19), arose from Wuhan, Hubei Province, China. It spread rapidly and to date has killed 3,242 persons with more than 81,000 cases of infection in China and causing over 126,000 global cases and 5,414 deaths in 166 other countries around the world, especially Italy. SARS-CoV-2 would seem to have come from a bat, but the intermediate reservoir continues to be unknown. Nonetheless, as for SARS-CoV and MERS CoV, the Spillover effect linked to animal-human promiscuity, human activities including deforestation, illegal bush-trafficking and bushmeat, cannot be excluded. Recently, however, evidence of inter-human only transmission of SARS-CoV-2 has been accumulated and thus, the outbreak seems to be spreading by human-to-human transmission throughout a large part of the world. Herein we will provide with an update on the main features of COVID-19 and suggest possible solutions how to halt the expansion of this novel pandemic. Copyright © 2020 Contini et al.

Huang, R., Liu, M., Ding, Y.

Spatial-temporal distribution of COVID-19 in China and its prediction: A data-driven modeling analysis

Abstract:
Currently, the outbreak of COVID-19 is rapidly spreading especially in Wuhan city, and threatens 14 million people in central China. In the present study we applied the Moran index, a strong statistical tool, to the spatial panel to show that COVID-19 infection is spatially dependent and mainly spread from Hubei Province in Central China to neighbouring areas. Logistic model was employed according to the trend of available data, which shows the difference between Hubei Province and outside of it. We also calculated the reproduction number R0 for the range of [2.23, 2.51] via SEIR model. The measures to reduce or prevent the virus spread should be implemented, and we expect our data-driven modeling analysis providing some insights to identify and prepare for the future virus control. Copyright © 2020 Huang et al.

Hormati, A., Shahhamzeh, A., Afifian, M., Khodadust, F., Ahmadvour, S.

Can COVID-19 present unusual GI symptoms?
Pan, X.-B.
**Application of personal-oriented digital technology in preventing transmission of COVID-19, China**
(2020) Irish Journal of Medical Science

**Abstract:**
We reported several personal-oriented and mobile phone-based information technologies which were recently developed and widely used during the outbreak of COVID-19 in China. These technologies help reduce the transmission of COVID-19 and maintain normal social order. © 2020, Royal Academy of Medicine in Ireland.

Mareiniss, D.P.
**The impending storm: COVID-19, pandemics and our overwhelmed emergency departments**
(2020) American Journal of Emergency Medicine

Rubino, S., Kelvin, N., Bermejo-Martin, J.F., Kelvin, D.J.
**As COVID-19 cases, deaths and fatality rates surge in Italy, underlying causes require investigation**

**Abstract:**
COVID-19 case fatalities surged during the month of March 2020 in Italy, reaching over 10,000 by 28 March 2020. This number exceeds the number of fatalities in China (3,301) recorded from January to March, even though the number of diagnosed cases was similar (85,000 Italy vs. 80,000 China). Case Fatality Rates (CFR) could be somewhat unreliable because the estimation of total case numbers is limited by several factors, including insufficient testing and limitations in test kits and materials, such as NP swabs and PPE for testers. Sero prevalence of SARS-CoV-2 antibodies may help in more accurate estimations of the total number of cases. Nevertheless, the disparity in the differences in the total number of fatalities between Italy and China suggests that investigation into several factors, such as demographics, sociological interactions, availability of medical equipment (ICU beds and PPE), variants in immune proteins (e.g., HLA, IFNs), past immunity to related CoVs, and mutations in SARS-CoV-2, could impact survival of severe COVID-19 illness survival and the number of case fatalities. Copyright © 2020 Rubino et al.

Spinelli, A., Pellino, G.
**COVID-19 pandemic: perspectives on an unfolding crisis**
(2020) British Journal of Surgery

De Ceukelaire, W., Bodini, C.
**We Need Strong Public Health Care to Contain the Global Corona Pandemic**
(2020) International Journal of Health Services

**Abstract:**
The corona virus (COVID-19) outbreak has spread from China to over a hundred countries in less than 2 months. Now is the time to take stock and to assess the responses of different countries to the outbreak so far. What we can learn from the global Corona pandemic so far is that strong public health systems have the resilience to address massive health threats with the collective responses
they require. Privatization of health services and individualization of risks might further undermine our ability to address this and future global pandemics. © The Author(s) 2020.

Ye, Z., Zhang, Y., Wang, Y., Huang, Z., Song, B.
Chest CT manifestations of new coronavirus disease 2019 (COVID-19): a pictorial review
(2020) European Radiology
Abstract:
Coronavirus disease 2019 (COVID-19) outbreak, first reported in Wuhan, China, has rapidly swept around the world just within a month, causing global public health emergency. In diagnosis, chest computed tomography (CT) manifestations can supplement parts of limitations of real-time reverse transcription polymerase chain reaction (RT-PCR) assay. Based on a comprehensive literature review and the experience in the frontline, we aim to review the typical and relatively atypical CT manifestations with representative COVID-19 cases at our hospital, and hope to strengthen the recognition of these features with radiologists and help them make a quick and accurate diagnosis.

Key Points • Ground glass opacities, consolidation, reticular pattern, and crazy paving pattern are typical CT manifestations of COVID-19. • Emerging atypical CT manifestations, including airway changes, pleural changes, fibrosis, nodules, etc., were demonstrated in COVID-19 patients. • CT manifestations may associate with the progression and prognosis of COVID-19. © 2020, European Society of Radiology.

Clinical progression of patients with COVID-19 in Shanghai, China
(2020) Journal of Infection
Abstract:
Background: Studies on the 2019 novel coronavirus disease (COVID-19) have generally been limited to the description of the epidemiology and initial clinical characteristics. We investigated the temporal progression in patients with COVID-19. Methods: In this retrospective, single-center study, we included confirmed cases of COVID-19 from Jan 20 to Feb 6, 2020 in Shanghai. Final date of follow-up was February 25, 2020. Results: Of the 249 patients enrolled, the median age was 51 years old, and 126 (50.6%) were male. The duration from onset of symptoms to hospitalization was 4 (2–7) days in symptomatic patients. Fever was occurred in 235 (94.3%) patients. A total of 215 (86.3%) patients had been discharged after 16 (12–20) days hospitalization. The estimated median duration of fever in all the patients with fever was 10 days (95 confidential intervals [CIs]: 8–11 days) after onset of symptoms. Patients who were transferred to intensive care units (ICU) had significantly longer duration of fever as compared to those not in ICU (31 days v.s. 9 days after onset of symptoms, respectively, P <0.0001). Radiological aggravation of initial image was observed in 163 (65.7%) patients on day 7 after onset of symptoms. 154 (94.5%) of these patients showed radiological improvement on day 14. The median duration to negative reverse-transcriptase PCR tests of upper respiratory tract samples was 11 days (95 CIs: 10–12 days). Viral clearance was more likely to be delayed in patients in ICU than those not in ICU (P <0.0001). In multivariate logistical analysis, age (Odds ratio [OR] = 1.06) and CD4 T cell count (OR = 0.55 per 100 cells/ul increase) were independently associated with ICU admission. Conclusions: The majority of COVID-19 cases are mild. The clinical progression pattern suggests that early control of viral replication and application of host-directed therapy in later stage is essential to improve the prognosis of CVOID-19. © 2020
Abstract:
The current coronavirus (COVID-19) pandemic is again reminding us of the importance of using telehealth to deliver care, especially as means of reducing the risk of cross-contamination caused by close contact. For telehealth to be effective as part of an emergency response it first needs to become a routinely used part of our health system. Hence, it is time to step back and ask why telehealth is not mainstreamed. In this article, we highlight key requirements for this to occur. Strategies to ensure that telehealth is used regularly in acute, post-acute and emergency situations, alongside conventional service delivery methods, include flexible funding arrangements, training and accrediting our health workforce. Telehealth uptake also requires a significant change in management effort and the redesign of existing models of care. Implementing telehealth proactively rather than reactively is more likely to generate greater benefits in the long-term, and help with the everyday (and emergency) challenges in healthcare. © The Author(s) 2020.

Popescu, S.
Roadblocks to Infection Prevention Efforts in Healthcare SARS-CoV-2/COVID-19 Response
(2020) Disaster Medicine and Public Health Preparedness
Abstract:
The outbreak of a novel coronavirus, COVID-19, is challenging international public health and healthcare efforts. As hospitals work to acquire enough personal protective equipment and brace for potential cases, the role of infection prevention efforts and programs has become increasingly important. Lessons from the 2003 SARS-CoV outbreak in Toronto and 2015 MERS-CoV outbreak in South Korea have unveiled the critical role that hospitals play in outbreaks, especially of novel coronaviruses. Their ability to amplify the spread of disease can rapidly fuel transmission of the disease and often those failures in infection prevention and general hospital practices contribute to such events. While efforts to enhance infection prevention measures and hospital readiness are underway in the United States, it is important to understand why these programs were not able to maintain continued, sustainable levels of readiness. History has shown that infection prevention programs are primarily responsible for preparing hospitals and responding to biological events but face under-staffing and focused efforts defined by administrators. The current U.S. healthcare system though, is built upon a series of priorities that often view biopreparedness as a costly endeavor. Awareness of these competing priorities and the challenges infection prevention programs face when working to maintain biopreparedness is critical in adequately addressing this critical infrastructure in the face of an international outbreak. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.

Cossarizza, A., De Biasi, S., Guaraldi, G., Girardis, M., Mussini, C., for the Modena Covid-19 Working Group (MoCo19)#
SARS-CoV-2, the Virus that Causes COVID-19: Cytometry and the New Challenge for Global Health
(2020) Cytometry Part A
**Bashyam, A.M.,** Feldman, S.R.

**Should patients stop their biologic treatment during the COVID-19 pandemic**

(2020) Journal of Dermatological Treatment

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**Seddighi, H.**

**Trust in humanitarian aid from the earthquake 2017 to COVID-19 in Iran: A policy analysis**

(2020) Disaster Medicine and Public Health Preparedness

**Abstract:**
The earthquake of November 2017, the great flood of April 2019, and the COVID-19 outbreak in 2020 are three major emergencies in Iran during the last three years. A common issue in all these crises seems to be the issue of "trust". Official authorities including Iranian President, ministers, and the Judiciary system tried to gain people's trust by either changing policies or developing new ones. In August 2019, the new law on crisis management in Iran went into effect and the issue of people donation has been considered too. Also, in their response to COVID-19 outbreak, Iranian officials ordered to all sectors to cooperate with Ministry of Health and provide it with all necessary facilities. Therefore, it seems that new policies are still needed to overcome mistrust in Iran at the times of emergency. Developing a policy on donation management was the first step, while there are several factors could have contributing to the perception of the mistrust and failure in emergency missions. Mistrust can be the result of different causes including but not limited to lack of knowledge on capabilities and efficiencies of humanitarian organizations, engagement of a wide range of organizations from different categories, extending of mistrust of an organization to other emergency organizations in the area or all of operation, lack of unity in emergency response; and poor public relations. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.

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**Gagliano, A.,** Villani, P.G., Cò, F.M., Paglia, S., Bisagni, P.A.G., Perotti, G.M., Storti, E., Lombardo, M.

**2019-ncov's epidemic in middle province of northern Italy: Impact, logistic & strategy in the first line hospital**

(2020) Disaster Medicine and Public Health Preparedness

**Abstract:**
The novel coronavirus (2019-nCoV) began in China in early December 2019 and rapidly has spread to many countries around the globe, with the number of confirmed cases increasing every day. An epidemic has been recorded since February 20 in a middle province in Northern Italy (Lodi's province, in the low Po Valley). The first line Hospital had to redesign its logistical and departmental structure to respond to the influx of 2019-ncov positive patients who needed hospitalisation. Logistical and structural strategies were guided by the crisis unit, managing in 8 days from the beginning of the epidemic to prepare the hospital ready to welcome more than 200 positive COVID19 patients with different ventilatory requirements, keeping clean emergency access lines and restoring surgical interventions and deferred urgent ordinary activity. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.

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**Clinical features and treatment of COVID-19 patients in northeast Chongqing**
Abstract:
The outbreak of the novel coronavirus in China (SARS-CoV-2) that began in December 2019 presents a significant and urgent threat to global health. This study was conducted to provide the international community with a deeper understanding of this new infectious disease. Epidemiological, clinical features, laboratory findings, radiological characteristics, treatment, and clinical outcomes of 135 patients in northeast Chongqing were collected and analyzed in this study. A total of 135 hospitalized patients with COVID-19 were enrolled. The median age was 47 years (interquartile range, 36-55), and there was no significant gender difference (53.3% men). The majority of patients had contact with people from the Wuhan area. Forty-three (31.9%) patients had underlying disease, primarily hypertension (13 [9.6%]), diabetes (12 [8.9%]), cardiovascular disease (7 [5.2%]), and malignancy (4 [3.0%]). Common symptoms included fever (120 [88.9%]), cough (102 [76.5%]), and fatigue (44 [32.5%]). Chest computed tomography scans showed bilateral patchy shadows or ground glass opacity in the lungs of all the patients. All patients received antiviral therapy (135 [100%]) (Kaletra and interferon were both used), antibacterial therapy (59 [43.7%]), and corticosteroids (36 [26.7%]). In addition, many patients received traditional Chinese medicine (TCM) (124 [91.8%]). It is suggested that patients should receive Kaletra early and should be treated by a combination of Western and Chinese medicines. Compared to the mild cases, the severe ones had lower lymphocyte counts and higher plasma levels of Pt, APTT, d-dimer, lactate dehydrogenase, PCT, ALB, C-reactive protein, and aspartate aminotransferase. This study demonstrates the clinic features and therapies of 135 COVID-19 patients. Kaletra and TCM played an important role in the treatment of the viral pneumonia. Further studies are required to explore the role of Kaletra and TCM in the treatment of COVID-19. © 2020 Wiley Periodicals, Inc.

Zhu, L., Xu, X., Ma, K., Yang, J., Guan, H., Chen, S., Chen, Z., Chen, G.
Successful recovery of COVID-19 pneumonia in a renal transplant recipient with long-term immunosuppression
(2020) American Journal of Transplantation
Abstract:
The current outbreak of Coronavirus Disease 2019 (COVID-19) has raised great concern worldwide, but its impact on transplant recipients is unknown. We report here the clinical features and therapeutic course of the first reported renal transplant recipient with confirmed COVID-19 pneumonia. This is a 52-year-old man who received kidney transplantation 12 years ago. His overall clinical characteristics (symptoms, laboratory examinations, and chest CT) were similar to those of non-transplanted COVID-19 patients. Following a treatment regimen consisting of reduced immunosuppressant use and low dose methylprednisolone-based therapy, the COVID-19 pneumonia in this long-term immunosuppressive patient was successfully recovered. This effectively treated case has reference value for the future treatment of other transplant patients with COVID-19 pneumonia. © 2020 The American Society of Transplantation and the American Society of Transplant Surgeons

Nakazawa, E., Ino, H., Akabayashi, A.
Chronology of COVID-19 cases on the Diamond Princess cruise ship and ethical considerations: A report from Japan
(2020) Disaster Medicine and Public Health Preparedness
Abstract:
Fact: The Diamond Princess cruise ship has been anchored at the Yokohama port in Japan since February 3, 2020. A total of 691 cases of COVID-19 infection had been confirmed as of February 23. The government initially assumed that the infection was not spreading aboard and therefore indicated that any persons who either tested negative for the virus or were asymptomatic should immediately disembark. However, on February 5, the government set a 14-day health observation period because of the severity of the infection. Passengers confirmed to free from infection began disembarking on Day 15 of quarantine (February 19).

Facts to be examined: The effectiveness and validity of infection control, justification for the timing of inspections, and even the nature of COVID-19 itself are now all in question.

Ethical considerations: The ethical considerations related to cruise ship infection control include the reasonable justification for isolation, the psychological fragility and quality of life of the isolated passengers and crew members, the procedural justice inherent in a forced quarantine, and the optimization of control measures.

Public health preparedness: The international coordination framework and the global ramifications of such outbreaks should be reevaluated by the international community. Denying a ship's entry based on local politics is incompatible with global justice. Events such as these require an international response and global regulations that seek to reduce disparities. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.


Transcriptomic characteristics of bronchoalveolar lavage fluid and peripheral blood mononuclear cells in COVID-19 patients

Abstract:
Circulating in China and 158 other countries and areas, the ongoing COVID-19 outbreak has caused devastating mortality and posed a great threat to public health. However, efforts to identify effectively supportive therapeutic drugs and treatments has been hampered by our limited understanding of host immune response for this fatal disease. To characterize the transcriptional signatures of host inflammatory response to SARS-CoV-2 (HCoV-19) infection, we carried out transcriptome sequencing of the RNAs isolated from the bronchoalveolar lavage fluid (BALF) and peripheral blood mononuclear cells (PBMC) specimens of COVID-19 patients. Our results reveal distinct host inflammatory cytokine profiles to SARS-CoV-2 infection in patients, and highlight the association between COVID-19 pathogenesis and excessive cytokine release such as CCL2/MCP-1, CXCL10/IP-10, CCL3/MIP-1A, and CCL4/MIP1B. Furthermore, SARS-CoV-2 induced activation of apoptosis and P53 signalling pathway in lymphocytes may be the cause of patients’ lymphopenia. The transcriptome dataset of COVID-19 patients would be a valuable resource for clinical guidance on anti-inflammatory medication and understanding the molecular mechanisms of host response. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.

Kaplan, E.H.

Containing 2019-nCoV (Wuhan) coronavirus
(2020) Health Care Management Science

Abstract:
The novel coronavirus 2019-nCoV first appeared in December 2019 in Wuhan, China. While most of the initial cases were linked to the Huanan Seafood Wholesale Market, person-to-person
transmission has been verified. Given that a vaccine cannot be developed and deployed for at least a year, preventing further transmission relies upon standard principles of containment, two of which are the isolation of known cases and the quarantine of persons believed at high risk of exposure. This note presents probability models for assessing the effectiveness of case isolation and quarantine within a community during the initial phase of an outbreak with illustrations based on early observations from Wuhan. © 2020, Springer Science+Business Media, LLC, part of Springer Nature.

Bo, H.-X., Li, W., Yang, Y., Wang, Y., Zhang, Q., Cheung, T., Wu, X., Xiang, Y.-T.  
**Posttraumatic stress symptoms and attitude toward crisis mental health services among clinically stable patients with COVID-19 in China**  
(2020) Psychological Medicine

Li, L., Yang, Z., Dang, Z., Meng, C., Huang, J., Meng, H., Wang, D., Chen, G., Zhang, J., Peng, H., Shao, Y.  
**Propogation analysis and prediction of the COVID-19**  
*Abstract:*  
Based on the official data modeling, this paper studies the transmission process of the Corona Virus Disease 2019 (COVID-19). The error between the model and the official data curve is quite small. At the same time, it realized forward prediction and backward inference of the epidemic situation, and the relevant analysis help relevant countries to make decisions. © 2020 The Authors

Craig, A.T., Heywood, A.E., Hall, J.  
**Risk of COVID-19 importation to the Pacific islands through global air travel**  
(2020) Epidemiology and Infection  
*Abstract:*  
On 30 January 2020, WHO declared coronavirus (COVID-19) a global public health emergency. As of 12 March 2020, 125,048 confirmed COVID-19 cases in 118 countries had been reported. On 12 March 2020, the first case in the Pacific islands was reported in French Polynesia; no other Pacific island country or territory has reported cases. The purpose of our analysis is to show how travellers may introduce COVID-19 into the Pacific islands and discuss the role robust health systems play in protecting health and reducing transmission risk. We analyse travel- A nd Global Health Security Index-data using a scoring tool to produce quantitative estimates of COVID-19 importation risk, by departing and arriving country. Our analysis indicates that, as of 12 March 2020, the highest risk air routes by which COVID-19 may be imported into the Pacific islands are from east Asian countries (specifically, China, Korea and Japan) to north Pacific airports (likely Guam, Commonwealth of the Northern Mariana Islands or, to a less extent, Palau); or from China, Japan, Singapore, the United States of America or France to south Pacific ports (likely, Fiji, Papua New Guinea French Polynesia, or New Caledonia). Other importation routes include from other east Asian countries to Guam, and from Australia, New Zealand and other European countries to the south Pacific. The tool provides a useful method for assessing COVID-19 importation risk and may be useful in other settings. © 2020 Cambridge University Press. All rights reserved.

Global epidemiology of coronavirus disease 2019 (COVID-19): disease incidence, daily cumulative index, mortality, and their association with country healthcare resources and economic status

(2020) International Journal of Antimicrobial Agents, art. no. 105946

Abstract:
It has been 2 months since the first case of coronavirus disease 2019 (COVID-19) was reported in Wuhan, China. So far, COVID-19 has affected 85 403 patients in 57 countries/territories and has caused 2924 deaths in 9 countries. However, epidemiological data differ between countries. Although China had higher morbidity and mortality than other sites, the number of new daily cases in China has been lower than outside of China since 26 February 2020. The incidence ranged from 61.44 per 1 000 000 people in the 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 29 February 2020) was greatest in China (1320.85), followed by the Republic of Korea (78.78), Iran (43.11) and Italy (30.62). However, the DCIs in other countries/territories were <10 per day. Several effective measures including restricting travel from China, controlling the distribution of masks, extensive investigation of COVID-19 spread, and once-daily press conferences by the government to inform and educate people were aggressively conducted in Taiwan. This is probably the reason why there was only 39 cases (as of 29 February 2020) with a DCI of 1 case per day in Taiwan, which is much lower than that of nearby countries such as the Republic of Korea and Japan. In addition, the incidence and mortality were correlated with the DCI. However, further study and continued monitoring are needed to better understand the underlying mechanism of COVID-19. © 2020 The Authors

Wang, Y., Di, Y., Ye, J., Wei, W.

Study on the public psychological states and its related factors during the outbreak of coronavirus disease 2019 (COVID-19) in some regions of China

(2020) Psychology, Health and Medicine

Abstract:
Background: As COVID-19 occurs suddenly and is highly contagious, this will inevitably cause people anxiety, depression, etc. The study on the public psychological states and its related factors during the COVID-19 outbreak is of practical significance. Methods: 600 valid questionnaires were received. The Self-Rating Anxiety Scale (SAS) and the Self-Rating Depression Scale (SDS) were used. Results: Females’ anxiety risk was 3.01 times compared to males (95% CI 1.39–6.52). Compared with people below 40 years old, the anxiety risk of people above 40 years old was 0.40 times (95% CI 0.16–0.99). SDS results indicated that the difference between education level and occupation was statistically significant (p = 0.024, 0.005). Compared to people with a master’s degree or above, those with a bachelor’s degree group had a depression risk of 0.39 times (95% CI 0.17–0.87). Compared with professionals, industrial service workers and other staff had a depression risk of 0.31 times (95% CI 0.15–0.65) and 0.38 times (95% CI 0.15–0.93). Conclusions: 600 questionnaire participants were psychologically stable. Non-anxiety and non-depression rates were 93.67% and 82.83%, respectively. There were anxiety in 6.33% and depression in 17.17%. Therefore, we should pay attention to the psychological states of the public. © 2020, © 2020 Informa UK Limited, trading as Taylor & Francis Group.

Safety Recommendations for Evaluation and Surgery of the Head and Neck during the COVID-19 Pandemic
(2020) JAMA Otolaryngology - Head and Neck Surgery

Abstract:
Importance: The rapidly expanding novel coronavirus disease 2019 (COVID-19) pandemic, caused by severe acute respiratory syndrome coronavirus 2, has challenged the medical community to an unprecedented degree. Physicians and health care workers are at added risk of exposure and infection during the course of patient care. Because of the rapid spread of this disease through respiratory droplets, health care workers who come in close contact with the upper aerodigestive tract during diagnostic and therapeutic procedures, such as otolaryngologists-head and neck surgeons, are particularly at risk. A set of safety recommendations was created based on a review of the literature and communications with physicians with firsthand knowledge of safety procedures during the COVID-19 pandemic. Observations: A high number of health care workers were infected during the first phase of the pandemic in the city of Wuhan, China. Subsequently, by adopting strict safety precautions, other regions were able to achieve high levels of safety for health care workers without jeopardizing the care of patients. The most common procedures related to the examination and treatment of upper aerodigestive tract diseases were reviewed. Each category was reviewed based on the potential risk imposed to health care workers. Specific recommendations were made based on the literature, when available, or consensus best practices. Specific safety recommendations were made for performing tracheostomy in patients with COVID-19. Conclusions and Relevance: Preserving a highly skilled health care workforce is a top priority for any community and health care system. Based on the experience of health care systems in Asia and Europe, by following strict safety guidelines, the risk of exposure and infection of health care workers could be greatly reduced while providing high levels of care. The provided recommendations, which may evolve over time, could be used as broad guidance for all health care workers who are involved in the care of patients with COVID-19. © 2020 Cambridge University Press. All rights reserved.

Huang, Y.-C., Lee, P.-I., Hsueh, P.-R.
Evolving reporting criteria of COVID-19 in Taiwan during the epidemic
(2020) Journal of Microbiology, Immunology and Infection

Epidemiological, clinical and virological characteristics of 74 cases of coronavirus-infected disease 2019 (COVID-19) with gastrointestinal symptoms
(2020) Gut, art. no. 320926

Abstract:
Objective: The SARS-CoV-2-infected disease (COVID-19) outbreak is a major threat to human beings. Previous studies mainly focused on Wuhan and typical symptoms. We analysed 74 confirmed COVID-19 cases with GI symptoms in the Zhejiang province to determine epidemiological, clinical and virological characteristics. Design: COVID-19 hospital patients were admitted in the Zhejiang province from 17 January 2020 to 8 February 2020. Epidemiological, demographic, clinical, laboratory, management and outcome data of patients with GI symptoms
were analysed using multivariate analysis for risk of severe/critical type. Bioinformatics were used to analyse features of SARS-CoV-2 from Zhejiang province. Results: Among enrolled 651 patients, 74 (11.4%) presented with at least one GI symptom (nausea, vomiting or diarrhoea), average age of 46.14 years, 4-day incubation period and 10.8% had pre-existing liver disease. Of patients with COVID-19 with GI symptoms, 17 (22.97%) and 23 (31.08%) had severe/critical types and family clustering, respectively, significantly higher than those without GI symptoms, 47 (8.14%) and 118 (20.45%). Of patients with COVID-19 with GI symptoms, 29 (39.19%), 23 (31.08%), 8 (10.81%) and 16 (21.62%) had significantly higher rates of fever &gt;38.5°C, fatigue, shortness of breath and headache, respectively. Low-dose glucocorticoids and antibiotics were administered to 14.86% and 41.89% of patients, respectively. Sputum production and increased lactate dehydrogenase/glucose levels were risk factors for severe/critical type. Bioinformatics showed sequence mutation of SARS-CoV-2 with m6A methylation and changed binding capacity with ACE2. Conclusion: We report COVID-19 cases with GI symptoms with novel features outside Wuhan. Attention to patients with COVID-19 with non-classic symptoms should increase to protect health providers. © 2020 Author(s).

Khan, S., Peng, L., Siddique, R., Nabi, G., Nawsherwan, Xue, M., Liu, J., Han, G. 
Impact of COVID-19 infection on pregnancy outcomes and the risk of maternal-to-neonatal intrapartum transmission of COVID-19 during natural birth 
(2020) Infection Control and Hospital Epidemiology 
Abstract: 
Little is known about the maternal-to-neonatal intrapartum transmission of COVID-19 via vaginal route. In this study, we report the adverse pregnancy outcomes in pregnant women infected with COVID-19 pneumonia and the risk of intrapartum transmission of COVID-19 via vaginal route. None of the three neonates were infected with COVID-19 delivered via natural birth. Only one neonate was delivered prematurely. No neonatal death and stillbirth were observed in pregnant women infected with COVID-19. Moreover, all of the neonates had normal birth weight, birth length, and normal Apgar score. © 2020 by The Society for Healthcare Epidemiology of America. All rights reserved.

Roda, W.C., Varughese, M.B., Han, D., Li, M.Y. 
Why is it difficult to accurately predict the COVID-19 epidemic? 
(2020) Infectious Disease Modelling, 5, pp. 271-281. 
Abstract: 
Since the COVID-19 outbreak in Wuhan City in December of 2019, numerous model predictions on the COVID-19 epidemics in Wuhan and other parts of China have been reported. These model predictions have shown a wide range of variations. In our study, we demonstrate that nonidentifiability in model calibrations using the confirmed-case data is the main reason for such wide variations. Using the Akaike Information Criterion (AIC) for model selection, we show that an SIR model performs much better than an SEIR model in representing the information contained in the confirmed-case data. This indicates that predictions using more complex models may not be more reliable compared to using a simpler model. We present our model predictions for the COVID-19 epidemic in Wuhan after the lockdown and quarantine of the city on January 23, 2020. We also report our results of modeling the impacts of the strict quarantine measures undertaken in the city after February 7 on the time course of the epidemic, and modeling the potential of a second outbreak after the return-to-work in the city.
Featuring COVID-19 cases via screening symptomatic patients with epidemiologic link during flu season in a medical center of central Taiwan (2020) Journal of Microbiology, Immunology and Infection

Abstract:
Background: Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first reported in Wuhan, Hubei province, China has now rapidly spread over 50 countries. For the prevention and control of infection, Taiwan Centers for Disease Control initiated testing of SARS-CoV-2 on January 24th 2020 for persons suspected with this disease. Until February 28th, 43 flu-like symptomatic patients were screened in China Medical University Hospital. Methods: Two patients were confirmed positive for SARS-CoV-2 infection by rRT-PCR as COVID-19 patients A and B. Causative pathogens for included patients were detected using FilmArray™ Respiratory Panel. We retrospectively analyzed the clinical presentations, laboratory data, radiologic findings, and travel and exposure contact histories, of the COVID-19 patients in comparison to those with other respiratory infections. Results: Through contact with Taiwan No. 19 case patient on 27th January, COVID-19 patients A and B were infected. Both patients had no identified comorbidities and developed mild illness with temporal fever, persistent cough, and lung interstitial infiltrates. Owing to the persistence of positive SARS-CoV-2 in respiratory specimen, the two COVID-19 patients are still in the isolation rooms despite recovery until 10th of March. The results of FilmArray™ Respiratory Panel revealed 22 of the 41 non-COVID-19 patients were infected by particular pathogens. In general, seasonal respiratory pathogens are more prevalent than SARS-CoV-2 in symptomatic patients in non-COVID-19 endemic area during the flu season. Since all patients shared similar clinical and laboratory findings, expanded surveillance of detailed exposure history for suspected patients and application of rapid detection tools are highly recommended. © 2020

Han, X., Fan, Y., Wan, Y.-L., Shi, H.

Abstract:
Novel coronavirus has become a global health hazard and its high infectivity is alarming. The imaging findings of the 2019-nCoV infection in our young diabetic patient featured ground-glass opacities and consolidations in both lungs. The lung lesions may involute rapidly during the course. The patient showed improvement both clinically and on computed tomography imaging at discharged after 2 weeks'treatment. Computed tomography scans of patients helped monitor the changes continuously, which could timely provide the information of the evolution of the disease or therapeutic effect to clinicians. © 2020 Lippincott Williams and Wilkins. All rights reserved.

Host susceptibility to severe COVID-19 and establishment of a host risk score: Findings of 487 cases outside Wuhan (2020) Critical Care, 24 (1), art. no. 108

Ahmed, Q.A., Memish, Z.A.
The cancellation of mass gatherings (MGs)? Decision making in the time of COVID-19
(2020) Travel Medicine and Infectious Disease, art. no. 101631
Abstract:
Our recommendation, as experts who have monitored health hazards at the Hajj for over 15 years, especially if the situation with COVID-19 continues to escalate globally is that Hajj 2020 will be at risk of being suspended and a means for Muslims to fulfill their rights in the future either personally or even by proxy need to be announced. The same holds true for the Summer 2020 Olympics in Japan and for many other MGs and large gatherings. Decisions in the time of COVID-19 will be closely followed and will be a blueprint for other mass gatherings.

Liu, H., Liu, F., Li, J., Zhang, T., Wang, D., Lan, W.
Clinical and CT imaging features of the COVID-19 pneumonia: Focus on pregnant women and children
(2020) Journal of Infection
Abstract:
Background: The ongoing outbreak of COVID-19 pneumonia is globally concerning. We aimed to investigate the clinical and CT features in the pregnant women and children with this disease, which have not been well reported. Methods: Clinical and CT data of 59 patients with COVID-19 from January 27 to February 14, 2020 were retrospectively reviewed, including 14 laboratory-confirmed non-pregnant adults, 16 laboratory-confirmed and 25 clinically-diagnosed pregnant women, and 4 laboratory-confirmed children. The clinical and CT features were analyzed and compared. Findings: Compared with the non-pregnant adults group (n = 14), initial normal body temperature (9 [56%] and 16 [64%]), leukocytosis (8 [50%] and 9 [36%]) and elevated neutrophil ratio (14 [88%] and 20 [80%]), and lymphopenia (9 [56%] and 16 [64%]) were more common in the laboratory-confirmed (n = 16) and clinically-diagnosed (n = 25) pregnant groups. Totally 614 lesions were detected with predominantly peripheral and bilateral distributions in 54 (98%) and 37 (67%) patients, respectively. Pure ground-glass opacity (GGO) was the predominant presence in 94/131 (72%) lesions for the non-pregnant adults. Mixed consolidation and complete consolidation were more common in the laboratory-confirmed (70/161 [43%]) and clinically-diagnosed (153/322 [48%]) pregnant groups than 37/131 (28%) in the non-pregnant adults (P = 0.007, P < 0.001). GGO with reticulation was less common in 9/161 (6%) and 16/322 (5%) lesions for the two pregnant groups than 24/131 (18%) for the non-pregnant adults (P = 0.001, P < 0.001). The pulmonary involvement in children with COVID-19 was mild with a focal GGO or consolidation. Twenty-three patients underwent follow-up CT, revealing progression in 9/13 (69%) at 3 days whereas improvement in 8/10 (80%) at 6–9 days after initial CT scans. Interpretation: Atypical clinical findings of pregnant women with COVID-19 could increase the difficulty in initial identification. Consolidation was more common in the pregnant groups. The clinically-diagnosed cases were vulnerable to more pulmonary involvement. CT was the modality of choice for early detection, severity assessment, and timely therapeutic effects evaluation for the cases with epidemic and clinical features of COVID-19 with or without laboratory confirmation. The exposure history and clinical symptoms were more helpful for screening in children versus chest CT. © 2020

Imaging Features of Coronavirus disease 2019 (COVID-19): Evaluation on Thin-Section CT
(2020) Academic Radiology
Abstract:
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: Forty-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. © 2020 The Association of University Radiologists


Abstract:
Middle East Respiratory Syndrome Coronavirus (MERS-CoV) has plagued the Middle East since it was first reported in 2012. Recently, at the end of December 2019, a cluster of pneumonia cases were reported from Wuhan city, Hubei Province, China, linked to a wet seafood market with a new coronavirus identified as the etiologic agent currently named SARS-CoV-2. Most cases are in Mainland China with international spread to 25 countries. The novelty of the virus, the rapid national and international spread, and the lack of therapeutic and preventative strategies have led the WHO International Health Regulation emergency committee to declare the disease as Public Health Emergency of International Concern (PHEIC) on January 30, 2020. As it relates to countries with the ongoing MERS-CoV community cases and hospital acquired infections, there will be a huge challenge for HCWs to deal with both coronaviruses, especially with the lack of standardized and approved point of care testing. This challenge will now be faced by the whole global health community dealing with COVID-19 since both coronaviruses have similar presentation. Those patients should now be tested for both MERS-CoV and SARS-CoV-2 simultaneously, and with the continuing wide international spread of SARS-CoV-2, the travel history to China in the last 14 days will be of less significance. © 2020 The Authors.


Abstract:
Background: With its epicenter in Wuhan, China, the COVID-19 outbreak was declared a pandemic by the World Health Organization (WHO). While many countries have implemented flight restrictions to China, an increasing number of cases with or without travel background to China are confirmed daily. These developments support concerns on possible unidentified and unreported international COVID-19 cases, which could lead to new local disease epicenters. Methods: We have analyzed all available data on the development of international COVID-19 cases from January 20th, 2020 until February 18th, 2020. COVID-19 cases with and without travel history to China were
divided into cohorts according to the Healthcare Access and Quality Index (HAQ-Index) of each country. Chi-square and Post-hoc testing were performed. Results: While COVID-19 cases with travel history to China seem to peak for each HAQ-cohort, the number of non-travel related COVID-19 cases seem to continuously increase in the HAQ-cohort of countries with higher medical standards. Further analyses demonstrate a significantly lower proportion of reported COVID-19 cases without travel history to China in countries with lower HAQ (HAQ I vs. HAQ II, posthoc p < 0.01). Conclusions: Our data indicate that countries with lower HAQ-index may either underreport COVID-19 cases or are unable to adequately detect them. Although our data may be incomplete and must be interpreted with caution, inconsistencies in reporting COVID-19 cases is a serious problem which might sabotage efforts to contain the virus. © 2020

Kamel Boulos, M.N., Geraghty, E.M.

Geographical tracking and mapping of coronavirus disease COVID-19/severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic and associated events around the world: How 21st century GIS technologies are supporting the global fight against outbreaks and epidemics
(2020) International Journal of Health Geographics, 19 (1), art. no. 8

Abstract:
In December 2019, a new virus (initially called ‘Novel Coronavirus 2019-nCoV’ and later renamed to SARS-CoV-2) causing severe acute respiratory syndrome (coronavirus disease COVID-19) emerged in Wuhan, Hubei Province, China, and rapidly spread to other parts of China and other countries around the world, despite China’s massive efforts to contain the disease within Hubei. As with the original SARS-CoV epidemic of 2002/2003 and with seasonal influenza, geographic information systems and methods, including, among other application possibilities, online real- or near-real-time mapping of disease cases and of social media reactions to disease spread, predictive risk mapping using population travel data, and tracing and mapping super-spreader trajectories and contacts across space and time, are proving indispensible for timely and effective epidemic monitoring and response. This paper offers pointers to, and describes, a range of practical online/mobile GIS and mapping dashboards and applications for tracking the 2019/2020 coronavirus epidemic and associated events as they unfold around the world. Some of these dashboards and applications are receiving data updates in near-real-time (at the time of writing), and one of them is meant for individual users (in China) to check if the app user has had any close contact with a person confirmed or suspected to have been infected with SARS-CoV-2 in the recent past. We also discuss additional ways GIS can support the fight against infectious disease outbreaks and epidemics. © The Author(s) 2020.

Li, W., Cui, H., Li, K., Fang, Y., Li, S.

Chest computed tomography in children with COVID-19 respiratory infection
(2020) Pediatric Radiology

Abstract:
Background: Infection with COVID-19 is currently rare in children. Objective: To describe chest CT findings in children with COVID-19. Materials and methods: We studied children at a large tertiary-care hospital in China, during the period from 28 January 2019 to 8 February 2020, who had positive reverse transcriptase polymerase chain reaction (RT-PCR) for COVID-19. We recorded findings at any chest CT performed in the included children, along with core clinical observations. Results: We included five children from 10 months to 6 years of age (mean 3.4 years). All had at least one CT scan after admission. Three of these five had CT abnormality on the first CT scan (at 2 days, 4 days and 9 days, respectively, after onset of symptoms) in the form of
patchy ground-glass opacities; all normalised during treatment. Conclusion: Compared to reports in adults, we found similar but more modest lung abnormalities at CT in our small paediatric cohort. © 2020, Springer-Verlag GmbH Germany, part of Springer Nature.

Ammad Ud Din, M., Boppana, L.K.T.  
**An update on the 2019-nCoV outbreak**  
(2020) American Journal of Infection Control  
**Abstract:**  
Cases of 2019-nCoV are now being reported in different regions around the globe, concerning for a possible SARS like epidemic that infected for than 8000 people in 2002-03. Though, major health authorities are still working on understanding the virus and its transmission, here we present a brief report regarding the 2019-nCoV outbreak and what is known so far. © 2020 Association for Professionals in Infection Control and Epidemiology, Inc.

Fang, Y., Nie, Y., Penny, M.  
**Transmission dynamics of the COVID-19 outbreak and effectiveness of government interventions: A data-driven analysis**  
(2020) Journal of Medical Virology  
**Abstract:**  
Using the parameterized susceptible-exposed-infectious-recovered model, we simulated the spread dynamics of coronavirus disease 2019 (COVID-19) outbreak and impact of different control measures, conducted the sensitivity analysis to identify the key factor, plotted the trend curve of effective reproductive number (R), and performed data fitting after the simulation. By simulation and data fitting, the model showed the peak existing confirmed cases of 59,769 arriving on 15 February 2020, with the coefficient of determination close to 1 and the fitting bias 3.02%, suggesting high precision of the data-fitting results. More rigorous government control policies were associated with a slower increase in the infected population. Isolation and protective procedures would be less effective as more cases accrue, so the optimization of the treatment plan and the development of specific drugs would be of more importance. There was an upward trend of R in the beginning, followed by a downward trend, a temporary rebound, and another continuous decline. The feature of high infectiousness for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) led to an upward trend, and government measures contributed to the temporary rebound and declines. The declines of R could be exploited as strong evidence for the effectiveness of the interventions. Evidence from the four-phase stringent measures showed that it was significant to ensure early detection, early isolation, early treatment, adequate medical supplies, patients’ being admitted to designated hospitals, and comprehensive therapeutic strategy. Collaborative efforts are required to combat the novel coronavirus, focusing on both persistent strict domestic interventions and vigilance against exogenous imported cases. © 2020 Wiley Periodicals, Inc.

**Safety and efficacy of different anesthetic regimens for parturients with COVID-19 undergoing Cesarean delivery: a case series of 17 patients [Sécurité et efficacité de différents modes d’anesthésie pour des parturientes infectées par la COVID-19 accouchant par césarienne : une série de 17 cas]**  
(2020) Canadian Journal of Anesthesia  
**Abstract:**
Purpose: To assess the management and safety of epidural or general anesthesia for Cesarean delivery in parturients with coronavirus disease (COVID-19) and their newborns, and to evaluate the standardized procedures for protecting medical staff. Methods: We retrospectively reviewed the cases of parturients diagnosed with severe acute respiratory syndrome coronavirus (SARS-CoV-2) infection disease (COVID-19). Their epidemiologic history, chest computed tomography scans, laboratory measurements, and SARS-CoV-2 nucleic acid positivity were evaluated. We also recorded the patients’ demographic and clinical characteristics, anesthesia and surgery-related data, maternal and neonatal complications, as well as the health status of the involved medical staff. Results: The clinical characteristics of 17 pregnant women infected with SARS-CoV-2 were similar to those previously reported in non-pregnant adult patients. All of the 17 patients underwent Cesarean delivery with anesthesia performed according to standardized anesthesia/surgery procedures. Fourteen of the patients underwent continuous epidural anesthesia with 12 experiencing significant intraoperative hypotension. Three patients received general anesthesia with tracheal intubation because emergency surgery was needed. Three of the parturients are still recovering from their Cesarean delivery and are receiving in-hospital treatment for COVID-19. Three neonates were born prematurely. There were no deaths or serious neonatal asphyxia events. All neonatal SARS-CoV-2 nucleic acid tests were negative. No medical staff were infected throughout the patient care period. Conclusions: Both epidural and general anesthesia were safely used for Cesarean delivery in the parturients with COVID-19. Nevertheless, the incidence of hypotension during epidural anesthesia appeared excessive. Proper patient transfer, medical staff access procedures, and effective biosafety precautions are important to protect medical staff from COVID-19. © 2020, Canadian Anesthesiologists' Society.

Yang, C.-W., Chen, M.-F.
Composition of human-specific slow codons and slow di-codons in SARS-CoV and 2019-nCoV are lower than other coronaviruses suggesting a faster protein synthesis rate of SARS-CoV and 2019-nCoV (2020) Journal of Microbiology, Immunology and Infection

Abstract:
Translation of a genetic codon without a cognate tRNA gene is affected by both the cognate tRNA availability and the interaction with non-cognate isoacceptor tRNAs. Moreover, two consecutive slow codons (slow di-codons) lead to a much slower translation rate. Calculating the composition of host specific slow codons and slow di-codons in the viral protein coding sequences can predict the order of viral protein synthesis rates between different virus strains. Comparison of human-specific slow codon and slow di-codon compositions in the genomes of 590 coronaviruses infect humans revealed that the protein synthetic rates of 2019 novel coronavirus (2019-nCoV) and severe acute respiratory syndrome-related coronavirus (SARS-CoV) may be much faster than other coronaviruses infect humans. Analysis of host-specific slow codon and di-codon compositions provides links between viral genomic sequences and capability of virus replication in host cells that may be useful for surveillance of the transmission potential of novel viruses. © 2020

Cheng, A.C., Williamson, D.A.

Middle East Respiratory Syndrome-Corona Virus (MERS-CoV) associated stress among medical students at a university teaching hospital in Saudi Arabia (2020) Journal of Infection and Public Health

Abstract:
Background and objectives: Middle East Respiratory Syndrome Corona Virus (MERS-CoV) outbreak in 2014 was associated with high public anxiety in the affected countries. Media speculations may have increased this psychological distress. The healthcare community was the most distressed because they were at the highest risk of infection. This study is the first to explore MERS-CoV epidemic impact on medical students’ perception and determinants of their psychological distress during this outbreak. Methods: We randomly selected and surveyed 200 students from the College of Medicine at King Saud University, Riyadh, Saudi Arabia. A predesigned questionnaire was answered by participants, and the collected data were statistically analyzed. Results: One hundred and seventy-four (87%) responded. Female students had a significantly higher mean stress level than males (P < 0.001). Participants had a mean GAD score of 2.7 ± 3.1 and a median of 2. Perceived sufficiency of information score was the highest mean and median (17.4 ± 4.2 and 18 respectively). College and hospital announcements were the most common source of information (25.4%). One hundred and thirty-four (77%) reported minimal anxiety, thirty-two (18.4%) reported mild anxiety, 8 (4.6%) reported moderate anxiety, and none of them reported severe anxiety (score >14). The stress level (as reported on 1–10 scale) shows significant correlation with Generalized Anxiety Disorder (GAD-7) score. We found in this study that significant predictors in our model, in terms of more significant to the least, were: an increased self-report on hygienic habits, self-reported social avoidance, the generalized anxiety score and finally being female gender while other variables including numbers of resources access, agreeing with public fear and knowledge score on MERS-CoV all were found to be non-significant. However, the number of accessed resources, as per students, has borderline significant correlation with higher self-reported anxiety from MERS-CoV. Conclusions: Medical students’ psychological needs during the MERS-CoV outbreak should be addressed appropriately. Our results highlight the need to establish psychological support programs for medical students during an infectious disease outbreak. © 2020


Abstract:
Objective: This multicenter, single-arm phase II study (UMIN000008429) aimed to evaluate the efficacy and safety of capecitabine plus oxaliplatin (CapOX) as postoperative adjuvant chemotherapy for patients with locally advanced rectal cancer. Methods: Patients with resectable clinical Stage II or III rectal cancer were enrolled to receive eight cycles of CapOX therapy (130 mg/m2 oxaliplatin on day 1 and 2000 mg/m2 oral capecitabine on days 1–14, every 3 weeks) after curative surgical resection. The primary endpoint was 3-year relapse-free survival (RFS) rate, and secondary endpoints were 3-year overall survival (OS) rate, treatment compliance, and safety. Results: A total of 40 patients (Stage II, 21; Stage III, 19) were enrolled between September 2012 and November 2015 from seven institutions. Thirty-nine patients (97%) received R0 resection, and 32 patients (84%) received postoperative CapOX therapy. The completion rate of all eight cycles of CapOX therapy was 66%. Relative dose intensities were 87% for oxaliplatin and 84% for capecitabine. At a median follow-up period of 46 months, disease recurrence was observed in nine
patients, including three with local recurrence. Three-year RFS and OS rates were 75% (95% CI 57–86%) and 96% (95% CI 80–99%), respectively. Frequencies of Grade ≥ 3 hematological and non-hematologic adverse events were 19% and 38%, respectively. Conclusion: CapOX therapy is feasible as adjuvant chemotherapy for locally advanced rectal cancer. © 2019, The Author(s).


Clinical course and outcomes of critically ill patients with SARS-CoV-2 pneumonia in Wuhan, China: a single-centered, retrospective, observational study
(2020) The Lancet Respiratory Medicine

Abstract:
Background: An ongoing outbreak of pneumonia associated with the severe acute respiratory coronavirus 2 (SARS-CoV-2) started in December, 2019, in Wuhan, China. Information about critically ill patients with SARS-CoV-2 infection is scarce. We aimed to describe the clinical course and outcomes of critically ill patients with SARS-CoV-2 pneumonia. Methods: In this single-centered, retrospective, observational study, we enrolled 52 critically ill adult patients with SARS-CoV-2 pneumonia who were admitted to the intensive care unit (ICU) of Wuhan Jinyintan hospital (Wuhan, China) between late December, 2019, and Jan 26, 2020. Demographic data, symptoms, laboratory values, comorbidities, treatments, and clinical outcomes were all collected. Data were compared between survivors and non-survivors. The primary outcome was 28-day mortality, as of Feb 9, 2020. Secondary outcomes included incidence of SARS-CoV-2-related acute respiratory distress syndrome (ARDS) and the proportion of patients requiring mechanical ventilation.

Findings: Of 710 patients with SARS-CoV-2 pneumonia, 52 critically ill adult patients were included. The mean age of the 52 patients was 59·7 (SD 13·3) years, 35 (67%) were men, 21 (40%) had chronic illness, 51 (98%) had fever. 32 (61·5%) patients had died at 28 days, and the median duration from admission to the intensive care unit (ICU) to death was 7 (IQR 3–11) days for non-survivors. Compared with survivors, non-survivors were older (64·6 years [11·2] vs 51·9 years [12·9]), more likely to develop ARDS (26 [81%] patients vs 9 [45%] patients), and more likely to receive mechanical ventilation (30 [94%] patients vs 7 [35%] patients), either invasively or non-invasively. Most patients had organ function damage, including 35 (67%) with ARDS, 15 (29%) with acute kidney injury, 12 (23%) with cardiac injury, 15 (29%) with liver dysfunction, and one (2%) with pneumothorax. 37 (71%) patients required mechanical ventilation. Hospital-acquired infection occurred in seven (13·5%) patients. Interpretation: The mortality of critically ill patients with SARS-CoV-2 pneumonia is considerable. The survival time of the non-survivors is likely to be within 1–2 weeks after ICU admission. Older patients (>65 years) with comorbidities and ARDS are at increased risk of death. The severity of SARS-CoV-2 pneumonia poses great strain on critical care resources in hospitals, especially if they are not adequately staffed or resourced. Funding: None.


Clinical findings in a group of patients infected with the 2019 novel coronavirus (SARS-Cov-2) outside of Wuhan, China: Retrospective case series
(2020) The BMJ, 368, art. no. m606

Abstract:
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. © Published by the BMJ Publishing Group Limited. For permission to use (where not already granted under a licence) please go to.

Zhang, J.-J., Dong, X., Cao, Y.-Y., Yuan, Y.-D., Yang, Y.-B., Yan, Y.-Q., Akdis, C.A., Gao, Y.-D. Clinical characteristics of 140 patients infected with SARS-CoV-2 in Wuhan, China (2020) Allergy: European Journal of Allergy and Clinical Immunology

Abstract: Background: Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has been widely spread. We aim to investigate the clinical characteristic and allergy status of patients infected with SARS-CoV-2. Methods: Electronic medical records including demographics, clinical manifestation, comorbidities, laboratory data, and radiological materials of 140 hospitalized COVID-19 patients, with confirmed result of SARS-CoV-2 viral infection, were extracted and analyzed. Results: An approximately 1:1 ratio of male (50.7%) and female COVID-19 patients was found, with an overall median age of 57.0 years. All patients were community-acquired cases. Fever (91.7%), cough (75.0%), fatigue (75.0%), and gastrointestinal symptoms (39.6%) were the most common clinical manifestations, whereas hypertension (30.0%) and diabetes mellitus (12.1%) were the most common comorbidities. Drug hypersensitivity (11.4%) and urticaria (1.4%) were self-reported by several patients. Asthma or other allergic diseases were not reported by any of the patients. Chronic obstructive pulmonary disease (COPD, 1.4%) patients and current smokers (1.4%) were rare. Bilateral ground-glass or patchy opacity (89.6%) was the most common sign of radiological finding. Lymphopenia (75.4%) and eosinopenia (52.9%) were observed in most patients. Blood eosinophil counts correlate positively with lymphocyte counts in severe (r =.486, P <.001) and nonsevere (r =.469, P <.001) patients after hospital admission. Significantly higher levels of D-dimer, C-reactive protein, and procalcitonin were associated with severe patients compared to nonsevere patients (all P <.001). Conclusion: Detailed clinical investigation of 140 hospitalized COVID-19 cases suggests eosinopenia together with lymphopenia may be a potential indicator for diagnosis. Allergic diseases, asthma, and COPD are not risk factors for SARS-CoV-2 infection. Older age, high number of comorbidities, and more prominent laboratory abnormalities were associated with severe patients. © 2020 EAAI and John Wiley and Sons A/S. Published by John Wiley and Sons Ltd.
Young, B.E., Ong, S.W.X., Kalimuddin, S., (...), Leo, Y.-S., Lye, D.C.

**Epidemiologic Features and Clinical Course of Patients Infected with SARS-CoV-2 in Singapore**

(2020) JAMA - Journal of the American Medical Association

**Abstract:**

Importance: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) emerged in Wuhan, China, in December 2019 and has spread globally with sustained human-to-human transmission outside China. Objective: To report the initial experience in Singapore with the epidemiologic investigation of this outbreak, clinical features, and management. Design, Setting, and Participants: Descriptive case series of the first 18 patients diagnosed with polymerase chain reaction (PCR)-confirmed SARS-CoV-2 infection at 4 hospitals in Singapore from January 23 to February 3, 2020; final follow-up date was February 25, 2020. Exposures: Confirmed SARS-CoV-2 infection. Main Outcomes and Measures: Clinical, laboratory, and radiologic data were collected, including PCR cycle threshold values from nasopharyngeal swabs and viral shedding in blood, urine, and stool. Clinical course was summarized, including requirement for supplemental oxygen and intensive care and use of empirical treatment with lopinavir-ritonavir. Results: Among the 18 hospitalized patients with PCR-confirmed SARS-CoV-2 infection (median age, 47 years; 9 [50%] women), clinical presentation was an upper respiratory tract infection in 12 (67%), and viral shedding from the nasopharynx was prolonged for 7 days or longer among 15 (83%). Six individuals (33%) required supplemental oxygen; of these, 2 required intensive care. There were no deaths. Virus was detectable in the stool (4/8 [50%]) and blood (1/12 [8%]) by PCR but not in urine. Five individuals requiring supplemental oxygen were treated with lopinavir-ritonavir. For 3 of the 5 patients, fever resolved and supplemental oxygen requirement was reduced within 3 days, whereas 2 deteriorated with progressive respiratory failure. Four of the 5 patients treated with lopinavir-ritonavir developed nausea, vomiting, and/or diarrhea, and 3 developed abnormal liver function test results. Conclusions and Relevance: Among the first 18 patients diagnosed with SARS-CoV-2 infection in Singapore, clinical presentation was frequently a mild respiratory tract infection. Some patients required supplemental oxygen and had variable clinical outcomes following treatment with an antiretroviral agent. © 2020 The Author(s).

Xia, J., Tong, J., Liu, M., Shen, Y., Guo, D.

**Evaluation of coronavirus in tears and conjunctival secretions of patients with SARS-CoV-2 infection**

(2020) Journal of Medical Virology

**Abstract:**

Objective: This study aimed to assess the presence of novel coronavirus in tears and conjunctival secretions of patients with SARS–CoV-2 infection. Methods: A prospective interventional case series study was performed, and 30 confirmed novel coronavirus pneumonia (NCP) patients were selected at the First Affiliated Hospital of Zhejiang University from 26 January 2020 to 9 February 2020. At an interval of 2 to 3 days, tear and conjunctival secretions were collected twice with disposable sampling swabs for reverse-transcription polymerase chain reaction (RT-PCR) assay. Results: Twenty-one common-type and nine severe-type NCP patients were enrolled. Two samples of tear and conjunctival secretions were obtained from the only one patient with conjunctivitis yielded positive RT-PCR results. Fifty-eight samples from other patients were all negative. Conclusion: We speculate that SARS-CoV-2 may be detected in the tears and conjunctival secretions in NCP patients with conjunctivitis. © 2020 Wiley Periodicals, Inc.

Letko, M., Marzi, A., Munster, V.
Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses

Abstract:
Over the past 20 years, several coronaviruses have crossed the species barrier into humans, causing outbreaks of severe, and often fatal, respiratory illness. Since SARS-CoV was first identified in animal markets, global viromics projects have discovered thousands of coronavirus sequences in diverse animals and geographic regions. Unfortunately, there are few tools available to functionally test these viruses for their ability to infect humans, which has severely hampered efforts to predict the next zoonotic viral outbreak. Here, we developed an approach to rapidly screen lineage B betacoronaviruses, such as SARS-CoV and the recent SARS-CoV-2, for receptor usage and their ability to infect cell types from different species. We show that host protease processing during viral entry is a significant barrier for several lineage B viruses and that bypassing this barrier allows several lineage B viruses to enter human cells through an unknown receptor. We also demonstrate how different lineage B viruses can recombine to gain entry into human cells, and confirm that human ACE2 is the receptor for the recently emerging SARS-CoV-2. © 2020, The Author(s), under exclusive licence to Springer Nature Limited.

Yan, R., Zhang, Y., Li, Y., Xia, L., Guo, Y., Zhou, Q.
Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2

Abstract:
Angiotensin-converting enzyme 2 (ACE2) is the cellular receptor for severe acute respiratory syndrome–coronavirus (SARS-CoV) and the new coronavirus (SARS-CoV-2) that is causing the serious coronavirus disease 2019 (COVID-19) epidemic. Here, we present cryo–electron microscopy structures of full-length human ACE2 in the presence of the neutral amino acid transporter B0AT1 with or without the receptor binding domain (RBD) of the surface spike glycoprotein (S protein) of SARS-CoV-2, both at an overall resolution of 2.9 angstroms, with a local resolution of 3.5 angstroms at the ACE2-RBD interface. The ACE2-B0AT1 complex is assembled as a dimer of heterodimers, with the collectrin-like domain of ACE2 mediating homodimerization. The RBD is recognized by the extracellular peptidase domain of ACE2 mainly through polar residues. These findings provide important insights into the molecular basis for coronavirus recognition and infection. © 2020 American Association for the Advancement of Science. All rights reserved.

Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2
(2020) Journal of Medical Virology

Abstract:
From the beginning of 2002 and 2012, severe respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) crossed the species barriers to infect humans, causing thousands of infections and hundreds of deaths, respectively. Currently, a novel coronavirus (SARS-CoV-2), which has become the cause of the outbreak of Coronavirus Disease 2019 (COVID-19), was discovered. Until 18 February 2020, there were 72 533 confirmed COVID-19 cases (including 10 644 severe cases) and 1872 deaths in China. SARS-CoV-2 is spreading among the public and causing substantial burden due to its human-to-human transmission. However, the intermediate host of SARS-CoV-2 is still unclear. Finding the possible intermediate host of
SARS-CoV-2 is imperative to prevent further spread of the epidemic. In this study, we used systematic comparison and analysis to predict the interaction between the receptor-binding domain (RBD) of coronavirus spike protein and the host receptor, angiotensin-converting enzyme 2 (ACE2). The interaction between the key amino acids of S protein RBD and ACE2 indicated that, other than pangolins and snakes, as previously suggested, turtles (Chrysemys picta bellii, Chelonia mydas, and Pelodiscus sinensis) may act as the potential intermediate hosts transmitting SARS-CoV-2 to humans. © 2020 Wiley Periodicals, Inc.


Imaging and clinical features of patients with 2019 novel coronavirus SARS-CoV-2

Abstract:
Background: The pneumonia caused by the 2019 novel coronavirus (SARS-CoV-2, also called 2019-nCoV) recently break out in Wuhan, China, and was named as COVID-19. With the spread of the disease, similar cases have also been confirmed in other regions of China. We aimed to report the imaging and clinical characteristics of these patients infected with SARS-CoV-2 in Guangzhou, China. Methods: All patients with laboratory-identified SARS-CoV-2 infection by real-time polymerase chain reaction (PCR) were collected between January 23, 2020, and February 4, 2020, in a designated hospital (Guangzhou Eighth People’s Hospital). This analysis included 90 patients (39 men and 51 women; median age, 50 years (age range, 18–86 years). All the included SARS-CoV-2-infected patients underwent non-contrast enhanced chest computed tomography (CT). We analyzed the clinical characteristics of the patients, as well as the distribution characteristics, pattern, morphology, and accompanying manifestations of lung lesions. In addition, after 1–6 days (mean 3.5 days), follow-up chest CT images were evaluated to assess radiological evolution. Findings: The majority of infected patients had a history of exposure in Wuhan or to infected patients and mostly presented with fever and cough. More than half of the patients presented bilateral, multifocal lung lesions, with peripheral distribution, and 53 (59%) patients had more than two lobes involved. Of all included patients, COVID-19 pneumonia presented with ground glass opacities in 65 (72%), consolidation in 12 (13%), crazy paving pattern in 11 (12%), interlobular thickening in 33 (37%), adjacent pleura thickening in 50 (56%), and linear opacities combined in 55 (61%). Pleural effusion, pericardial effusion, and lymphadenopathy were uncommon findings. In addition, baseline chest CT did not show any abnormalities in 21 patients (23%), but 3 patients presented bilateral ground glass opacities on the second CT after 3–4 days. Conclusion: SARS-CoV-2 infection can be confirmed based on the patient’s history, clinical manifestations, imaging characteristics, and laboratory tests. Chest CT examination plays an important role in the initial diagnosis of the novel coronavirus pneumonia. Multiple patchy ground glass opacities in bilateral multiple lobular with periphery distribution are typical chest CT imaging features of the COVID-19 pneumonia. © 2020, Springer-Verlag GmbH Germany, part of Springer Nature.

Li, X., Zai, J., Zhao, Q., Nie, Q., Li, Y., Foley, B.T., Chaillon, A.

Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2
(2020) Journal of Medical Virology

Abstract:
To investigate the evolutionary history of the recent outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in China, a total of 70 genomes of virus strains from China and
elsewhere with sampling dates between 24 December 2019 and 3 February 2020 were analyzed. To explore the potential intermediate animal host of the SARS-CoV-2 virus, we reanalyzed virome data sets from pangolins and representative SARS-related coronaviruses isolates from bats, with particular attention paid to the spike glycoprotein gene. We performed phylogenetic, split network, transmission network, likelihood-mapping, and comparative analyses of the genomes. Based on Bayesian time-scaled phylogenetic analysis using the tip-dating method, we estimated the time to the most recent common ancestor and evolutionary rate of SARS-CoV-2, which ranged from 22 to 24 November 2019 and 1.19 to 1.31 × 10⁻³ substitutions per site per year, respectively. Our results also revealed that the BetaCoV/bat/Yunnan/RaTG13/2013 virus was more similar to the SARS-CoV-2 virus than the coronavirus obtained from the two pangolin samples (SRR10168377 and SRR10168378). We also identified a unique peptide (PRRA) insertion in the human SARS-CoV-2 virus, which may be involved in the proteolytic cleavage of the spike protein by cellular proteases, and thus could impact host range and transmissibility. Interestingly, the coronavirus carried by pangolins did not have the RRAR motif. Therefore, we concluded that the human SARS-CoV-2 virus, which is responsible for the recent outbreak of COVID-19, did not come directly from pangolins. © 2020 Wiley Periodicals, Inc.

Bouadma, L., Lescure, F.-X., Lucet, J.-C., Yazdanpanah, Y., Timsit, J.-F.
Severe SARS-CoV-2 infections: practical considerations and management strategy for intensivists
(2020) Intensive Care Medicine, 46 (4), pp. 579-582.

Lai, A., Bergna, A., Acciarri, C., Galli, M., Zehender, G.
Early phylogenetic estimate of the effective reproduction number of SARS-CoV-2
(2020) Journal of Medical Virology
Abstract:
To reconstruct the evolutionary dynamics of the 2019 novel-coronavirus recently causing an outbreak in Wuhan, China, 52 SARS-CoV-2 genomes available on 4 February 2020 at Global Initiative on Sharing All Influenza Data were analyzed. The two models used to estimate the reproduction number (coalescent-based exponential growth and a birth-death skyline method) indicated an estimated mean evolutionary rate of 7.8 × 10⁻⁴ subs/site/year (range, 1.1 × 10⁻⁴–15 × 10⁻⁴) and a mean tMRCA of the tree root of 73 days. The estimated R value was 2.6 (range, 2.1-5.1), and increased from 0.8 to 2.4 in December 2019. The estimated mean doubling time of the epidemic was between 3.6 and 4.1 days. This study proves the usefulness of phylogeny in supporting the surveillance of emerging new infections even as the epidemic is growing. © 2020 Wiley Periodicals, Inc.

Xu, J., Zhao, S., Teng, T., Abdalla, A.E., Zhu, W., Xie, L., Wang, Y., Guo, X.
Systematic comparison of two animal-to-human transmitted human coronaviruses: SARS-CoV-2 and SARS-CoV
(2020) Viruses, 12 (2), art. no. 244
Abstract:
After the outbreak of the severe acute respiratory syndrome (SARS) in the world in 2003, human coronaviruses (HCoVs) have been reported as pathogens that cause severe symptoms in respiratory tract infections. Recently, a new emerged HCoV isolated from the respiratory epithelium of unexplained pneumonia patients in the Wuhan seafood market caused a major disease outbreak and
has been named the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This virus causes acute lung symptoms, leading to a condition that has been named as "coronavirus disease 2019" (COVID-19). The emergence of SARS-CoV-2 and of SARS-CoV caused widespread fear and concern and has threatened global health security. There are some similarities and differences in the epidemiology and clinical features between these two viruses and diseases that are caused by these viruses. The goal of this work is to systematically review and compare between SARS-CoV and SARS-CoV-2 in the context of their virus incubation, origins, diagnosis and treatment methods, genomic and proteomic sequences, and pathogenic mechanisms. © 2020 by the authors.

Zhang, H., Penninger, J.M., Li, Y., Zhong, N., Slutsky, A.S.
Angiotensin-converting enzyme 2 (ACE2) as a SARS-CoV-2 receptor: molecular mechanisms and potential therapeutic target

Viral load kinetics of SARS-CoV-2 infection in first two patients in Korea
(2020) Journal of Korean Medical Science, 35 (7), art. no. e86
Abstract:
As of February 2020, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) outbreak started in China in December 2019 has been spreading in many countries in the world. With the numbers of confirmed cases are increasing, information on the epidemiologic investigation and clinical manifestation have been accumulated. However, data on viral load kinetics in confirmed cases are lacking. Here, we present the viral load kinetics of the first two confirmed patients with mild to moderate illnesses in Korea in whom distinct viral load kinetics are shown. This report suggests that viral load kinetics of SARS-CoV-2 may be different from that of previously reported other coronavirus infections such as SARS-CoV. © 2020 The Korean Academy of Medical Sciences.

Phan, T.
Genetic diversity and evolution of SARS-CoV-2
(2020) Infection, Genetics and Evolution, 81, art. no. 104260
Abstract:
COVID-19 is a viral respiratory illness caused by a new coronavirus called SARS-CoV-2. The World Health Organization declared the SARS-CoV-2 outbreak a global public health emergency. We performed genetic analyses of eighty-six complete or near-complete genomes of SARS-CoV-2 and revealed many mutations and deletions on coding and non-coding regions. These observations provided evidence of the genetic diversity and rapid evolution of this novel coronavirus. © 2020 Elsevier B.V.

Liu, R., Han, H., Liu, F., Lv, Z., Wu, K., Liu, Y., Feng, Y., Zhu, C.
Positive rate of RT-PCR detection of SARS-CoV-2 infection in 4880 cases from one hospital in Wuhan, China, from Jan to Feb 2020
Abstract:
Background: There's an outbreak of a novel coronavirus (SARS-CoV-2) infection since December 2019, first in China, and currently with more than 80 thousand confirmed infection globally in 29 countries till March 2, 2020. Identification, isolation and caring for patients early are essential to
limit human-to-human transmission including reducing secondary infections among close contacts and health care workers, preventing transmission amplification events. The RT-PCR detection of viral nucleic acid test (NAT) was one of the most quickly established laboratory diagnosis method in a novel viral pandemic, just as in this COVID-19 outbreak. Methods: 4880 cases that had respiratory infection symptoms or close contact with COVID-19 patients in hospital in Wuhan, China, were tested for SARS-CoV-2 infection by use of quantitative RT-PCR (qRT-PCR) on samples from the respiratory tract. Positive rates were calculated in groups divided by genders or ages. Results: The positive rate was about 38% for the total 4880 specimens. Male and older population had a significant higher positive rates. However, 57% was positive among the specimens from the Fever Clinics. Binary logistic regression analysis showed that age, not gender, was the risk factor for SARS-CoV-2 infection in fever clinics. Conclusions: Therefore, we concluded that viral NAT played an important role in identifying SARS-CoV-2 infection. © 2020 Elsevier B.V.


Abstract:
Background: Coronavirus disease 2019 (COVID-19) is a disease caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), first detected in China in December, 2019. In January, 2020, state, local, and federal public health agencies investigated the first case of COVID-19 in Illinois, USA. Methods: Patients with confirmed COVID-19 were defined as those with a positive SARS-CoV-2 test. Contacts were people with exposure to a patient with COVID-19 on or after the patient's symptom onset date. Contacts underwent active symptom monitoring for 14 days following their last exposure. Contacts who developed fever, cough, or shortness of breath became persons under investigation and were tested for SARS-CoV-2. A convenience sample of 32 asymptomatic health-care personnel contacts were also tested. Findings: Patient 1—a woman in her 60s—returned from China in mid-January, 2020. One week later, she was hospitalised with pneumonia and tested positive for SARS-CoV-2. Her husband (Patient 2) did not travel but had frequent close contact with his wife. He was admitted 8 days later and tested positive for SARS-CoV-2. Overall, 372 contacts of both cases were identified; 347 underwent active symptom monitoring, including 152 community contacts and 195 health-care personnel. Of monitored contacts, 43 became persons under investigation, in addition to Patient 2. These 43 persons under investigation and all 32 asymptomatic health-care personnel tested negative for SARS-CoV-2. Interpretation: Person-to-person transmission of SARS-CoV-2 occurred between two people with prolonged, unprotected exposure while Patient 1 was symptomatic. Despite active symptom monitoring and testing of symptomatic and some asymptomatic contacts, no further transmission was detected. Funding: None.


Clinical characteristics of laboratory confirmed positive cases of SARS-CoV-2 infection in Wuhan, China: A retrospective single center analysis (2020) Travel Medicine and Infectious Disease, art. no. 101606

Clinical and computed tomographic imaging features of novel coronavirus pneumonia caused by SARS-CoV-2

Abstract:
Purpose: To investigate the clinical and imaging characteristics of computed tomography (CT) in novel coronavirus pneumonia (NCP) caused by SARS-CoV-2. Materials and methods: A retrospective analysis was performed on the imaging findings of patients confirmed with COVID-19 pneumonia who had chest CT scanning and treatment after disease onset. The clinical and imaging data were analyzed. Results: Fifty patients were enrolled, including mild type in nine, common in 28, severe in 10 and critically severe in the rest three. Mild patients (29 years) were significantly (P<0.03) younger than either common (44.5 years) or severe (54.7) and critically severe (65.7 years) patients, and common patients were also significantly (P<0.03) younger than severe and critically severe patients. Mild patients had low to moderate fever (<39.1 °C), 49 (98%) patients had normal or slightly reduced leukocyte count, 14 (28%) had decreased counts of lymphocytes, and 26 (52%) patients had increased C-reactive protein. Nine mild patients were negative in CT imaging. For all the other types of NCP, the lesion was in the right upper lobe in 30 cases, right middle lobe in 22, right lower lobe in 39, left upper lobe in 33 and left lower lobe in 36. The lesion was primarily located in the peripheral area under the pleura with possible extension towards the pulmonary hilum. Symmetrical lesions were seen in 26 cases and asymmetrical in 15. The density of lesion was mostly uneven with ground glass opacity as the primary presentation accompanied by partial consolidation and fibrosis. Conclusion: CT imaging presentations of NCP are mostly patchy ground glass opacities in the peripheral areas under the pleura with partial consolidation which will be absorbed with formation of fibrotic stripes if improved. CT scanning provides important bases for early diagnosis and treatment of NCP. © 2020 The British Infection Association


Potential impact of seasonal forcing on a SARS-CoV-2 pandemic
(2020) Swiss medical weekly, 150, p. w20224.

Abstract:
A novel coronavirus (SARS-CoV-2) first detected in Wuhan, China, has spread rapidly since December 2019, causing more than 100,000 confirmed infections and 4000 fatalities (as of 10 March 2020). The outbreak has been declared a pandemic by the WHO on Mar 11, 2020. Here, we explore how seasonal variation in transmissibility could modulate a SARS-CoV-2 pandemic. Data from routine diagnostics show a strong and consistent seasonal variation of the four endemic coronaviruses (229E, HKU1, NL63, OC43) and we parameterise our model for SARS-CoV-2 using these data. The model allows for many subpopulations of different size with variable parameters. Simulations of different scenarios show that plausible parameters result in a small peak in early 2020 in temperate regions of the Northern Hemisphere and a larger peak in winter 2020/2021. Variation in transmission and migration rates can result in substantial variation in prevalence between regions. While the uncertainty in parameters is large, the scenarios we explore show that transient reductions in the incidence rate might be due to a combination of seasonal variation and infection control efforts but do not necessarily mean the epidemic is contained. Seasonal forcing on SARS-CoV-2 should thus be taken into account in the further monitoring of the global transmission.
The likely aggregated effect of seasonal variation, infection control measures, and transmission rate variation is a prolonged pandemic wave with lower prevalence at any given time, thereby providing a window of opportunity for better preparation of health care systems.

Pfefferle, S., Reucher, S., Nörz, D., Lütgehetmann, M.  
**Evaluation of a quantitative RT-PCR assay for the detection of the emerging coronavirus SARS-CoV-2 using a high throughput system**  
(2020) Eurosurveillance, 25 (9), art. no. 2000152  
**Abstract:**  
Facing the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), high-volume respiratory testing is demanded in laboratories worldwide. We evaluated the performance of a molecular assay for the detection of SARS-CoV-2 on a high-throughput platform, the cobas 6800, using the 'open channel' for integration of a laboratory-developed assay. We observed good analytical performance in clinical specimens. The fully automated workflow enables highthroughput testing with minimal hands-on time, while offering fast and reliable results. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

**Virus isolation from the first patient with SARS-CoV-2 in Korea**  
(2020) Journal of Korean Medical Science, 35 (7), art. no. e84  
**Abstract:**  
Novel coronavirus (SARS-CoV-2) is found to cause a large outbreak started from Wuhan since December 2019 in China and SARS-CoV-2 infections have been reported with epidemiological linkage to China in 25 countries until now. We isolated SARS-CoV-2 from the oropharyngeal sample obtained from the patient with the first laboratory-confirmed SARS-CoV-2 infection in Korea. Cytopathic effects of SARS-CoV-2 in the Vero cell cultures were confluent 3 days after the first blind passage of the sample. Coronavirus was confirmed with spherical particle having a fringe reminiscent of crown on transmission electron microscopy. Phylogenetic analyses of whole genome sequences showed that it clustered with other SARS-CoV-2 reported from Wuhan. © 2020 The Korean Academy of Medical Sciences.

Koo, J.R., Cook, A.R., Park, M., Sun, Y., Sun, H., Lim, J.T., Tam, C., Dickens, B.L.  
**Interventions to mitigate early spread of SARS-CoV-2 in Singapore: a modelling study**  
(2020) The Lancet Infectious Diseases  
**Abstract:**  
Background: Since the coronavirus disease 2019 outbreak began in the Chinese city of Wuhan on Dec 31, 2019, 68 imported cases and 175 locally acquired infections have been reported in Singapore. We aimed to investigate options for early intervention in Singapore should local containment (eg, preventing disease spread through contact tracing efforts) be unsuccessful.  
Methods: We adapted an influenza epidemic simulation model to estimate the likelihood of human-to-human transmission of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in a simulated Singaporean population. Using this model, we estimated the cumulative number of SARS-CoV-2 infections at 80 days, after detection of 100 cases of community transmission, under three infectivity scenarios (basic reproduction number [R0] of 1·5, 2·0, or 2·5) and assuming 7·5% of infections are asymptomatic. We first ran the model assuming no intervention was in place.
(baseline scenario), and then assessed the effect of four intervention scenarios compared with a baseline scenario on the size and progression of the outbreak for each R0 value. These scenarios included isolation measures for infected individuals and quarantining of family members (hereafter referred to as quarantine); quarantine plus school closure; quarantine plus workplace distancing; and quarantine, school closure, and workplace distancing (hereafter referred to as the combined intervention). We also did sensitivity analyses by altering the asymptomatic fraction of infections (22.7%, 30.0%, 40.0%, and 50.0%) to compare outbreak sizes under the same control measures.

Findings: For the baseline scenario, when R0 was 1.5, the median cumulative number of infections at day 80 was 279,000 (IQR 245,000–320,000), corresponding to 7.4% (IQR 6.5–8.5) of the resident population of Singapore. The median number of infections increased with higher infectivity: 727,000 cases (670,000–776,000) when R0 was 2.0, corresponding to 19.3% (17.8–20.6) of the Singaporean population, and 1,207,000 cases (1,164,000–1,249,000) when R0 was 2.5, corresponding to 32% (30.9–33.1) of the Singaporean population. Compared with the baseline scenario, the combined intervention was the most effective, reducing the estimated median number of infections by 99.3% (IQR 92.6–99.9) when R0 was 1.5, by 93.0% (81.5–99.7) when R0 was 2.0, and by 78.2% (59.0–94.4) when R0 was 2.5. Assuming increasing asymptomatic fractions up to 50.0%, up to 277,000 infections were estimated to occur at day 80 with the combined intervention relative to 1,800 for the baseline at R0 of 1.5. Interpretation: Implementing the combined intervention of quarantining infected individuals and their family members, workplace distancing, and school closure once community transmission has been detected could substantially reduce the number of SARS-CoV-2 infections. We therefore recommend immediate deployment of this strategy if local secondary transmission is confirmed within Singapore. However, quarantine and workplace distancing should be prioritised over school closure because at this early stage, symptomatic children have higher withdrawal rates from school than do symptomatic adults from work. At higher asymptomatic proportions, intervention effectiveness might be substantially reduced requiring the need for effective case management and treatments, and preventive measures such as vaccines.

Funding: Singapore Ministry of Health, Singapore Population Health Improvement Centre.


Temporal profiles of viral load in posterior oropharyngeal saliva samples and serum antibody responses during infection by SARS-CoV-2: an observational cohort study

(2020) The Lancet Infectious Diseases

Abstract:

Background: Coronavirus disease 2019 (COVID-19) causes severe community and nosocomial outbreaks. Comprehensive data for serial respiratory viral load and serum antibody responses from patients infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) are not yet available. Nasopharyngeal and throat swabs are usually obtained for serial viral load monitoring of respiratory infections but gathering these specimens can cause discomfort for patients and put health-care workers at risk. We aimed to ascertain the serial respiratory viral load of SARS-CoV-2 in posterior oropharyngeal (deep throat) saliva samples from patients with COVID-19, and serum antibody responses. Methods: We did a cohort study at two hospitals in Hong Kong. We included patients with laboratory-confirmed COVID-19. We obtained samples of blood, urine, posterior oropharyngeal saliva, and rectal swabs. Serial viral load was ascertained by reverse transcriptase
quantitative PCR (RT-qPCR). Antibody levels against the SARS-CoV-2 internal nucleoprotein (NP) and surface spike protein receptor binding domain (RBD) were measured using EIA. Whole-genome sequencing was done to identify possible mutations arising during infection. Findings: Between Jan 22, 2020, and Feb 12, 2020, 30 patients were screened for inclusion, of whom 23 were included (median age 62 years [range 37–75]). The median viral load in posterior oropharyngeal saliva or other respiratory specimens at presentation was 5·2 log10 copies per mL (IQR 4·1–7·0). Salivary viral load was highest during the first week after symptom onset and subsequently declined with time (slope −0·15, 95% CI −0·19 to −0·11; R2=0·71). In one patient, viral RNA was detected 25 days after symptom onset. Older age was correlated with higher viral load (Spearman’s ρ=0·48, 95% CI 0·074–0·75; p=0·020). For 16 patients with serum samples available 14 days or longer after symptom onset, rates of seropositivity were 94% for anti-NP IgG (n=15), 88% for anti-NP IgM (n=14), 100% for anti-RBD IgG (n=16), and 94% for anti-RBD IgM (n=15). Anti-SARS-CoV-2-NP or anti-SARS-CoV-2-RBD IgG levels correlated with virus neutralisation titre (R2>0·9). No genome mutations were detected on serial samples. Interpretation: Posterior oropharyngeal saliva samples are a non-invasive specimen more acceptable to patients and health-care workers. Unlike severe acute respiratory syndrome, patients with COVID-19 had the highest viral load near presentation, which could account for the fast-spreading nature of this epidemic. This finding emphasises the importance of stringent infection control and early use of potent antiviral agents, alone or in combination, for high-risk individuals. Serological assay can complement RT-qPCR for diagnosis. Funding: Richard and Carol Yu, May Tam Mak Mei Yin, The Shaw Foundation Hong Kong, Michael Tong, Marina Lee, Government Consultancy Service, and Sanming Project of Medicine.

Alonso Díaz, C., López Maestro, M., Moral Pumarega, M.T., Flores Antón, B., Pallás Alonso, C.  
**First case of neonatal infection due to SARS-CoV-2 in Spain** [Primer caso de infección neonatal por SARS-CoV-2 en España]  
(2020) Anales de Pediatria

**Epidemiological update on SARS-CoV-2 infection in Spain. Comments on the management of infection in pediatrics** [Actualización de la situación epidemiológica de la infección por SARS-CoV-2 en España. Comentarios a las recomendaciones de manejo de la infección en pediatría]  
(2020) Anales de Pediatria

**Predicting the angiotensin converting enzyme 2 (ACE2) utilizing capability as the receptor of SARS-CoV-2**  
(2020) Microbes and Infection

Abstract:
SARS-CoV-2, the newly identified human coronavirus causing severe pneumonia pandemic, was probably originated from Chinese horseshoe bats. However, direct transmission of the virus from bats to humans is unlikely due to lack of direct contact, implying the existence of unknown intermediate hosts. Angiotensin converting enzyme 2 (ACE2) is the receptor of SARS-CoV-2, but only ACE2s of certain species can be utilized by SARS-CoV-2. Here, we evaluated and ranked the receptor-utilizing capability of ACE2s from various species by phylogenetic clustering and sequence alignment with the currently known ACE2s utilized by SARS-CoV-2. As a result, we predicted that SARS-CoV-2 tends to utilize ACE2s of various mammals, except murines, and some birds, such as pigeon. This prediction may help to screen the intermediate hosts of SARS-CoV-2. © 2020 Institut Pasteur

Giovanetti, M., Angeletti, S., Benvenuto, D., Ciccozzi, M.
A doubt of multiple introduction of SARS-CoV-2 in Italy: A preliminary overview
(2020) Journal of Medical Virology
Abstract:
The emergence of the novel betacoronavirus, recently renamed as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has raised serious concerns due to the virus's rapid dissemination worldwide. Nevertheless, there is limited information about the genomic epidemiology of SARS-CoV-2 circulating in Italy from surveillance studies. The shortage of complete genomic sequences available impairs our understanding of the SARS-CoV-2 introduction and establishment in the country. To better understand its dynamics in Italy, we analyzed complete genomes of SARS-CoV-2 isolates, obtained directly from clinical samples. Our phylogenetic reconstructions suggest possible multiple introduction of SARS-CoV-2. Continued genomic surveillance strategies are needed to improve monitoring and understanding of the current SARS-CoV-2 epidemics, which might help to attenuate public health impact of infectious diseases. © 2020 Wiley Periodicals, Inc.

Ma, X., Su, L., Zhang, Y., Zhang, X., Gai, Z., Zhang, Z.
Do children need a longer time to shed SARS-CoV-2 in stool than adults?
(2020) Journal of Microbiology, Immunology and Infection
Abstract:
SARS-CoV-2 can be shed in the stool of patients in the recovery phase. Children show a longer shedding time than adults. We analyzed the possible causes of this finding and recommend that a negative stool sample be included in a patient's discharge criteria. © 2020

Leung, C.
The difference in the incubation period of 2019 novel coronavirus (SARS-CoV-2) infection between travelers to Hubei and non-travelers: The need of a longer quarantine period
(2020) Infection Control and Hospital Epidemiology
Abstract:
Data collected from the individual cases reported by the media were used to estimate the distribution of the incubation period of travelers to Hubei and non-travelers. Upon the finding of longer and more volatile incubation period in travelers, the duration of quarantine should be extended to three weeks. © 2020 by The Society for Healthcare Epidemiology of America. All rights reserved.

Zheng, M., Song, L.
Novel antibody epitopes dominate the antigenicity of spike glycoprotein in SARS-CoV-2 compared to SARS-CoV
(2020) Cellular and Molecular Immunology


Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-CoV-2): Immunoinformatics approach
(2020) Journal of Medical Virology

Abstract:
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. © 2020 Wiley Periodicals, Inc.

Ghosal, S., Sengupta, S., Majumder, M., Sinha, B.
Prediction of the number of deaths in India due to SARS-CoV-2 at 5–6 weeks

Abstract:
Introduction: and Aims: No valid treatment or preventative strategy has evolved till date to counter the SARS-CoV-2 (Novel Coronavirus) epidemic that originated in China in late 2019 and have since wrought havoc on millions across the world with illness, socioeconomic recession and death. This analysis was aimed at tracing a trend related to death counts expected at the 5th and 6th week of the COVID-19 in India. Material and methods: Validated database was used to procure global and Indian data related to coronavirus and related outcomes. Multiple regression and linear regression analyses were used interchangeably. Since the week 6 death count data was not correlated significantly with any of the chosen inputs, an auto-regression technique was employed to improve the predictive ability of the regression model. Results: A linear regression analysis predicted average week 5 death count to be 211 with a 95% CI: 1.31–2.60). Similarly, week 6 death count, in spite of a strong correlation with input variables, did not pass the test of statistical significance. Using auto-regression technique and using week 5 death count as input the linear regression model predicted week 6 death count in India to be 467, while keeping at the back of our mind the risk of over-estimation by most of the risk-based models. Conclusion: According to our analysis, if situation continue in present state; projected death rate (n) is 211 and467 at the end of the 5th and 6th week from now, respectively. © 2020 Diabetes India

Zhang, J., Zeng, H., Gu, J., Li, H., Zheng, L., Zou, Q.
Progress and prospects on vaccine development against sars-cov-2
(2020) Vaccines, 8 (2), art. no. 153

Abstract:
In December 2019, the outbreak of pneumonia caused by a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has led to a serious pandemic in China and other countries worldwide. So far, more than 460,000 confirmed cases were diagnosed in nearly 190 countries, causing globally over 20,000 deaths. Currently, the epidemic is still spreading and there is no effective means to prevent the infection. Vaccines are proved to be the most effective and economical means to prevent and control infectious diseases. Several countries, companies, and institutions announced their programs and progress on vaccine development against the virus. While most of the vaccines are under design and preparation, there are some that have entered efficacy evaluation in animals and initial clinical trials. This review mainly focused on the progress and our prospects on field of vaccine development against SARS-CoV-2. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Atypical presentation of SARS-CoV-2 infection: A case report
Abstract:
BACKGROUND The first case of pneumonia subsequently attributed to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) occurred in Wuhan, Hubei Province on December 8, 2019. The symptoms included fever, coughing, and breathing difficulties. A few patients with this infection may only have atypical symptoms, which could lead to a misdiagnosis and subsequently further facilitate the spread of the virus. CASE SUMMARY A 74-year-old female patient complained of severe diarrhea. She did not have fever, coughing, or breathing difficulties. A physical examination revealed no obvious positive signs. The patient had been hypertensive for more than 10 years. Her blood pressure was well controlled. On January 9, 2020, the patient's son visited a colleague who was later confirmed positive for SARS-CoV-2 and his first close contact with our patient was on January 17. The patient was first diagnosed with gastrointestinal dysfunction. However, considering her indirect contact with a SARS-CoV-2-infected individual, we suggested that an atypical pneumonia virus infection should be ruled out. A computed tomography scan was performed on January 26, and showed ground-glass nodules scattered along the two lungs, suggestive of viral pneumonia. Given the clinical characteristics, epidemiological history, and examination, the patient was diagnosed with coronavirus disease-2019 (COVID-19).
CONCLUSION Our patient had atypical symptoms of COVID-19. Careful acquisition of an epidemiological history is necessary to make a correct diagnosis and strategize a treatment plan. © The Author(s) 2020.

Ferioli, M., Cisternino, C., Leo, V., Pisani, L., Palange, P., Nava, S.
Protecting healthcare workers from sars-cov-2 infection: Practical indications
Abstract:
The World Health Organization has recently defined the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection a pandemic. The infection, that may cause a potentially very severe respiratory disease, now called coronavirus disease 2019 (COVID-19), has airborne transmission via droplets. The rate of transmission is quite high, higher than common influenza. Healthcare workers are at high risk of contracting the infection particularly when applying respiratory devices such as oxygen cannulas or noninvasive ventilation. The aim of this article is to provide evidence-based recommendations for the correct use of “respiratory devices” in the COVID-19 emergency and protect healthcare workers from contracting the SARS-CoV-2 infection. © ERS 2020.

**Enhanced isolation of SARS-CoV-2 by TMPRSS2- expressing cells**

**Abstract:**
A novel betacoronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which caused a large respiratory outbreak in Wuhan, China in December 2019, is currently spreading across many countries globally. Here, we show that a TMPRSS2- expressing VeroE6 cell line is highly susceptible to SARS-CoV-2 infection, making it useful for isolating and propagating SARS-CoV-2. Our results reveal that, in common with SARS- and Middle East respiratory syndrome-CoV, SARS-CoV-2 infection is enhanced by TMPRSS2. © 2020 National Academy of Sciences. All rights reserved.

Richard, N.A., Robert, D., Valentin, D., Emma, H.B., Jan, A.

**Potential impact of seasonal forcing on a SARS-CoV-2 pandemic**
(2020) Swiss Medical Weekly, 150 (11-12), art. no. e20224

**Abstract:**
A novel coronavirus (SARS-CoV-2) first detected in Wuhan, China, has spread rapidly since December 2019, causing more than 100,000 confirmed infections and 4000 fatalities (as of 10 March 2020). The outbreak has been declared a pandemic by the WHO on Mar 11, 2020. Here, we explore how seasonal variation in transmissibility could modulate a SARS-CoV-2 pandemic. Data from routine diagnostics show a strong and consistent seasonal variation of the four endemic coronaviruses (229E, HKU1, NL63, OC43) and we parameterise our model for SARS-CoV-2 using these data. The model allows for many subpopulations of different size with variable parameters. Simulations of different scenarios show that plausible parameters result in a small peak in early 2020 in temperate regions of the Northern Hemisphere and a larger peak in winter 2020/2021. Variation in transmission and migration rates can result in substantial variation in prevalence between regions. While the uncertainty in parameters is large, the scenarios we explore show that transient reductions in the incidence rate might be due to a combination of seasonal variation and infection control efforts but do not necessarily mean the epidemic is contained. Seasonal forcing on SARS-CoV-2 should thus be taken into account in the further monitoring of the global transmission. The likely aggregated effect of seasonal variation, infection control measures, and transmission rate variation is a prolonged pandemic wave with lower prevalence at any given time, thereby providing a window of opportunity for better preparation of health care systems. © 2020 EMH Swiss Medical Publishers Ltd.. All rights reserved.

Luo, C., Yao, L., Zhang, L., Yao, M., Chen, X., Wang, Q., Shen, H.

**Possible Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in a Public Bath Center in Huai’an, Jiangsu Province, China**

Rehman, S.U., Shafique, L., Ihsan, A., Liu, Q.

**Evolutionary trajectory for the emergence of novel coronavirus SARS-CoV-2**
(2020) Pathogens, 9 (3), art. no. 240
Abstract:
Over the last two decades, the world experienced three outbreaks of coronaviruses with elevated morbidity rates. Currently, the global community is facing emerging virus SARS-CoV-2 belonging to Betacoronavirus, which appears to be more transmissible but less deadly than SARS-CoV. The current study aimed to track the evolutionary ancestors and different evolutionary strategies that were genetically adapted by SARS-CoV-2. Our whole-genome analysis revealed that SARS-CoV-2 was the descendant of Bat SARS/SARS-like CoVs and bats served as a natural reservoir. SARS-CoV-2 used mutations and recombination as crucial strategies in different genomic regions including the envelop, membrane, nucleocapsid, and spike glycoproteins to become a novel infectious agent. We confirmed that mutations in different genomic regions of SARS-CoV-2 have specific influence on virus reproductive adaptability, allowing for genotype adjustment and adaptations in rapidly changing environments. Moreover, for the first time we identified nine putative recombination patterns in SARS-CoV-2, which encompass spike glycoprotein, RdRp, helicase and ORF3a. Six recombination regions were spotted in the S gene and are undoubtedly important for evolutionary survival, meanwhile this permitted the virus to modify superficial antigenicity to find a way from immune reconnaissance in animals and adapt to a human host. With these combined natural selected strategies, SARS-CoV-2 emerged as a novel virus in human society. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Emma, H.B.
Preliminary case report on the SARS-CoV-2 cluster in the UK, France, and Spain
(2020) Swiss Medical Weekly, 150 (9-10), art. no. e20212
Abstract:
Almost half of the confirmed COVID-19 cases detected so far in the United Kingdom are part of a large cluster of 13 British nationals who tested positive for SARS-CoV-2 in the UK, Spain, and France. Transmissions among this cluster occurred at a ski resort in France, and originated from a single infected traveller returning from a conference in Singapore where he acquired the virus. At least 21 individuals were exposed to the virus, tested, and quarantined, with 13 of those testing positive between the period of 6th February and 15th February. Here, all publicly available information about the primarily UK/France cluster is consolidated, providing a complete and accessible summary of the cases and their connections. Notable in this cluster are the number of individuals infected, the apparent absence of any severe illness among those infected, and a case of a “delayed positive” test during isolation after initially testing negative, at least 7 days after last possible contact. © 2020 EMH Swiss Medical Publishers Ltd.. All rights reserved.

Hodcroft, E.B.
Preliminary case report on the SARS-CoV-2 cluster in the UK, France, and Spain
(2020) Swiss medical weekly, 150 (9-10)
Abstract:
Almost half of the confirmed COVID-19 cases detected so far in the United Kingdom are part of a large cluster of 13 British nationals who tested positive for SARS-CoV-2 in the UK, Spain, and France. Transmissions among this cluster occurred at a ski resort in France, and originated from a single infected traveller returning from a conference in Singapore where he acquired the virus. At least 21 individuals were exposed to the virus, tested, and quarantined, with 13 of those testing positive between the period of 6th February and 15th February. Here, all publicly available information about the primarily UK/France cluster is consolidated, providing a complete and accessible summary of the cases and their connections. Notable in this cluster are the number of individuals infected, the apparent absence of any severe illness among those infected, and a case of a “delayed positive” test during isolation after initially testing negative, at least 7 days after last possible contact. © 2020 EMH Swiss Medical Publishers Ltd.. All rights reserved.
accessible summary of the cases and their connections. Notable in this cluster are the number of individuals infected, the apparent absence of any severe illness among those infected, and a case of a “delayed positive” test during isolation after initially testing negative, at least 7 days after last possible contact. EMH Swiss Medical Publishers Ltd.


**Genomic characterization and phylogenetic analysis of SARS-COV-2 in Italy**

(2020) Journal of Medical Virology

**Abstract:**
This report describes the isolation, molecular characterization, and phylogenetic analysis of the first three complete genomes of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) isolated from three patients involved in the first outbreak of COVID-19 in Lombardy, Italy. Early molecular epidemiological tracing suggests that SARS-CoV-2 was present in Italy weeks before the first reported cases of infection. © 2020 Wiley Periodicals, Inc.

Oliveira, T.C., Abranches, M.V., Lana, R.M.

**Food (in)security in Brazil in the context of the SARS-CoV-2 pandemic**

((In)Segurança alimentar no contexto da pandemia por SARS-CoV-2]


Ma, Q.-X., Shan, H., Zhang, H.-L., Li, G.-M., Yang, R.-M., Chen, J.-M.

Potential utilities of mask-wearing and instant hand hygiene for fighting SARS-CoV-2

(2020) Journal of Medical Virology

**Abstract:**
The surge of patients in the pandemic of COVID-19 caused by the novel coronavirus SARS-CoV-2 may overwhelm the medical systems of many countries. Mask-wearing and handwashing can slow the spread of the virus, but currently, masks are in shortage in many countries, and timely handwashing is often impossible. In this study, the efficacy of three types of masks and instant hand wiping was evaluated using the avian influenza virus to mock the coronavirus. Virus quantification was performed using real-time reverse transcription-polymerase chain reaction. Previous studies on mask-wearing were reviewed. The results showed that instant hand wiping using a wet towel soaked in water containing 1.00% soap powder, 0.05% active chlorine, or 0.25% active chlorine from sodium hypochlorite removed 98.36%, 96.62%, and 99.98% of the virus from hands, respectively. N95 masks, medical masks, and homemade masks made of four-layer kitchen paper and one-layer cloth could block 99.98%, 97.14%, and 95.15% of the virus in aerosols. Medical mask-wearing which was supported by many studies was opposed by other studies possibly due to erroneous judgment. With these data, we propose the approach of mask-wearing plus instant hand hygiene (MIH) to slow the exponential spread of the virus. This MIH approach has been supported by the experiences of seven countries in fighting against COVID-19. Collectively, a simple approach to slow the exponential spread of SARS-CoV-2 was proposed with the support of experiments, literature review, and control experiences. © 2020 Wiley Periodicals, Inc.

Fantini, J., Di Scala, C., Chahinian, H., Yahi, N.

**Structural and molecular modelling studies reveal a new mechanism of action of chloroquine and hydroxychloroquine against SARS-CoV-2 infection**

(2020) International Journal of Antimicrobial Agents, art. no. 105960
Abstract:
The recent emergence of the novel pathogenic SARS-coronavirus 2 (SARS-CoV-2) is responsible for a worldwide pandemic. Given the global health emergency, drug repositioning is the most reliable option to design an efficient therapy for infected patients without delay. The first step of the viral replication cycle [i.e. attachment to the surface of respiratory cells, mediated by the spike (S) viral protein] offers several potential therapeutic targets. The S protein uses the angiotension-converting enzyme-2 (ACE-2) receptor for entry, but also sialic acids linked to host cell surface gangliosides. Using a combination of structural and molecular modelling approaches, this study showed that chloroquine (CLQ), one of the drugs currently under investigation for SARS-CoV-2 treatment, binds sialic acids and gangliosides with high affinity. A new type of ganglioside-binding domain at the tip of the N-terminal domain of the SARS-CoV-2 S protein was identified. This domain (111–158), which is fully conserved among clinical isolates worldwide, may improve attachment of the virus to lipid rafts and facilitate contact with the ACE-2 receptor. This study showed that, in the presence of CLQ [or its more active derivative, hydroxychloroquine (CLQ-OH)], the viral S protein is no longer able to bind gangliosides. The identification of this new mechanism of action of CLQ and CLQ-OH supports the use of these repositioned drugs to cure patients infected with SARS-CoV-2. The in-silico approaches used in this study might also be used to assess the efficiency of a broad range of repositioned and/or innovative drug candidates before clinical evaluation. © 2020 Elsevier B.V. and International Society of Chemotherapy


Phylogenetic analysis of the first four SARS-CoV-2 cases in Chile
(2020) Journal of Medical Virology

Abstract:
The current pandemic caused by the new coronavirus is a worldwide public health concern. To aboard this emergency, and like never before, scientific groups around the world have been working in a fast and coordinated way to get the maximum of information about this virus when it has been almost 3 months since the first cases were detected in Wuhan province in China. The complete genome sequences of around 450 isolates are available, and studies about similarities and differences among them and with the close related viruses that caused similar epidemics in this century. In this work, we studied the complete genome of the first four cases of the new coronavirus disease in Chile, from patients who traveled to Europe and Southeast Asia. Our findings reveal at least two different viral variants entries to Chilean territory, coming from Europe and Asia. We also sub-classified the isolates into variants according to punctual mutations in the genome. Our work contributes to global information about transmission dynamics and the importance to take control measures to stop the spread of the infection. © 2020 Wiley Periodicals, Inc.

Ong, S.W.X., Tan, Y.K., Sutjipto, S., Chia, P.Y., Young, B.E., Gum, M., Lau, S.K., Chan, M., Vasoo, S., Mendis, S., Toh, B.K., Leong, J., Barkham, T., Ang, B.S.P., Tan, B.H., Leo, Y.-S., Marimuthu, K., Wong, M.S.Y., Ng, O.T.

Absence of contamination of personal protective equipment (PPE) by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)
(2020) Infection Control and Hospital Epidemiology


SARS-CoV-2: fear versus data
(2020) International Journal of Antimicrobial Agents, art. no. 105947
Abstract:
SARS-CoV-2, the novel coronavirus from China, is spreading around the world, causing a huge reaction despite its current low incidence outside China and the Far East. Four common coronaviruses are in current circulation and cause millions of cases worldwide. This article compares the incidence and mortality rates of these four common coronaviruses with those of SARS-CoV-2 in Organisation for Economic Co-operation and Development countries. It is concluded that the problem of SARS-CoV-2 is probably being overestimated, as 2.6 million people die of respiratory infections each year compared with less than 4000 deaths for SARS-CoV-2 at the time of writing.

Faccincani, R., Pascucci, F., Lennquist, S.
How to surge to face SARS-CoV-2 outbreak. Lessons learned from Lumbardy, Italy
(2020) Disaster Medicine and Public Health Preparedness

Abstract:
Italy is fighting against one of the worst medical emergency since the 1918 Spanish Flu. Pressure on the hospitals is tremendous as for official data on March 14th: 8372 admitted in hospitals, 1518 in ICU, 1441 deaths (175 more than the day before). Unfortunately hospitals are not prepared: even where a plan for massive influx of patients is present, it usually focuses on sudden onset disaster trauma victims (the most probable case scenario), and it has not been tested, validated or propagated to the staff. Despite this, the All Hazards Approach (AHA) for management of major incidents and disasters is still valid and the "4S" theory for surge capacity can guide to respond to this disaster. Copyright © 2020 Society for Disaster Medicine and Public Health, Inc.

Srinivasan, S., Cui, H., Gao, Z., Liu, M., Lu, S., Mkandawire, W., Narykov, O., Sun, M., Korkin, D.
Structural genomics of SARS-COV-2 indicates evolutionary conserved functional regions of viral proteins
(2020) Viruses, 12 (4), art. no. 360

Abstract:
During its first two and a half months, the recently emerged 2019 novel coronavirus, SARS-CoV-2, has already infected over one-hundred thousand people worldwide and has taken more than four thousand lives. However, the swiftly spreading virus also caused an unprecedentedly rapid response from the research community facing the unknown health challenge of potentially enormous proportions. Unfortunately, the experimental research to understand the molecular mechanisms behind the viral infection and to design a vaccine or antivirals is costly and takes months to develop. To expedite the advancement of our knowledge, we leveraged data about the related coronaviruses that is readily available in public databases and integrated these data into a single computational pipeline. As a result, we provide comprehensive structural genomics and interactomics roadmaps of SARS-CoV-2 and use this information to infer the possible functional differences and similarities with the related SARS coronavirus. All data are made publicly available to the research community. © 2020 by the authors.

SARS-CoV-2 infection during pregnancy. Information and proposal of management care. CNGOF [Infection par le SARS-CoV-2 chez les femmes enceintes. État des connaissances et proposition de prise en charge. CNGOF]

(2020) Gynecologie Obstetrique Fertilite et Senologie

Abstract:
A new coronavirus (SARS-CoV-2) highlighted at the end of 2019 in China is spreading across all continents. Most often at the origin of a mild infectious syndrome, associating mild symptoms (fever, cough, myalgia, headache and possible digestive disorders) to different degrees, SARS-Covid-2 can cause serious pulmonary pathologies and sometimes death. Data on the consequences during pregnancy are limited. The first Chinese data published seem to show that the symptoms in pregnant women are the same as those of the general population. There are no cases of intrauterine maternal-fetal transmission, but cases of newborns infected early suggest that there could be vertical perpartum or neonatal transmission. Induced prematurity and cases of respiratory distress in newborns of infected mothers have been described. Pregnancy is known as a period at higher risk for the consequences of respiratory infections, as for influenza, so it seems important to screen for Covid-19 in the presence of symptoms and to monitor closely pregnant women. In this context of the SARS-Covid-2 epidemic, the societies of gynecology-obstetrics, infectious diseases and neonatology have proposed a French protocol for the management of possible and proven cases of SARS-Covid-2 in pregnant women. These proposals may evolve on a daily basis with the advancement of the epidemic and knowledge in pregnant women. Subsequently, an in-depth analysis of cases in pregnant women will be necessary in order to improve knowledge on the subject.

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Establishment and validation of a pseudovirus neutralization assay for SARS-CoV-2


Abstract:
Pseudoviruses are useful virological tools because of their safety and versatility, especially for emerging and re-emerging viruses. Due to its high pathogenicity and infectivity and the lack of effective vaccines and therapeutics, live SARS-CoV-2 has to be handled under biosafety level 3 conditions, which has hindered the development of vaccines and therapeutics. Based on a VSV pseudovirus production system, a pseudovirus-based neutralization assay has been developed for evaluating neutralizing antibodies against SARS-CoV-2 in biosafety level 2 facilities. The key parameters for this assay were optimized, including cell types, cell numbers, virus inoculum. When tested against the SARS-CoV-2 pseudovirus, SARS-CoV-2 convalescent patient sera showed high neutralizing potency, which underscore its potential as therapeutics. The limit of detection for this assay was determined as 22.1 and 43.2 for human and mouse serum samples respectively using a panel of 120 negative samples. The cutoff values were set as 30 and 50 for human and mouse serum samples, respectively. This assay showed relatively low coefficient of variations with 15.9% and 16.2% for the intra- and inter-assay analyses respectively. Taken together, we established a robust pseudovirus-based neutralization assay for SARS-CoV-2 and are glad to share pseudoviruses and related protocols with the developers of vaccines or therapeutics to fight against this lethal virus. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.
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)

(2020) Journal of Medical Virology

Abstract:
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. © 2020 Wiley Periodicals, Inc.
The potential chemical structure of anti-SARS-CoV-2 RNA-dependent RNA polymerase
(2020) Journal of Medical Virology

Abstract:
An outbreak of coronavirus disease 2019 (COVID-19) occurred in Wuhan and it has rapidly spread to almost all parts of the world. For coronaviruses, RNA-dependent RNA polymerase (RdRp) is an important protease that catalyzes the replication of RNA from RNA template and is an attractive therapeutic target. In this study, we screened these chemical structures from traditional Chinese medicinal compounds proven to show antiviral activity in severe acute respiratory syndrome coronavirus (SARS-CoV) and the similar chemical structures through a molecular docking study to target RdRp of SARS-CoV-2, SARS-CoV, and Middle East respiratory syndrome coronavirus (MERS-CoV). We found that theaflavin has a lower idock score in the catalytic pocket of RdRp in SARS-CoV-2 (−9.11 kcal/mol), SARS-CoV (−8.03 kcal/mol), and MERS-CoV (−8.26 kcal/mol) from idock. To confirm the result, we discovered that theaflavin has lower binding energy of −8.8 kcal/mol when it docks in the catalytic pocket of SARS-CoV-2 RdRp by using the Blind Docking server. Regarding contact modes, hydrophobic interactions contribute significantly in binding and additional hydrogen bonds were found between theaflavin and RdRp. Moreover, one π-cation interaction was formed between theaflavin and Arg553 from the Blind Docking server. Our results suggest that theaflavin could be a potential SARS-CoV-2 RdRp inhibitor for further study. © 2020 Wiley Periodicals, Inc.


Practical recommendations for the perioperative management of the patient with suspicion or serious infection by coronavirus SARS-CoV [Recomendaciones prácticas para el manejo perioperatorio del paciente con sospecha o infección grave por coronavirus SARS-CoV-2]
(2020) Revista Española de Anestesiología y Reanimacion

Abstract:
In December 2019, the Wuhan Municipal Health and health Commission (Hubei Province, China) reported a series of cases of pneumonia of unknown etiology. On January 7, 2020, the Chinese authorities identified as a causative agent of the outbreak a new type of virus of the Coronaviridiae family, called SARS-CoV-2. Since then, thousands of cases have been reported with global dissemination. Infections in humans cause a broad clinical spectrum ranging from mild upper respiratory tract infection, to severe acute respiratory distress syndrome and sepsis. There is not specific treatment for SARS-CoV-2, which is why the fundamental aspects are to establish adequate prevention measures and support treatment and management of complications. © 2020 Sociedad Española de Anestesiología, Reanimación y Terapéutica del Dolor

Kandeel, M., Ibrahim, A., Fayez, M., Al-Nazawi, M.

From SARS and MERS CoVs to SARS-CoV-2: Moving toward more biased codon usage in viral structural and nonstructural genes
(2020) Journal of Medical Virology

Abstract:
Background: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an emerging disease with fatal outcomes. In this study, a fundamental knowledge gap question is to be resolved by evaluating the differences in biological and pathogenic aspects of SARS-CoV-2 and the changes in SARS-CoV-2 in comparison with the two prior major COV epidemics, SARS and Middle East respiratory syndrome (MERS) coronaviruses. Methods: The genome composition, nucleotide analysis, codon usage indices, relative synonymous codons usage, and effective number of codons (ENc) were analyzed in the four structural genes; Spike (S), Envelope (E), membrane (M), and Nucleocapsid (N) genes, and two of the most important nonstructural genes comprising RNA-dependent RNA polymerase and main protease (Mpro) of SARS-CoV-2, Beta-CoV from pangolins, bat SARS, MERS, and SARS CoVs. Results: SARS-CoV-2 prefers pyrimidine rich codons to purines. Most high-frequency codons were ending with A or T, while the low frequency and rare codons were ending with G or C. SARS-CoV-2 structural proteins showed 5 to 20 lower ENc values, compared with SARS, bat SARS, and MERS CoVs. This implies higher codon bias and higher gene expression efficiency of SARS-CoV-2 structural proteins. SARS-CoV-2 encoded the highest number of over-biased and negatively biased codons. Pangolin Beta-CoV showed little differences with SARS-CoV-2 ENc values, compared with SARS, bat SARS, and MERS CoV. Conclusion: Extreme bias and lower ENc values of SARS-CoV-2, especially in Spike, Envelope, and Mpro genes, are suggestive for higher gene expression efficiency, compared with SARS, bat SARS, and MERS CoVs.
Life Sciences:

- Agricultural and Biological Sciences
- Biochemistry, Genetics, and Molecular Biology
- Immunology and Microbiology
- Neuroscience
- Pharmacology, Toxicology, and Pharmaceutics
Detection of 2019 novel coronavirus (2019-nCoV) by real-time RT-PCR
(2020) Eurosurveillance, 25 (3), art. no. 2000045

Abstract:
Background: The ongoing outbreak of the recently emerged novel coronavirus (2019-nCoV) poses a challenge for public health laboratories as virus isolates are unavailable while there is growing evidence that the outbreak is more widespread than initially thought, and international spread through travellers does already occur. Aim: We aimed to develop and deploy robust diagnostic methodology for use in public health laboratory settings without having virus material available. Methods: Here we present a validated diagnostic workflow for 2019-nCoV, its design relying on close genetic relatedness of 2019-nCoV with SARS coronavirus, making use of synthetic nucleic acid technology. Results: The workflow reliably detects 2019-nCoV, and further discriminates 2019-nCoV from SARS-CoV. Through coordination between academic and public laboratories, we confirmed assay exclusivity based on 297 original clinical specimens containing a full spectrum of human respiratory viruses. Control material is made available through European Virus Archive Global (EVAg), a European Union infrastructure project. Conclusion: The present study demonstrates the enormous response capacity achieved through coordination of academic and public laboratories in national and European research networks. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Cross-species transmission of the newly identified coronavirus 2019-nCoV

Abstract:
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 coronavirus 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. © 2020 Wiley Periodicals, Inc.

Drug treatment options for the 2019-new coronavirus (2019-nCoV)
(2020) BioScience Trends, 14 (1), art. no. 1020

Abstract:
As of January 22, 2020, a total of 571 cases of the 2019-new coronavirus (2019-nCoV) have been reported in 25 provinces (districts and cities) in China. At present, there is no vaccine or antiviral treatment for human and animal coronavirus, so that identifying the drug treatment options as soon as possible is critical for the response to the 2019-nCoV outbreak. Three general methods, which include existing broad-spectrum antiviral drugs using standard assays, screening of a chemical library containing many existing compounds or databases, and the redevelopment of new specific drugs based on the genome and biophysical understanding of individual coronaviruses, are used to
discover the potential antiviral treatment of human pathogen coronavirus. Lopinavir /Ritonavir, Nucleoside analogues, Neuraminidase inhibitors, Remdesivir, peptide (EK1), arbidol, RNA synthesis inhibitors (such as TDF, 3TC), anti-inflammatory drugs (such as hormones and other molecules), Chinese traditional medicine, such ShuFengJieDu Capsules and Lianhuaqingwen Capsule, could be the drug treatment options for 2019-nCoV. However, the efficacy and safety of these drugs for 2019-nCoV still need to be further confirmed by clinical experiments. © 2020 International Advancement Center for Medicine and Health Research Co., Ltd.

Wang, W., Tang, J., Wei, F.

**Updated understanding of the outbreak of 2019 novel coronavirus (2019-nCoV) in Wuhan, China**


**Abstract:**

To help health workers and the public recognize and deal with the 2019 novel coronavirus (2019-nCoV) quickly, effectively, and calmly with an updated understanding. A comprehensive search from Chinese and worldwide official websites and announcements was performed between 1 December 2019 and 9:30 am 26 January 2020 (Beijing time). A latest summary of 2019-nCoV and the current outbreak was drawn. Up to 24 pm, 25 January 2020, a total of 1975 cases of 2019-nCoV infection were confirmed in mainland China with a total of 56 deaths having occurred. The latest mortality was approximately 2.84% with a total of 2684 cases still suspected. The China National Health Commission reported the details of the first 17 deaths up to 24 pm, 22 January 2020. The deaths included 13 males and 4 females. The median age of the people who died was 75 (range 48-89) years. Fever (64.7%) and cough (52.9%) were the most common first symptoms among those who died. The median number of days from the occurrence of the first symptom to death was 14.0 (range 6-41) days, and it tended to be shorter among people aged 70 years or more (11.5 [range 6-19] days) than those aged less than 70 years (20 [range 10-41] days; P =.033). The 2019-nCoV infection is spreading and its incidence is increasing nationwide. The first deaths occurred mostly in elderly people, among whom the disease might progress faster. The public should still be cautious in dealing with the virus and pay more attention to protecting the elderly people from the virus. © 2020 Wiley Periodicals, Inc.


**Molecular and serological investigation of 2019-nCoV infected patients: implication of multiple shedding routes**


**Abstract:**

In December 2019, a novel coronavirus (2019-nCoV) caused an outbreak in Wuhan, China, and soon spread to other parts of the world. It was believed that 2019-nCoV was transmitted through respiratory tract and then induced pneumonia, thus molecular diagnosis based on oral swabs was used for confirmation of this disease. Likewise, patient will be released upon two times of negative detection from oral swabs. However, many coronaviruses can also be transmitted through oral–fecal route by infecting intestines. Whether 2019-nCoV infected patients also carry virus in other organs like intestine need to be tested. We conducted investigation on patients in a local hospital who were infected with this virus. We found the presence of 2019-nCoV in anal swabs and blood as well, and more anal swab positives than oral swab positives in a later stage of infection, suggesting shedding and thereby transmitted through oral–fecal route. We also showed serology test can improve detection positive rate thus should be used in future epidemiology. Our report provides a cautionary warning that 2019-nCoV may be shed through multiple routes. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.
Chen, J.


Abstract:
A zoonotic coronavirus, tentatively labeled as 2019-nCoV by the World Health Organization (WHO), has been identified as the causative agent of the viral pneumonia outbreak in Wuhan, China, at the end of 2019. Although 2019-nCoV can cause a severe respiratory illness like SARS and MERS, evidence from clinics suggested that 2019-nCoV is generally less pathogenic than SARS-CoV, and much less than MERS-CoV. The transmissibility of 2019-nCoV is still debated and needs to be further assessed. To avoid the 2019-nCoV outbreak turning into an epidemic or even a pandemic and to minimize the mortality rate, China activated emergency response procedures, but much remains to be learned about the features of the virus to refine the risk assessment and response. Here, the current knowledge in 2019-nCoV pathogenicity and transmissibility is summarized in comparison with several commonly known emerging viruses, and information urgently needed for a better control of the disease is highlighted. © 2020 The Author(s)

Paraskevis, D., Kostaki, E.G., Magiorkinis, G., Panayiotakopoulos, G., Sourvinos, G., Tsiodras, S.

Full-genome evolutionary analysis of the novel corona virus (2019-nCoV) rejects the hypothesis of emergence as a result of a recent recombination event (2020) Infection, Genetics and Evolution, 79, art. no. 104212

Abstract:
Background: A novel coronavirus (2019-nCoV) associated with human to human transmission and severe human infection has been recently reported from the city of Wuhan in China. Our objectives were to characterize the genetic relationships of the 2019-nCoV and to search for putative recombination within the subgenus of sarbecovirus. Methods: Putative recombination was investigated by RDPhylo and Simplot v3.5.1 and discordant phylogenetic clustering in individual genomic fragments was confirmed by phylogenetic analysis using maximum likelihood and Bayesian methods. Results: Our analysis suggests that the 2019-nCoV although closely related to BatCoV RaTG13 sequence throughout the genome (sequence similarity 96.3%), shows discordant clustering with the Bat_SARS-like coronavirus sequences. Specifically, in the 5′-part spanning the first 11,498 nucleotides and the last 3′-part spanning 24,341–30,696 positions, 2019-nCoV and RaTG13 formed a single cluster with Bat_SARS-like coronavirus sequences, whereas in the middle region spanning the 3′-end of ORF1a, the ORF1b and almost half of the spike regions, 2019-nCoV and RaTG13 grouped in a separate distant lineage within the sarbecovirus branch. Conclusions: The levels of genetic similarity between the 2019-nCoV and RaTG13 suggest that the latter does not provide the exact variant that caused the outbreak in humans, but the hypothesis that 2019-nCoV has originated from bats is very likely. We show evidence that the novel coronavirus (2019-nCov) is not-mosaic consisting in almost half of its genome of a distinct lineage within the betacoronavirus. These genomic features and their potential association with virus characteristics and virulence in humans need further attention. © 2020 Elsevier B.V.


Abstract:
The outbreak of the 2019-nCoV infection began in December 2019 in Wuhan, Hubei province, and rapidly spread to many provinces in China as well as other countries. Here we report the epidemiological, clinical, laboratory, and radiological characteristics, as well as potential biomarkers for predicting disease severity in 2019-nCoV-infected patients in Shenzhen, China. All 12 cases of the 2019-nCoV-infected patients developed pneumonia and half of them developed acute respiratory distress syndrome (ARDS). The most common laboratory abnormalities were hypoalbuminemia, lymphopenia, decreased percentage of lymphocytes (LYM) and neutrophils (NEU), elevated C-reactive protein (CRP) and lactate dehydrogenase (LDH), and decreased CD8 count. The viral load of 2019-nCoV detected from patient respiratory tracts was positively linked to lung disease severity. ALB, LYM, LYM (%), LDH, NEU (%), and CRP were highly correlated to the acute lung injury. Age, viral load, lung injury score, and blood biochemistry indexes, albumin (ALB), CRP, LDH, LYM (%), LYM, and NEU (%), may be predictors of disease severity. Moreover, the Angiotensin II level in the plasma sample from 2019-nCoV infected patients was markedly elevated and linearly associated to viral load and lung injury. Our results suggest a number of potential diagnosis biomarkers and angiotensin receptor blocker (ARB) drugs for potential repurposing treatment of 2019-nCoV infection. © 2020, Science China Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China (2020) Science China Life Sciences

Abstract:
Previous studies have showed clinical characteristics of patients with the 2019 novel coronavirus disease (COVID-19) and the evidence of person-to-person transmission. Limited data are available for asymptomatic infections. This study aims to present the clinical characteristics of 24 cases with asymptomatic infection screened from close contacts and to show the transmission potential of asymptomatic COVID-19 virus carriers. Epidemiological investigations were conducted among all close contacts of COVID-19 patients (or suspected patients) in Nanjing, Jiangsu Province, China, from Jan 28 to Feb 9, 2020, both in clinic and in community. Asymptomatic carriers were laboratory-confirmed positive for the COVID-19 virus by testing the nucleic acid of the pharyngeal swab samples. Their clinical records, laboratory assessments, and chest CT scans were reviewed. As a result, none of the 24 asymptomatic cases presented any obvious symptoms while nucleic acid screening. Five cases (20.8%) developed symptoms (fever, cough, fatigue, etc.) during hospitalization. Twelve (50.0%) cases showed typical CT images of ground-glass chest and 5 (20.8%) presented stripe shadowing in the lungs. The remaining 7 (29.2%) cases showed normal CT image and had no symptoms during hospitalization. These 7 cases were younger (median age: 14.0 years; P=0.012) than the rest. None of the 24 cases developed severe COVID-19 pneumonia or died. The median communicable period, defined as the interval from the first day of positive nucleic acid tests to the first day of continuous negative tests, was 9.5 days (up to 21 days among the 24 asymptomatic cases). Through epidemiological investigation, we observed a typical asymptomatic transmission to the cohabiting family members, which even caused severe COVID-19 pneumonia. Overall, the asymptomatic carriers identified from close contacts were prone to be mildly ill during hospitalization. However, the communicable period could be up to three weeks and the communicated patients could develop severe illness. These results highlighted the importance of close contact tracing and longitudinally surveillance via virus nucleic acid tests. Further isolation recommendation and continuous nucleic acid tests may also be recommended to the patients discharged. © 2020, Science China Press and Springer-Verlag GmbH Germany, part of Springer Nature.
Learning from the Past: Possible Urgent Prevention and Treatment Options for Severe Acute Respiratory Infections Caused by 2019-nCoV

Abstract:
With the current trajectory of the 2019-nCoV outbreak unknown, public health and medicinal measures will both be needed to contain spreading of the virus and to optimize patient outcomes. Although little is known about the virus, an examination of the genome sequence shows strong homology with its better-studied cousin, SARS-CoV. The spike protein used for host cell infection shows key nonsynonymous mutations that might hamper the efficacy of previously developed therapeutics but remains a viable target for the development of biologics and macrocyclic peptides. Other key drug targets, including RNA-dependent RNA polymerase and coronavirus main proteinase (3CLpro), share a strikingly high (>95 %) homology to SARS-CoV. Herein, we suggest four potential drug candidates (an ACE2-based peptide, remdesivir, 3CLpro-1 and a novel vinylsulfone protease inhibitor) that could be used to treat patients suffering with the 2019-nCoV. We also summarize previous efforts into drugging these targets and hope to help in the development of broad-spectrum anti-coronaviral agents for future epidemics. © 2020 Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim

The spike glycoprotein of the new coronavirus 2019-nCoV contains a furin-like cleavage site absent in CoV of the same clade
(2020) Antiviral Research, 176, art. no. 104742

Abstract:
In 2019, a new coronavirus (2019-nCoV) infecting Humans has emerged in Wuhan, China. Its genome has been sequenced and the genomic information promptly released. Despite a high similarity with the genome sequence of SARS-CoV and SARS-like CoVs, we identified a peculiar furin-like cleavage site in the Spike protein of the 2019-nCoV, lacking in the other SARS-like CoVs. In this article, we discuss the possible functional consequences of this cleavage site in the viral cycle, pathogenicity and its potential implication in the development of antivirals. © 2020 Elsevier B.V.

Genomic variance of the 2019-nCoV coronavirus

Abstract:
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. © 2020 Wiley Periodicals, Inc.

Potential of large “first generation” human-to-human transmission of 2019-nCoV
Abstract:
To investigate the genetic diversity, time origin, and evolutionary history of the 2019-nCoV outbreak in China and Thailand, a total of 12 genome sequences of the virus with known sampling date (24 December 2019 and 13 January 2020) and geographic location (primarily Wuhan city, Hubei Province, China, but also Bangkok, Thailand) were analyzed. Phylogenetic and likelihood-mapping analyses of these genome sequences were performed. On the basis of our results, the star-like signal and topology of 2019-nCoV may be indicative of potentially large “first generation” human-to-human virus transmission. We estimated that 2019-nCoV likely originated in Wuhan on 9 November 2019 (95% credible interval: 25 September 2019 and 19 December 2019), and that Wuhan is the major hub for the spread of the 2019-nCoV outbreak in China and elsewhere. Our results could be useful for designing effective prevention strategies for 2019-nCoV in China and beyond. © 2020 Wiley Periodicals, Inc.

Sun, P., Qie, S., Liu, Z., Ren, J., Li, K., Xi, J.
Clinical characteristics of 50 466 hospitalized patients with 2019-nCoV infection (2020) Journal of Medical Virology

Abstract:
We aim to summarize reliable evidence of evidence-based medicine for the treatment and prevention of the 2019 novel coronavirus (2019-nCoV) by analyzing all the published studies on the clinical characteristics of patients with 2019-nCoV. PubMed, Cochrane Library, Embase, and other databases were searched. Several studies on the clinical characteristics of 2019-nCoV infection were collected for meta-analysis. Ten studies were included in the meta-analysis, including a total number of 50 466 patients with 2019-nCoV infection. Meta-analysis shows that among these patients, the incidence of fever was 89.1%, the incidence of cough was 72.2%, and the incidence of muscle soreness or fatigue was 42.5%. The incidence of acute respiratory distress syndrome (ARDS) was 14.8%, the incidence of abnormal chest computer tomography (CT) was 96.6%, the percentage of severe cases in all infected cases was 18.1%, and the case fatality rate of patients with 2019-nCoV infection was 4.3%. Fever and cough are the most common symptoms in patients with 2019-nCoV infection, and most of these patients have abnormal chest CT examination. Several people have muscle soreness or fatigue as well as ARDS. Diarrhea, hemoptysis, headache, sore throat, shock, and other symptoms only occur in a small number of patients. The case fatality rate of patients with 2019-nCoV infection is lower than that of the severe acute respiratory syndrome and Middle East respiratory syndrome. © 2020 Wiley Periodicals, Inc.

Lee, P.-I., Hsueh, P.-R.
Emerging threats from zoonotic coronaviruses-from SARS and MERS to 2019-nCoV (2020) Journal of Microbiology, Immunology and Infection

Giovanetti, M., Benvenuto, D., Angeletti, S., Ciccozzi, M.

Abstract:
A novel Coronavirus, 2019-nCoV, has been identified as the causal pathogen of an ongoing epidemic, with the first cases reported in Wuhan, China, last December 2019, and has since spread to other countries worldwide, included Europe and very recently Italy. In this short report, phylogenetic reconstruction was used to better understand the transmission dynamics of the virus from its first introduction in China focusing on the more recent evidence of infection in a couple of Chinese tourists arrived in Italy on 23rd January 2020 and labeled as Coronavirus Italian cases. A maximum clade credibility tree has been built using a dataset of 54 genome sequences of 2019-nCoV plus two closely related bat strains (SARS-like CoV) available in GenBank. Bayesian time-
scaled phylogenetic analysis was implemented in BEAST 1.10.4. The Bayesian phylogenetic reconstruction showed that 2019-2020 nCoV firstly introduced in Wuhan on 25 November 2019, started epidemic transmission reaching many countries worldwide, including Europe and Italy where the two strains isolated dated back 19 January 2020, the same that the Chinese tourists arrived in Italy. Strains isolated outside China were intermixed with strains isolated in China as evidence of likely imported cases in Rome, Italy, and Europe, as well. In conclusion, this report suggests that further spread of 2019-nCoV epidemic was supported by human mobility and that quarantine of suspected or diagnosed cases is useful to prevent further transmission. Viral genome phylogenetic analysis represents a useful tool for the evaluation of transmission dynamics and preventive action. © 2020 Wiley Periodicals, Inc.

Eurosurveillance Editorial Team

**Note from the editors: World Health Organization declares novel coronavirus (2019-nCoV) sixth public health emergency of international concern**

Porcheddu, R., Serra, C., Kelvin, D., Kelvin, N., Rubino, S.

**Similarity in Case Fatality Rates (CFR) of COVID-19/SARS-COV-2 in Italy and China**

**Abstract:**
As of 28 February 2020, Italy had 888 cases of SARS-CoV-2 infections, with most cases in Northern Italy in the Lombardia and Veneto regions. Travel-related cases were the main source of COVID-19 cases during the early stages of the current epidemic in Italy. The month of February, however, has been dominated by two large clusters of outbreaks in Northern Italy, south of Milan, with mainly local transmission the source of infections. Contact tracing has failed to identify patient zero in one of the outbreaks. As of 28 February 2020, twenty-one cases of COVID-19 have died. Comparison between case fatality rates in China and Italy are identical at 2.3. Additionally, deaths are similar in both countries with fatalities in mostly the elderly with known comorbidities. It will be important to develop point-of-care devices to aid clinicians in stratifying elderly patients as early as possible to determine the potential level of care they will require to improve their chances of survival from COVID-19 disease. © 2020 Porcheddu et al.

Baruah, V., Bose, S.

**Immunoinformatics-aided identification of T cell and B cell epitopes in the surface glycoprotein of 2019-nCoV**

**Abstract:**
The 2019 novel coronavirus (2019-nCoV) outbreak has caused a large number of deaths with thousands of confirmed cases worldwide, especially in East Asia. This study took an immunoinformatics approach to identify significant cytotoxic T lymphocyte (CTL) and B cell epitopes in the 2019-nCoV surface glycoprotein. Also, interactions between identified CTL epitopes and their corresponding major histocompatibility complex (MHC) class I supertype representatives prevalent in China were studied by molecular dynamics simulations. We identified five CTL epitopes, three sequential B cell epitopes and five discontinuous B cell epitopes in the viral surface glycoprotein. Also, during simulations, the CTL epitopes were observed to be binding MHC class I peptide-binding grooves via multiple contacts, with continuous hydrogen bonds and salt bridge anchors, indicating their potential in generating immune responses. Some of these identified epitopes can be potential candidates for the development of 2019-nCoV vaccines. © 2020 Wiley Periodicals, Inc.
Chen, Y., Guo, Y., Pan, Y., Zhao, Z.J.
Structure analysis of the receptor binding of 2019-nCoV
(2020) Biochemical and Biophysical Research Communications, 525 (1), pp. 135-140.

Abstract:
2019-nCoV is a newly identified coronavirus with high similarity to SARS-CoV. We performed a structural analysis of the receptor binding domain (RBD) of spike glycoprotein responsible for entry of coronaviruses into host cells. The RBDs from the two viruses share 72% identity in amino acid sequences, and molecular simulation reveals highly similar ternary structures. However, 2019-nCoV has a distinct loop with flexible glycy1 residues replacing rigid proly1 residues in SARS-CoV. Molecular modeling revealed that 2019-nCoV RBD has a stronger interaction with angiotensin converting enzyme 2 (ACE2). A unique phenylalanine F486 in the flexible loop likely plays a major role because its penetration into a deep hydrophobic pocket in ACE2. ACE2 is widely expressed with conserved primary structures throughout the animal kingdom from fish, amphibians, reptiles, birds, to mammals. Structural analysis suggests that ACE2 from these animals can potentially bind RBD of 2019-nCoV, making them all possible natural hosts for the virus. 2019-nCoV is thought to be transmitted through respiratory droplets. However, since ACE2 is predominantly expressed in intestines, testis, and kidney, fecal-oral and other routes of transmission are also possible. Finally, antibodies and small molecular inhibitors that can block the interaction of ACE2 with RBD should be developed to combat the virus. © 2020 The Authors

Transplantation of ACE2- Mesenchymal stem cells improves the outcome of patients with covid-19 pneumonia

Abstract:
A coronavirus (HCoV-19) has caused the novel coronavirus disease (COVID-19) outbreak in Wuhan, China. Preventing and reversing the cytokine storm may be the key to save the patients with severe COVID-19 pneumonia. Mesenchymal stem cells (MSCs) have been shown to possess a comprehensive powerful immunomodulatory function. This study aims to investigate whether MSC transplantation improves the outcome of 7 enrolled patients with COVID-19 pneumonia in Beijing YouAn Hospital, China, from Jan 23, 2020 to Feb 16, 2020. The clinical outcomes, as well as changes of inflammatory and immune function levels and adverse effects of 7 enrolled patients were assessed for 14 days after MSC injection. MSCs could cure or significantly improve the functional outcomes of seven patients without observed adverse effects. The pulmonary function and symptoms of these seven patients were significantly improved in 2 days after MSC transplantation. Among them, two common and one severe patient were recovered and discharged in 10 days after treatment. After treatment, the peripheral lymphocytes were increased, the C-reactive protein decreased, and the overactivated cytokine-secreting immune cells CXCR3+CD4+ T cells, CXCR3+CD8+ T cells, and CXCR3+ NK cells disappeared in 3-6 days. In addition, a group of CD14+CD11c+CD11bmid regulatory DC cell population dramatically increased. Meanwhile, the level of TNF-α was significantly decreased, while IL-10 increased in MSC treatment group compared to the placebo control group. Furthermore, the gene expression profile showed MSCs were ACE2- and TMPRSS2- which indicated MSCs are free from COVID-19 infection. Thus, the intravenous transplantation of MSCs was safe and effective for treatment in patients with COVID-19 pneumonia, especially for the patients in critically severe condition. © 2020 Leng Z et al. This is an open-access article distributed under the terms of the Creative
Abstract:
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 provinence. While zoonotic transmission appears to be the original source of infections, the most alarming development is that human-to-human transmission is now prevalent. 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. Copyright © 2020 Ralph et al.

Development and validation
Wang, A., Zhao, W., Xu, Z., Gu, J.
Timely blood glucose management for the outbreak of 2019 novel coronavirus disease (COVID-19) is urgently needed
(2020) Diabetes Research and Clinical Practice, 162, art. no. 108118

Angeletti, S., Benvenuto, D., Bianchi, M., Giovanetti, M., Pascarella, S., Ciccozzi, M.
COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis
(2020) Journal of Medical Virology
Abstract:
Last December 2019, a new virus, named novel Coronavirus (COVID-2019) causing many cases of severe pneumonia was reported in Wuhan, China. The virus knowledge is limited and especially about COVID-2019 pathogenesis. The Open Reading Frame 1ab (ORF1ab) of COVID-2019 has been analyzed to evidence the presence of mutation caused by selective pressure on the virus. For selective pressure analysis fast-unconstrained Bayesian approximation (FUBAR) was used. Homology modelling has been performed by SwissModel and HHPred servers. The presence of transmembrane helical segments in Coronavirus ORF1ab non structural protein 2 (nsp2) and nsp3
was tested by TMHMM, MEMSAT, and MEMPACK tools. Three-dimensional structures have been analyzed and displayed using PyMOL. FUBAR analysis revealed the presence of potential sites under positive selective pressure (P < .05). Position 723 in the COVID-2019 has a serine instead a glycine residue, while at aminoacidic position 1010 a proline instead an isoleucine. Significant (P < .05) pervasive negative selection in 2416 sites (55%) was found. The positive selective pressure could account for some clinical features of this virus compared with severe acute respiratory syndrome (SARS) and Bat SARS-like CoV. The stabilizing mutation falling in the endosome-associated-protein-like domain of the nsp2 protein could account for COVID-2019 high ability of contagious, while the destabilizing mutation in nsp3 proteins could suggest a potential mechanism differentiating COVID-2019 from SARS. These data could be helpful for further investigation aimed to identify potential therapeutic targets or vaccine strategy, especially in the actual moment when the epidemic is ongoing and the scientific community is trying to enrich knowledge about this new viral pathogen. © 2020 Wiley Periodicals, Inc.


2019 novel coronavirus disease (COVID-19) in Taiwan: Reports of two cases from Wuhan, China
(2020) Journal of Microbiology, Immunology and Infection
Abstract:
We reported two cases with community-acquired pneumonia caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) who returned from Wuhan, China in January, 2020. The reported cases highlight non-specific clinical presentations of 2019 novel coronavirus disease (COVID-19) as well as the importance of rapid laboratory-based diagnosis. © 2020

Shanmugaraj, B., Malla, A., Phoolcharoen, W.

Emergence of novel coronavirus 2019-nCoV: Need for rapid vaccine and biologics development
(2020) Pathogens, 9 (2), art. no. 148
Abstract:
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. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Wu, Y.

Compensation of ACE2 Function for Possible Clinical Management of 2019-nCoV-Induced Acute Lung Injury
(2020) Virologica Sinica
Elfiky, A.A.

**Anti-HCV, nucleotide inhibitors, repurposing against COVID-19**
(2020) Life Sciences, 248, art. no. 117477

**Abstract:**
Aims: A newly emerged Human Coronavirus (HCoV) is reported two months ago in Wuhan, China (COVID-19). Until today >2700 deaths from the 80,000 confirmed cases reported mainly in China and 40 other countries. Human to human transmission is confirmed for COVID-19 by China a month ago. Based on the World Health Organization (WHO) reports, SARS HCoV is responsible for >8000 cases with confirmed 774 deaths. Additionally, MERS HCoV is responsible for 858 deaths out of about 2500 reported cases. The current study aims to test anti-HCV drugs against COVID-19 RNA dependent RNA polymerase (RdRp). Materials and methods: In this study, sequence analysis, modeling, and docking are used to build a model for Wuhan COVID-19 RdRp. Additionally, the newly emerged Wuhan HCoV RdRp model is targeted by anti-polymerase drugs, including the approved drugs Sofosbuvir and Ribavirin. Key findings: The results suggest the effectiveness of Sofosbuvir, IDX-184, Ribavirin, and Remidisvir as potent drugs against the newly emerged HCoV disease. Significance: The present study presents a perfect model for COVID-19 RdRp enabling its testing in silico against anti-polymerase drugs. Besides, the study presents some drugs that previously proved its efficiency against the newly emerged viral infection. © 2020 Elsevier Inc.

Li, X., Wang, W., Zhao, X., Zai, J., Zhao, Q., Li, Y., Chaillon, A.

**Transmission dynamics and evolutionary history of 2019-nCoV**

**Abstract:**
To investigate the time origin, genetic diversity, and transmission dynamics of the recent 2019-nCoV outbreak in China and beyond, a total of 32 genomes of virus strains sampled from China, Thailand, and the USA with sampling dates between 24 December 2019 and 23 January 2020 were analyzed. Phylogenetic, transmission network, and likelihood-mapping analyses of the genome sequences were performed. On the basis of the likelihood-mapping analysis, the increasing tree-like signals (from 0% to 8.2%, 18.2%, and 25.4%) over time may be indicative of increasing genetic diversity of 2019-nCoV in human hosts. We identified three phylogenetic clusters using the Bayesian inference framework and three transmission clusters using transmission network analysis, with only one cluster identified by both methods using the above genome sequences of 2019-nCoV strains. The estimated mean evolutionary rate for 2019-nCoV ranged from $1.7926 \times 10^{-3}$ to $1.8266 \times 10^{-3}$ substitutions per site per year. On the basis of our study, undertaking epidemiological investigations and genomic data surveillance could positively impact public health in terms of guiding prevention efforts to reduce 2019-nCoV transmission in real-time. © 2020 Wiley Periodicals, Inc.

Pan, X., Ojcius, D.M., Gao, T., Li, Z., Pan, C., Pan, C.

**Lessons learned from the 2019-nCoV epidemic on prevention of future infectious diseases**

**Abstract:**
Only a month after the outbreak of pneumonia caused by 2019-nCoV, more than forty-thousand people were infected. This put enormous pressure on the Chinese government, medical healthcare provider, and the general public, but also made the international community deeply nervous. On the 25th day after the outbreak, the Chinese government implemented strict traffic restrictions on the area where the 2019-nCoV had originated—Hubei province, whose capital city is Wuhan. Ten days later, the rate of increase of cases in Hubei showed a significant difference ($p = 0.0001$) compared with the total rate of increase in other provinces of China. These preliminary data suggest
the effectiveness of a traffic restriction policy for this pandemic thus far. At the same time, solid financial support and improved research ability, along with network communication technology, also greatly facilitated the application of epidemic prevention measures. These measures were motivated by the need to provide effective treatment of patients, and involved consultation with three major groups in policy formulation—public health experts, the government, and the general public. It was also aided by media and information technology, as well as international cooperation. This experience will provide China and other countries with valuable lessons for quickly coordinating and coping with future public health emergencies. © 2020 Institut Pasteur

Tetro, J.A.

Is COVID-19 receiving ADE from other coronaviruses?

Abstract:
One of the most perplexing questions regarding the current COVID-19 coronavirus epidemic is the discrepancy between the severity of cases observed in the Hubei province of China and those occurring elsewhere in the world. One possible answer is antibody dependent enhancement (ADE) of SARS-CoV-2 due to prior exposure to other coronaviruses. ADE modulates the immune response and can elicit sustained inflammation, lymphopenia, and/or cytokine storm, one or all of which have been documented in severe cases and deaths. ADE also requires prior exposure to similar antigenic epitopes, presumably circulating in local viruses, making it a possible explanation for the observed geographic limitation of severe cases and deaths. © 2020 Institut Pasteur

Wu, J.T., Leung, K., Bushman, M., Kishore, N., Niehus, R., de Salazar, P.M., Cowling, B.J., Lipsitch, M., Leung, G.M.

Estimating clinical severity of COVID-19 from the transmission dynamics in Wuhan, China
(2020) Nature Medicine

Abstract:
As of 29 February 2020 there were 79,394 confirmed cases and 2,838 deaths from COVID-19 in mainland China. Of these, 48,557 cases and 2,169 deaths occurred in the epicenter, Wuhan. A key public health priority during the emergence of a novel pathogen is estimating clinical severity, which requires properly adjusting for the case ascertainment rate and the delay between symptoms onset and death. Using public and published information, we estimate that the overall symptomatic case fatality risk (the probability of dying after developing symptoms) of COVID-19 in Wuhan was 1.4% (0.9–2.1%), which is substantially lower than both the corresponding crude or naïve confirmed case fatality risk (2,169/48,557 = 4.5%) and the approximator1 of deaths/deaths + recoveries (2,169/2,169 + 17,572 = 11%) as of 29 February 2020. Compared to those aged 30–59 years, those aged below 30 and above 59 years were 0.6 (0.3–1.1) and 5.1 (4.2–6.1) times more likely to die after developing symptoms. The risk of symptomatic infection increased with age (for example, at ~4% per year among adults aged 30–60 years). © 2020, The Author(s), under exclusive licence to Springer Nature America, Inc.


Revisiting the one health approach in the context of COVID-19: A look into the ecology of this emerging disease

Han, Y., Yang, H.

The transmission and diagnosis of 2019 novel coronavirus infection disease (COVID-19): A Chinese perspective
Abstract:
2019 novel coronavirus (SARS-CoV-2), which originated in Wuhan, China, has attracted the world's attention over the last month. The Chinese government has taken emergency measures to control the outbreak and has undertaken initial steps in the diagnosis and treatment of 2019 novel coronavirus infection disease (COVID-19). However, SARS-CoV-2 possesses powerful pathogenicity as well as transmissibility and still holds many mysteries that are yet to be solved, such as whether the virus can be transmitted by asymptomatic patients or by mothers to their infants. Our research presents selected available cases of COVID-19 in China to better understand the transmission and diagnosis regarding this infectious disease. © 2020 Wiley Periodicals, Inc.

Ahmed, S.F., Quadeer, A.A., McKay, M.R.

Preliminary identification of potential vaccine targets for the COVID-19 Coronavirus (SARS-CoV-2) Based on SARS-CoV Immunological Studies
(2020) Viruses, 12 (3), art. no. 254

Abstract:
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. © 2020 by the authors.

Eurosurveillance Editorial Team

Note from the editors: novel coronavirus (2019-nCoV)
(2020) Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 25 (3)

Lippi, G., Plebani, M., Henry, B.M.

Thrombocytopenia is associated with severe coronavirus disease 2019 (COVID-19) infections: A meta-analysis

Abstract:
Background: Coronavirus disease 2019 (COVID-19) is a novel infectious disease with lack of established laboratory markers available to evaluate illness severity. In this study, we investigate whether platelet count could differentiate between COVID-19 patients with or without severe disease. Additionally, we evaluate if thrombocytopenia is associated with severe COVID-19. Methods: An electronic search in Medline, Scopus and Web of Science was performed to identify studies reporting data on platelet count in COVID-19 patients. A meta-analysis was performed, with calculation of weighted mean difference (WMD) of platelet number in COVID-19 patients with or without severe disease and odds ratio (OR) of thrombocytopenia for severe form of COVID-
Results: Nine studies with 1779 COVID-19 patients, 399 (22.4%) with severe disease, were included in the meta-analysis. The pooled analysis revealed that platelet count was significantly lower in patients with more severe COVID-19 (WMD $-31 \times 10^9/L$; 95% CI, from $-35$ to $-29 \times 10^9/L$). A subgroup analysis comparing patients by survival, found an even lower platelet count was observed with mortality (WMD, $-48 \times 10^9/L$; 95% CI, $-57$ to $-39 \times 10^9/L$). In the four studies (n = 1427) which reported data on rate of thrombocytopenia, a low platelet count was associated with over fivefold enhanced risk of severe COVID-19 (OR, 5.1; 95% CI, 1.8–14.6). Conclusions: Low platelet count is associated with increased risk of severe disease and mortality in patients with COVID-19, and thus should serve as clinical indicator of worsening illness during hospitalization.

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Cao, W., Fang, Z., Hou, G., Han, M., Xu, X., Dong, J., Zheng, J.
The psychological impact of the COVID-19 epidemic on college students in China
(2020) Psychiatry Research, 287, art. no. 112934

Abstract:
A COVID-19 epidemic has been spreading in China and other parts of the world since December 2019. The epidemic has brought not only the risk of death from infection but also unbearable psychological pressure. We sampled college students from Changzhi medical college by using cluster sampling. They responded to a questionnaire packet that included the 7-item Generalized Anxiety Disorder Scale (GAD-7) and those inquiring the participants’ basic information. We received 7,143 responses. Results indicated that 0.9% of the respondents were experiencing severe anxiety, 2.7% moderate anxiety, and 21.3% mild anxiety. Moreover, living in urban areas (OR = 0.810, 95% CI = 0.709 - 0.925), family income stability (OR = 0.726, 95% CI = 0.645 - 0.817) and living with parents (OR = 0.752, 95% CI = 0.596 - 0.950) were protective factors against anxiety. Moreover, having relatives or acquaintances infected with COVID-19 was a risk factor for increasing the anxiety of college students (OR = 3.007, 95% CI = 2.377 - 3.804). Results of correlation analysis indicated that economic effects, and effects on daily life, as well as delays in academic activities, were positively associated with anxiety symptoms (P <.001). However, social support was negatively correlated with the level of anxiety (P <.001). It is suggested that the mental health of college students should be monitored during epidemics. © 2020 Elsevier B.V.

Eurosurveillance Editorial Team

Updated rapid risk assessment from ECDC on the novel coronavirus disease 2019 (COVID-19) pandemic: increased transmission in the EU/EEA and the UK


Abstract:
At the end of December 2019, a novel coronavirus, 2019-nCoV, caused an outbreak of pneumonia spreading from Wuhan, Hubei province, to the whole country of China, which has posed great threats to public health and attracted enormous attention around the world. To date, there are no clinically approved vaccines or antiviral drugs available for these human coronavirus infections. Intensive research on the novel emerging human infectious coronaviruses is urgently needed to elucidate their route of transmission and pathogenic mechanisms, and to identify potential drug targets, which would promote the development of effective preventive and therapeutic countermeasures. Herein, we describe the epidemic and etiological characteristics of 2019-nCoV,
discuss its essential biological features, including tropism and receptor usage, summarize approaches for disease prevention and treatment, and speculate on the transmission route of 2019-nCoV. © 2020 Institut Pasteur

Benvenuto, D., Giovanetti, M., Salemi, M., Prosperi, M., De Flora, C., Junior Alcantara, L.C., Angeletti, S., Ciccozzi, M.

Abstract:
The global spread of the 2019-nCoV is continuing and is fast moving, as indicated by the WHO raising the risk assessment to high. In this article, we provide a preliminary phylodynamic and phylogeographic analysis of this new virus. A Maximum Clade Credibility tree has been built using the 29 available whole genome sequences of 2019-nCoV and two whole genome sequences that are highly similar sequences from Bat SARS-like Coronavirus available in GeneBank. We are able to clarify the mechanism of transmission among the countries which have provided the 2019-nCoV sequence isolates from their patients. The Bayesian phylogeographic reconstruction shows that the 2019–2020 nCoV most probably originated from the Bat SARS-like Coronavirus circulating in the Rhinolophus bat family. In agreement with epidemiological observations, the most likely geographic origin of the new outbreak was the city of Wuhan, China, where 2019-nCoV time of the most recent common ancestor emerged, according to molecular clock analysis, around November 25th, 2019. These results, together with previously recorded epidemics, suggest a recurring pattern of periodical epizootic outbreaks due to Betacoronavirus. Moreover, our study describes the same population genetic dynamic underlying the SARS 2003 epidemic, and suggests the urgent need for the development of effective molecular surveillance strategies of Betacoronavirus among animals and Rhinolophus of the bat family. © 2020, © 2020 Informa UK Limited, trading as Taylor & Francis Group.

Yang, C.-J., Chen, T.-C., Chen, Y.-H.
The preventive strategies of community hospital in the battle of fighting pandemic COVID-19 in Taiwan (2020) Journal of Microbiology, Immunology and Infection


Abstract:
This study aims to analyze the different clinical characteristics between children and their families infected with severe acute respiratory syndrome coronavirus 2. Clinical data from nine children and their 14 families were collected, including general status, clinical, laboratory test, and imaging characteristics. All the children were detected positive result after their families onset. Three children had fever (22.2%) or cough (11.2%) symptoms and six (66.7%) children had no symptom. Among the 14 adult patients, the major symptoms included fever (57.1%), cough (35.7%), chest tightness/pain (21.4%), fatigue (21.4%) and sore throat (7.1%). Nearly 70% of the patients had normal (71.4%) or decreased (28.6%) white blood cell counts, and 50% (7/14) had lymphocytopenia. There were 10 adults (71.4%) showed abnormal imaging. The main manifestations were pulmonary consolidation (70%), nodular shadow (50%), and ground glass opacity (50%). Five discharged children were admitted again because their stool showed positive result in SARS-CoV-2 PCR. COVID-19 in children is mainly caused by family transmission, and their symptoms are mild and prognosis is better than adult. However, their PCR result in stool showed longer time than their families. Because of the mild or asymptomatic clinical process, it is
Fedson, D.S., Opal, S.M., Rordam, O.M.

**Hiding in plain sight: An approach to treating patients with severe covid-19 infection**
(2020) mBio, 11 (2), art. no. e00398-20

**Abstract:**
 Patients with COVID-19 infection are at risk of acute respiratory disease syndrome (ARDS) and death. The tissue receptor for COVID-19 is ACE2, and higher levels of ACE2 can protect against ARDS. Angiotensin receptor blockers and statins upregulate ACE2. Clinical trials are needed to determine whether this drug combination might be used to treat patients with severe COVID-19 infection. © 2020 Fedson et al.

Tilocca, B., Soggiu, A., Musella, V., Britti, D., Sanguinetti, M., Urbani, A., Roncada, P.

**Molecular basis of COVID-19 relationships in different species: a one health perspective**
(2020) Microbes and Infection

**Abstract:**
 Outside the Hubei province, China, the mild form of infection and the progressive recover of the COVID-19 patients suggest the intervention of “unconventional” biological mechanisms worthy of attention. Based on the high-homology between the Spike protein epitopes of taxonomically-related coronaviruses, we hypothesized that past contact with infected dogs shield humans against the circulating SARS-CoV-2. Elseways, the recurrent virus exposure over a short time-lapse might result in the Antibody Dependent Enhancement, triggering the violent immune reaction responsible for the severe clinical outcomes observed in the Hubei province. Nevertheless, further experimental studies are desired for a confidential evaluation of the postulated hypotheses. © 2020 Institut Pasteur

Yen, M.-Y., Schwartz, J., Chen, S.-Y., King, C.-C., Yang, G.-Y., Hsueh, P.-R.

**Interrupting COVID-19 transmission by implementing enhanced traffic control bundling: Implications for global prevention and control efforts**
(2020) Journal of Microbiology, Immunology and Infection

**Abstract:**
 We argue that enhanced Traffic Control Bundling (eTCB) can interrupt the community-hospital-community transmission cycle, thereby limiting COVID-19’s impact. Enhanced TCB is an expansion of the traditional TCB that proved highly effective during Taiwan's 2003 SARS outbreak. TCB's success derived from ensuring that Health Care Workers (HCWs) and patients were protected from fomite, contact and droplet transmission within hospitals. Although TCB proved successful during SARS, achieving a similar level of success with the COVID-19 outbreak requires adapting TCB to the unique manifestations of this new disease. These manifestations include asymptomatic infection, a hyper-affinity to ACE2 receptors resulting in high transmissibility, false negatives, and an incubation period of up to 22 days. Enhanced TCB incorporates the necessary adaptations. In particular, eTCB includes expanding the TCB transition zone to incorporate a new sector – the quarantine ward. This ward houses patients exhibiting atypical manifestations or awaiting definitive diagnosis. A second adaptation involves enhancing the checkpoint hand disinfection and gowning up with Personal Protective Equipment deployed in traditional TCB. Under eTCB, checkpoint hand disinfection and donning of face masks are now required of all visitors who seek to enter hospitals. These enhancements ensure that transmissions by droplets, fomites and contact are disrupted both within hospitals and between hospitals and the...
broader community. Evidencing eTCB effectiveness is Taiwan's success to date in containing and controlling the community-hospital-community transmission cycle. © 2020

Wu, D., Yang, X.O.

**TH17 responses in cytokine storm of COVID-19: An emerging target of JAK2 inhibitor Fedratinib**
(2020) Journal of Microbiology, Immunology and Infection

**Abstract:**
COVID-19 emerges as a pandemic disease with high mortality. Development of effective prevention and treatment is an urgent need. We reviewed TH17 responses in patients with SARS-CoV-2 and proposed an FDA approved JAK2 inhibitor Fedratinib for reducing mortality of patients with TH17 type immune profiles. © 2020


**Analyzing the epidemiological outbreak of COVID-19: A visual exploratory data analysis approach**
(2020) Journal of Medical Virology

**Abstract:**
There is an obvious concern globally regarding the fact about the emerging coronavirus 2019 novel coronavirus (2019-nCoV) as a worldwide public health threat. As the outbreak of COVID-19 causes by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) progresses within China and beyond, rapidly available epidemiological data are needed to guide strategies for situational awareness and intervention. The recent outbreak of pneumonia in Wuhan, China, caused by the SARS-CoV-2 emphasizes the importance of analyzing the epidemiological data of this novel virus and predicting their risks of infecting people all around the globe. In this study, we present an effort to compile and analyze epidemiological outbreak information on COVID-19 based on the several open datasets on 2019-nCoV provided by the Johns Hopkins University, World Health Organization, Chinese Center for Disease Control and Prevention, National Health Commission, and DXY. An exploratory data analysis with visualizations has been made to understand the number of different cases reported (confirmed, death, and recovered) in different provinces of China and outside of China. Overall, at the outset of an outbreak like this, it is highly important to readily provide information to begin the evaluation necessary to understand the risks and begin containment activities. © 2020 Wiley Periodicals, Inc.

Sayed, A.S.M., Malek, S.S., Abushahba, M.F.N.

**Seroprevalence of Middle East Respiratory Syndrome Corona Virus in dromedaries and their traders in upper Egypt**

**Abstract:**
Introduction: Camel trade in Egypt depends mainly on importation. Seemingly healthy imported camels are responsible for the ingress of serious diseases into Egypt. A striking example of this concerning public health globally is the Middle East respiratory coronavirus (MERS-CoV) which causes case fatalities of over 34%. Here, we determined the seroepidemiological situation of the MERS-CoV in imported camels and their traders in Upper Egypt. Methodology: Sera of sixty-three dromedaries and twenty-eight camel traders were recruited (January 2015-December 2016). The age, gender, and sampling locality of each sampled camel and human were obtained. Semi-quantitative anti-MERS-CoV IgG ELISAs which utilize the purified spike protein domain S1 antigen of MERS coronavirus (MERS-CoV S1) were used to detect specific IgG antibodies against the virus. Results: The data showed that 58.73% of imported camels and 25% of traders had antibodies specific to MERS-CoV. Interestingly, like seroreactive camels, all seropositive humans were apparently healthy without any history of developing severe respiratory disease in the 14 days
prior to sampling. Having specific antibodies among the examined camel sera was significantly different (P < 0.0001) in relation to various sampling localities, gender and age groups. In contrast, the seropositivity rate of MERS-CoV IgG in humans did not differ significantly by any of the studied factors. Conclusions: The current study provides the first serological evidence of occupational exposure of humans to MERS-CoV in Africa. Additionally, it reports that imported camels could be implicated in introducing MERS-CoV into Egypt. Accordingly, application of strict control measures to camel importation is a priority. © 2020 Sayed et al.


Vicarious traumatization in the general public, members, and non-members of medical teams aiding in COVID-19 control
(2020) Brain, Behavior, and Immunity

Abstract:
Since December 2019, more than 79,000 people have been diagnosed with infection of the Corona Virus Disease 2019 (COVID-19). A large number of medical staff was sent to Wuhan city and Hubei province to aid COVID-19 control. Psychological stress, especially vicarious traumatization caused by the COVID-19 pandemic, should not be ignored. To address this concern, the study employed a total of 214 general public and 526 nurses (i.e., 234 front-line nurses and 292 non-front-line nurses) to evaluate vicarious traumatization scores via a mobile app-based questionnaire. Front-line nurses are engaged in the process of providing care for patients with COVID-19. The results showed that the vicarious traumatization scores for front-line nurses including scores for physiological and psychological responses, were significantly lower than those of non-front-line nurses (P < 0.001). Interestingly, the vicarious traumatization scores of the general public were significantly higher than those of the front-line nurses (P < 0.001); however, no statistical difference was observed compared to the scores of non-front-line nurses (P > 0.05). Therefore, increased attention should be paid to the psychological problems of the medical staff, especially non-front-line nurses, and general public under the situation of the spread and control of COVID-19. Early strategies that aim to prevent and treat vicarious traumatization in medical staff and general public are extremely necessary. © 2020 Elsevier Inc.

Lee, N.-Y., Li, C.-W., Tsai, H.-P., Chen, P.-L., Syue, L.-S., Li, M.-C., Tsai, C.-S., Lo, C.-L., Hsueh, P.-R., Ko, W.-C.

A case of COVID-19 and pneumonia returning from Macau in Taiwan: Clinical course and anti-SARS-CoV-2 IgG dynamic
(2020) Journal of Microbiology, Immunology and Infection

Abstract:
A 46-year-old woman presented to the emergency department with 2-day fever and cough at seven days after returning from Macau. COVID-19 and pneumonia was diagnosed based on the positive real-time RT-PCR tests for oropharyngeal swab samples and the presence of anti-SARS-2019-nCoV IgG starting from the illness day 11 and post-exposure 18–21 days. © 2020

Zhou, Y., Hou, Y., Shen, J., Huang, Y., Martin, W., Cheng, F.

(2020) Cell Discovery, 6 (1), art. no. 14

Abstract:
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. © 2020, The Author(s).


Shell disorder analysis predicts greater resilience of the SARS-CoV-2 (COVID-19) outside the body and in body fluids
(2020) Microbial Pathogenesis, 144, art. no. 104177

Abstract:
The coronavirus (CoV) family consists of viruses that infects a variety of animals including humans with various levels of respiratory and fecal-oral transmission levels depending on the behavior of the viruses' natural hosts and optimal viral fitness. A model to classify and predict the levels of respective respiratory and fecal-oral transmission potentials of the various viruses was built before the outbreak of MERS-CoV using AI and empirically-based molecular tools to predict the disorder level of proteins. Using the percentages of intrinsic disorder (PID) of the nucleocapsid (N) and membrane (M) proteins of CoV, the model easily clustered the viruses into three groups with the SARS-CoV (M PID = 8%, N PID = 50%) falling into Category B, in which viruses have intermediate levels of both respiratory and fecal-oral transmission potentials. Later, MERS-CoV (M PID = 9%, N PID = 44%) was found to be in Category C, which consists of viruses with lower respiratory transmission potential but with higher fecal-oral transmission capabilities. Based on the peculiarities of disorder distribution, the SARS-CoV-2 (M PID = 6%, N PID = 48%) has to be placed in Category B. Our data show however, that the SARS-CoV-2 is very strange with one of the hardest protective outer shell, (M PID = 6%) among coronaviruses. This means that it might be expected to be highly resilient in saliva or other body fluids and outside the body. An infected body is likelier to shed greater numbers of viral particles since the latter is more resistant to antimicrobial enzymes in body fluids. These particles are also likelier to remain active longer. These factors could account for the greater contagiousness of the SARS-CoV-2 and have implications for efforts to prevent its spread. © 2020 Elsevier Ltd

Fahmi, M., Kubota, Y., Ito, M.

Nonstructural proteins NS7b and NS8 are likely to be phylogenetically associated with evolution of 2019-nCoV
(2020) Infection, Genetics and Evolution, 81, art. no. 104272

Abstract:
The seventh novel human infecting Betacoronavirus that causes pneumonia (2019 novel coronavirus, 2019-nCoV) originated in Wuhan, China. The evolutionary relationship between 2019-nCoV and the other human respiratory illness-causing coronavirus is not closely related. We sought to characterize the relationship of the translated proteins of 2019-nCoV with other species of Orthocoronavirinae. A phylogenetic tree was constructed from the genome sequences. A cluster tree was developed from the profiles retrieved from the presence and absence of homologs of ten 2019-nCoV proteins. The combined data were used to characterize the relationship of the translated proteins of 2019-nCoV to other species of Orthocoronavirinae. Our analysis reliably suggests that 2019-nCoV is most closely related to BatCoV RaTG13 and belongs to subgenus Sarbecovirus of Betacoronavirus, together with SARS coronavirus and Bat-SARS-like coronavirus. The phylogenetic profiling cluster of homolog proteins of one annotated 2019-nCoV protein against other genome sequences revealed two clades of ten 2019-nCoV proteins. Clade 1 consisted of a group of conserved proteins in Orthocoronavirinae comprising Orf1ab polyprotein, Nucleocapsid protein, Spike glycoprotein, and Membrane protein. Clade 2 comprised six proteins exclusive to Sarbecovirus and Hibecovirus. Two of six Clade 2 nonstructural proteins, NS7b and NS8, were exclusively conserved among 2019-nCoV, BetaCoV_RaTG, and BatSARS-like Cov. NS7b and NS8 have previously been shown to affect immune response signaling in the SARS-CoV experimental model. Thus, we speculated that knowledge of the functional changes in the NS7b and NS8 proteins during evolution may provide important information to explore the human infective property of 2019-nCoV. © 2020 The Authors

Li, R., Tian, J., Yang, F., Lv, L., Yu, J., Sun, G., Ma, Y., Yang, X., Ding, J.
Clinical characteristics of 225 patients with COVID-19 in a tertiary Hospital near Wuhan, China
(2020) Journal of Clinical Virology, 127, art. no. 104363

Lupia, T., Scabini, S., Mornese Pinna, S., Di Perri, G., De Rosa, F.G., Corcione, S.

Abstract:
Objectives: Following the public-health emergency of international concern (PHEIC) declared by the World Health Organization (WHO) on 30 January 2020 and the recent outbreak caused by 2019 novel coronavirus (2019-nCoV) [officially renamed severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)] in China and 29 other countries, we aimed to summarise the clinical aspects of the novelBetacoronavirus disease (COVID-19) and its possible clinical presentations together with suggested therapeutic algorithms for patients who may require antimicrobial treatment. Methods: The currently available literature was reviewed for microbiologically confirmed infections by 2019-nCoV or COVID-19 at the time of writing (13 February 2020). A literature search was performed using the PubMed database and Cochrane Library. Search terms included ‘novel coronavirus’ or ‘2019-nCoV’ or ‘COVID-19’. Results: Published cases occurred mostly in males (age range, 8–92 years). Cardiovascular, digestive and endocrine system diseases were commonly reported, except previous chronic pulmonary diseases [e.g. chronic obstructive pulmonary disease (COPD), asthma, bronchiectasis] that were surprisingly underreported. Fever was present in all of the case series available, flanked by cough, dyspnoea, myalgia and fatigue. Multiple bilateral lobular and subsegmental areas of consolidation or bilateral ground-glass opacities were the main reported radiological features of 2019-nCoV infection, at least in the early phases of the disease. Conclusion: The new 2019-nCoV epidemic is mainly associated with respiratory disease and few extrapulmonary signs. However, there is a low rate of associated pre-existing respiratory co-morbidities. © 2020

Han, Y., Jiang, M., Xia, D., He, L., Lv, X., Liao, X., Meng, J.
COVID-19 in a patient with long-term use of glucocorticoids: A study of a familial cluster
(2020) Clinical Immunology, 214, art. no. 108413

Abstract:
Clusters of patients with novel coronavirus disease 2019 (COVID-19) have been successively reported globally. Studies show clear person-to-person transmission. The average incubation period is 2–14 days, and mostly 3–7 days. However, in some patients, this period may be longer. Here, we report a familial cluster of COVID-19 where a 47-year-old woman with long-term use of glucocorticoids did not develop any symptoms within the 14-day quarantine period but was confirmed with COVID-19 by tested positive of antibody on day 40 after she left Wuhan. Almost at the same time, her father and sister were diagnosed with COVID-19. The results suggest that the long-term use of glucocorticoids might cause atypical infections, a long incubation period, and extra transmission of COVID-19. © 2020 Elsevier Inc.

Esler, M., Esler, D.
Can angiotensin receptor-blocking drugs perhaps be harmful in the COVID-19 pandemic?

Desjardins, M.R., Hohl, A., Delmelle, E.M.
Rapid surveillance of COVID-19 in the United States using a prospective space-time scan statistic: Detecting and evaluating emerging clusters
(2020) Applied Geography, 118, art. no. 102202

Abstract:
Coronavirus disease 2019 (COVID-19) was first identified in Wuhan, China in December 2019, and is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). COVID-19 is a pandemic with an estimated death rate between 1% and 5%; and an estimated R0 between 2.2 and 6.7 according to various sources. As of March 28th, 2020, there were over 649,000 confirmed cases and 30,249 total deaths, globally. In the United States, there were over 115,500 cases and 1891 deaths and this number is likely to increase rapidly. It is critical to detect clusters of COVID-19 to better allocate resources and improve decision-making as the outbreaks continue to grow. Using daily case data at the county level provided by Johns Hopkins University, we conducted a prospective spatial-temporal analysis with SaTScan. We detect statistically significant space-time clusters of COVID-19 at the county level in the U.S. between January 22nd-March 9th, 2020, and January 22nd-March 27th, 2020. The space-time prospective scan statistic detected “active” and emerging clusters that are present at the end of our study periods – notably, 18 more clusters were detected when adding the updated case data. These timely results can inform public health officials and decision makers about where to improve the allocation of resources, testing sites; also, where to implement stricter quarantines and travel bans. As more data becomes available, the statistic can be rerun to support timely surveillance of COVID-19, demonstrated here. Our research is the first geographic study that utilizes space-time statistics to monitor COVID-19 in the U.S. © 2020 The Authors

Moazzami, B., Razavi-Khorasani, N., Dooghaie Moghadam, A., Farokhi, E., Rezaei, N.
COVID-19 and telemedicine: Immediate action required for maintaining healthcare providers well-being
(2020) Journal of Clinical Virology, 126, art. no. 104345

Abstract:
The well-being of the health care workforce is the cornerstone of every well-functioning health system. As a result of the pandemic, medical healthcare providers are under an enormous amount of workload pressure along with increased total health expenditures. The overwhelming burden of
COVID-19 illness could lead to caregiver burnout. Direct-to-consumer telemedicine can enable patients to connect with their healthcare provider at a distance. This virtual platform could be used by smartphones or webcam-enabled computers and allows physicians to effectively screen patients with early signs of COVID-19 before they reach to hospital. © 2020 Elsevier B.V.

Prevalence and predictors of PTSS during COVID-19 outbreak in China hardest-hit areas: Gender differences matter
(2020) Psychiatry Research, 287, art. no. 112921
Abstract:
The outbreak of COVID-19 in China in December 2019 has been identified as a pandemic and a health emergency of global concern. Our objective was to investigate the prevalence and predictors of posttraumatic stress symptoms (PTSS) in China hardest-hit areas during COVID-19 outbreak, especially exploring the gender difference existing in PTSS. One month after the December 2019 COVID-19 outbreak in Wuhan China, we surveyed PTSS and sleep qualities among 285 residents in Wuhan and surrounding cities using the PTSD Checklist for DSM-5 (PCL-5) and 4 items from the Pittsburgh Sleep Quality Index (PSQI). Hierarchical regression analysis and non-parametric test were used to analyze the data. Results indicated that the prevalence of PTSS in China hardest-hit areas a month after the COVID-19 outbreak was 7%. Women reported significant higher PTSS in the domains of re-experiencing, negative alterations in cognition or mood, and hyper-arousal. Participants with better sleep quality or less frequency of early awakenings reported lower PTSS. Professional and effective mental health services should be designed in order to aid the psychological wellbeing of the population in affected areas, especially those living in hardest-hit areas, females and people with poor sleep quality. © 2020 Elsevier B.V.

CT imaging changes of corona virus disease 2019(COVID-19): a multi-center study in Southwest China
Abstract:
BACKGROUND: Since the first case of a coronavirus disease 2019 (COVID-19) infection pneumonia was detected in Wuhan, China, a series of confirmed cases of the COVID-19 were found in Southwest China. The aim of this study was to describe the imaging manifestations of hospitalized patients with confirmed COVID-19 infection in southwest China. METHODS: In this retrospective study, data were collected from 131 patients with confirmed coronavirus disease 2019 (COVID-19) from 3 Chinese hospitals. Their common clinical manifestations, as well as characteristics and evolvement features of chest CT images, were analyzed. RESULTS: A total of 100 (76%) patients had a history of close contact with people living in Wuhan, Hubei. The clinical manifestations of COVID-19 included cough, fever. Most of the lesions identified in chest CT images were multiple lesions of bilateral lungs, lesions were more localized in the peripheral lung, 109 (83%) patients had more than two lobes involved, 20 (15%) patients presented with patchy ground glass opacities, patchy ground glass opacities and consolidation of lesions co-existing in 61 (47%) cases. Complications such as pleural thickening, hydrothorax, pericardial effusion, and enlarged mediastinal lymph nodes were detected but only in rare cases. For the follow-up chest CT examinations (91 cases), We found 66 (73%) cases changed very quickly, with an average of 3.5 days, 25 cases (27%) presented absorbed lesions, progression was observed in 41 cases (46%). 25 (27%) cases showed no significant changes. CONCLUSION: Chest CT plays an important role in diagnosing COVID-19. The imaging pattern of multifocal peripheral ground glass or mixed consolidation is highly suspicious of COVID-19, that can quickly change over a short period of time.
Zhang, T., Wu, Q., Zhang, Z.
Probable Pangolin Origin of SARS-CoV-2 Associated with the COVID-19 Outbreak

Abstract:
An outbreak of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) began in the city of Wuhan in China and has widely spread worldwide. Currently, it is vital to explore potential intermediate hosts of SARS-CoV-2 to control COVID-19 spread. Therefore, we reinvestigated published data from pangolin lung samples from which SARS-CoV-like CoVs were detected by Liu et al. [1]. We found genomic and evolutionary evidence of the occurrence of a SARS-CoV-2-like CoV (named Pangolin-CoV) in dead Malayan pangolins. Pangolin-CoV is 91.02% and 90.55% identical to SARS-CoV-2 and BatCoV RaTG13, respectively, at the whole-genome level. Aside from RaTG13, Pangolin-CoV is the most closely related CoV to SARS-CoV-2. The S1 protein of Pangolin-CoV is much more closely related to SARS-CoV-2 than to RaTG13. Five key amino acid residues involved in the interaction with human ACE2 are completely consistent between Pangolin-CoV and SARS-CoV-2, but four amino acid mutations are present in RaTG13. Both Pangolin-CoV and RaTG13 lost the putative furin recognition sequence motif at S1/S2 cleavage site that can be observed in the SARS-CoV-2. Conclusively, this study suggests that pangolin species are a natural reservoir of SARS-CoV-2-like CoVs. © 2020 Elsevier Inc.

The emerging SARS-coronavirus 2 (SARS-CoV-2) poses tremendous threat to human health. Zhang, Wu et al. show that like bats, pangolin species are a natural reservoir of SARS-CoV-2-like CoVs. This finding might help to find the intermediate host of SARS-CoV-2 for blocking a global coronavirus pandemic. © 2020 Elsevier Inc.

Rabby, M.I.I.
Current drugs with potential for treatment of covid-19: A literature review

Abstract:
Purpose: SARS-CoV-2 first emerged in China in December 2019 and rapidly spread worldwide. No vaccine or approved drug is available to eradicate the virus, however, some drugs that are indicated for other afflictions seems to be potentially beneficial to treat the infection albeit without unequivocal evidence. The aim of this article is to review the published background on the effectiveness of these drugs against COVID-19 Methods: A thorough literature search was conducted on recently published studies which have published between January 1 to March 25, 2020. PubMed, Google Scholar and Science Direct databases were searched Results: A total 22 articles were found eligible. 8 discuss about treatment outcomes from their applied drugs during treatment of COVID-19 patients, 4 report laboratory tests, one report animal trial and other 9 articles discuss recommendations and suggestions based on the treatment process and clinical outcomes of other diseases such as malaria, ebola, severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS). The data and/or recommendations are categorized in 4 classes: (a) anti-viral and anti-inflammatory drugs, (b) anti-malaria drugs, (c) traditional Chinese drugs and (d) other treatments/drugs. Conclusion: All examined treatments, although potentiality effective against COVID-19, need either appropriate drug development or clinical trial to be suitable for clinical use. © 2020, Canadian Society for Pharmaceutical Sciences. All rights reserved.

Zhang, C., Zheng, W., Huang, X., Bell, E.W., Zhou, X., Zhang, Y.
Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1

Abstract:
As the infection of 2019-nCoV coronavirus is quickly developing into a global pneumonia epidemic, the careful analysis of its transmission and cellular mechanisms is sorely needed. In this Communication, we first analyzed two recent studies that concluded that snakes are the intermediate hosts of 2019-nCoV and that the 2019-nCoV spike protein insertions share a unique similarity to HIV-1. However, the reimplementation of the analyses, built on larger scale data sets using state-of-the-art bioinformatics methods and databases, presents clear evidence that rebuts these conclusions. Next, using metagenomic samples from Manis javanica, we assembled a draft genome of the 2019-nCoV-like coronavirus, which shows 73% coverage and 91% sequence identity to the 2019-nCoV genome. In particular, the alignments of the spike surface glycoprotein receptor binding domain revealed four times more variations in the bat coronavirus RaTG13 than in the Manis coronavirus compared with 2019-nCoV, suggesting the pangolin as a missing link in the transmission of 2019-nCoV from bats to human.

Sjödin, H., Wilder-Smith, A., Osman, S., Farooq, Z., Rocklöv, J.
Only strict quarantine measures can curb the coronavirus disease (COVID-19) outbreak in Italy, 2020
(2020) Eurosurveillance, 25 (13)

Abstract:
Several Italian towns are under lockdown to contain the COVID-19 outbreak. The level of transmission reduction required for physical distancing interventions to mitigate the epidemic is a crucial question. We show that very high adherence to community quarantine (total stay-home policy) and a small household size is necessary for curbing the outbreak in a locked-down town. The larger the household size and amount of time in the public, the longer the lockdown period needed. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Verelst, F., Kuylen, E., Beutels, P.
Indications for healthcare surge capacity in European countries facing an exponential increase in coronavirus disease (COVID-19) cases, March 2020
(2020) Eurosurveillance, 25 (13)

Abstract:
European healthcare systems face extreme pressure from coronavirus disease (COVID-19). We relate country-specific accumulated COVID-19 deaths (intensity approach) and active COVID-19 cases (magnitude approach) to measures of healthcare system capacity: hospital beds, healthcare workers and healthcare expenditure. Modelled by the intensity approach with a composite measure for healthcare capacity, the countries experiencing the highest pressure on 25 March 2020 - relative to Italy on 11 March - were Italy, Spain, the Netherlands and France (www.covid-hcpressure.org). © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Baker, E.N.
Visualizing an unseen enemy; mobilizing structural biology to counter COVID-19

Baker, E.N.
Visualizing an unseen enemy; mobilizing structural biology to counter COVID-19
Kirigia, J.M., Muthuri, R.N.D.K.
The fiscal value of human lives lost from coronavirus disease (COVID-19) in China
(2020) BMC Research Notes, 13 (1), art. no. 198

Abstract:
Objective: According to the WHO coronavirus disease (COVID-19) situation report 35, as of 24th February 2020, there was a total of 77,262 confirmed COVID-19 cases in China. That included 2595 deaths. The specific objective of this study was to estimate the fiscal value of human lives lost due to COVID-19 in China as of 24th February 2020. Results: The deaths from COVID-19 had a discounted (at 3%) total fiscal value of Int$ 924,346,795 in China. Out of which, 63.2% was borne by people aged 25-49 years, 27.8% by people aged 50-64 years, and 9.0% by people aged 65 years and above. The average fiscal value per death was Int$ 356,203. Re-estimation of the economic model alternately with 5% and 10 discount rates led to a reduction in the expected total fiscal value by 21.3% and 50.4%, respectively. Furthermore, the re-estimation of the economic model using the world's highest average life expectancy of 87.1 years (which is that of Japanese females), instead of the national life expectancy of 76.4 years, increased the total fiscal value by Int$ 229,456,430 (24.8%). © 2020 The Author(s).

Tolksdorf, K., Buda, S., Schuler, E., Wieler, L.H., Haas, W.
Influenza-associated pneumonia as reference to assess seriousness of coronavirus disease (COVID-19)
(2020) Eurosurveillance, 25 (11), art. no. 2000258

Abstract:
Information on severity of coronavirus disease (COVID-19) (transmissibility, disease seriousness, impact) is crucial for preparation of healthcare sectors. We present a simple approach to assess disease seriousness, creating a reference cohort of pneumonia patients from sentinel hospitals. First comparisons exposed a higher rate of COVID-19 patients requiring ventilation. There were more case fatalities among COVID-19 patients without comorbidities than in the reference cohort. Hospitals should prepare for high utilisation of ventilation and intensive care resources. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Coronavirus disease (COVID-19) in a paucisymptomatic patient: Epidemiological and clinical challenge in settings with limited community transmission, Italy, February 2020
(2020) Eurosurveillance, 25 (11), art. no. 2000230

Abstract:
Data concerning the transmission of the novel severe acute respiratory syndrome coronavirus (SARS-CoV-2) in paucisymptomatic patients are lacking. We report an Italian paucisymptomatic case of coronavirus disease 2019 with multiple biological samples positive for SARS-CoV-2. This case was detected using the World Health Organization protocol on cases and contact investigation. Current discharge criteria and the impact of extra-pulmonary SARS-CoV-2 samples are discussed. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.
Yuen, K.-S., Ye, Z.-W., Fung, S.-Y., Chan, C.-P., Jin, D.-Y.

**SARS-CoV-2 and COVID-19: The most important research questions**
(2020) Cell and Bioscience, 10 (1), art. no. 40

**Abstract:**
Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an ongoing global health emergency. Here we highlight nine most important research questions concerning virus transmission, asymptomatic and presymptomatic virus shedding, diagnosis, treatment, vaccine development, origin of virus and viral pathogenesis. © 2020 The Author(s).

Rong, X., Yang, L., Chu, H., Fan, M.

**Effect of delay in diagnosis on transmission of COVID-19**

**Abstract:**
The outbreak of COVID-19 caused by SARS-CoV-2 in Wuhan and other cities of China is a growing global concern. Delay in diagnosis and limited hospital resources lead to a rapid spread of COVID-19. In this study, we investigate the effect of delay in diagnosis on the disease transmission with a new formulated dynamic model. Sensitivity analyses and numerical simulations reveal that, improving the proportion of timely diagnosis and shortening the waiting time for diagnosis can not eliminate COVID-19 but can effectively decrease the basic reproduction number, significantly reduce the transmission risk, and effectively prevent the endemic of COVID-19, e.g., shorten the peak time and reduce the peak value of new confirmed cases and new infection, decrease the cumulative number of confirmed cases and total infection. More rigorous prevention measures and better treatment of patients are needed to control its further spread, e.g., increasing available hospital beds, shortening the period from symptom onset to isolation of patients, quarantining and isolating the suspected cases as well as all confirmed patients. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)

Zhou, W., Wang, A., Xia, F., Xiao, Y., Tang, S.

**Effects of media reporting on mitigating spread of COVID-19 in the early phase of the outbreak**

**Abstract:**
The 2019 novel coronavirus disease (COVID-19) is running rampant in China and is swiftly spreading to other countries in the world, which causes a great concern on the global public health. The absence of specific therapeutic treatment or effective vaccine against COVID-19 call for other avenues of the prevention and control measures. Media reporting is thought to be effective to curb the spreading of an emergency disease in the early stage. Cross-correlation analysis based on our collected data demonstrated a strong correlation between media data and the infection case data. Thus we proposed a deterministic dynamical model to examine the interaction of the disease progression and the media reports and to investigate the effectiveness of media reporting on mitigating the spread of COVID-19. The basic reproduction number was estimated as 5.3167 through parameterization of the model with the number of cumulative confirmed cases, the number of cumulative deaths and the daily number of media items. Sensitivity analysis suggested that, during the early phase of the COVID-19 outbreak, enhancing the response rate of the media reporting to the severity of COVID-19, and enhancing the response rate of the public awareness to the media reports, both can bring forward the peak time and reduce the peak size of the infection significantly. These findings suggested that besides improving the medical levels, media coverage can be considered as an effective way to mitigate the disease spreading during the initial stage of an outbreak. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed
Yin, F., Lv, J., Zhang, X., Xia, X., Wu, J.


**Abstract:**
The outbreak of a novel coronavirus (COVID-19) generated an outbreak of public opinions in the Chinese Sina-microblog. To help in designing effective communication strategies during a major public health emergency, we propose a multiple-information susceptible-discussing-immune (M-SDI) model in order to understand the patterns of key information propagation on social networks. We develop the M-SDI model, based on the public discussion quantity and take into account of the behavior that users may re-enter another related topic or Weibo after discussing one. Data fitting using the real data of COVID-19 public opinion obtained from Chinese Sina-microblog can parameterize the model to make accurate prediction of the public opinion trend until the next major news item occurs. The reproduction ratio has fallen from 1.7769 and maintained around 0.97, which reflects the peak of public opinion has passed but it will continue for a period of time. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)

Bar-On, Y.M., Flamholz, A., Phillips, R., Milo, R.

*Sars-cov-2 (Covid-19) by the numbers* (2020) eLife, 9

**Abstract:**
The current SARS-CoV-2 pandemic is a harsh reminder of the fact that, whether in a single human host or a wave of infection across continents, viral dynamics is often a story about the numbers. In this snapshot, our aim is to provide a one-stop, curated graphical source for the key numbers that help us understand the virus driving our current global crisis. The discussion is framed around two broad themes: 1) the biology of the virus itself and 2) the characteristics of the infection of a single human host. Our one-page summary provides the key numbers pertaining to SARS-CoV-2, based mostly on peer-reviewed literature. The numbers reported in summary format are substantiated by the annotated references below. Readers are urged to remember that much uncertainty remains and knowledge of this pandemic and the virus driving it is rapidly evolving. In the paragraphs below we provide “back of the envelope” calculations that exemplify the insights that can be gained from knowing some key numbers and using quantitative logic. These calculations serve to improve our intuition through sanity checks, but do not replace detailed epidemiological analysis. © 2020, eLife Sciences Publications Ltd. All rights reserved.

MacKenzie, J.S., Smith, D.W.


**Abstract:**
At the end of December, 2019, a new disease of unknown aetiology appeared in Wuhan, China. It was quickly identified as a novel betacoronavirus, and related to SARS-CoV and a number of other bat-borne SARS-like coronaviruses. The virus rapidly spread to all provinces in China, as well as a number of countries overseas, and was declared a Public Health Emergency of International Concern by the Director General of the World Health Organization on 30 January 2020. This paper describes the evolution of the outbreak, and the known properties of the novel virus, SARS-CoV-2 and the clinical disease it causes, COVID-19, and comments on some of the important gaps in our knowledge of the virus and the disease it causes. The virus is the third
zoonotic coronavirus, after SARS-CoV and MERS-CoV, but appears to be the only one with pandemic potential. © 2020 CSIRO. All rights reserved.


**Cancer care delivery challenges amidst coronavirus disease -19 (covid-19) outbreak: Specific precautions for cancer patients and cancer care providers to prevent spread**


**Abstract:**
Coronavirus outbreak has affected thousands of people in at least 186 countries which has affected the cancer care delivery system apart from affecting the overall health system. Cancer patients are more susceptible to coronavirus infection than individuals without cancer as they are in an immunosuppressive state because of the malignancy and anticancer treatment. Oncologists should be more attentive to detect coronavirus infection early, as any type of advanced cancer is at much higher risk for unfavorable outcomes. Oncology communities must ensure that cancer patients should spend more time at home and less time out in the community. Oncologists and other health care professionals involved in cancer care have a critical opportunity to communicate to their patients to pass on right information regarding practice modifications in view of COVID-19 outbreaks. Countries must isolate, test, treat and trace to control the coronavirus pandemic. There is a paucity of information on novel coronavirus infection and its impact on cancer patients and cancer care providers. To date, there is no scientific guideline regarding management of cancer patients in a background of coronavirus outbreak. © 2020, Asian Pacific Organization for Cancer Prevention.

Zhao, S., Chen, H.

**Modeling the epidemic dynamics and control of COVID-19 outbreak in China**


**Abstract:**
Background: The coronavirus disease 2019 (COVID-19) is rapidly spreading in China and more than 30 countries over last two months. COVID-19 has multiple characteristics distinct from other infectious diseases, including high infectivity during incubation, time delay between real dynamics and daily observed number of confirmed cases, and the intervention effects of implemented quarantine and control measures. Methods: We develop a Susceptible, Un-quarantined infected, Quarantined infected, Confirmed infected (SUQC) model to characterize the dynamics of COVID-19 and explicitly parameterize the intervention effects of control measures, which is more suitable for analysis than other existing epidemic models. Results: The SUQC model is applied to the daily released data of the confirmed infections to analyze the outbreak of COVID-19 in Wuhan, Hubei (excluding Wuhan), China (excluding Hubei) and four first-tier cities of China. We found that, before January 30, 2020, all these regions except Beijing had a reproductive number $R > 1$, and after January 30, all regions had a reproductive number $R < 1$, indicating that the quarantine and control measures are effective in preventing the spread of COVID-19. The confirmation rate of Wuhan estimated by our model is 0.0643, substantially lower than that of Hubei excluding Wuhan (0.1914), and that of China excluding Hubei (0.2189), but it jumps to 0.3229 after February 12 when clinical evidence was adopted in new diagnosis guidelines. The number of unquarantined infected cases in Wuhan on February 12, 2020 is estimated to be 3,509 and declines to 334 on February 21, 2020. After fitting the model with data as of February 21, 2020, we predict that the end time of COVID-19 in Wuhan and Hubei is around late March, around mid March for China excluding Hubei, and before early March 2020 for the four tier-one cities. A total of 80,511 individuals are estimated to be infected in China, among which 49,510 are from Wuhan, 17,679 from Hubei (excluding Wuhan), and the rest 13,322 from other regions of China (excluding Hubei). Note that the estimates are from a deterministic ODE model and should be interpreted with some
uncertainty. Conclusions: We suggest that rigorous quarantine and control measures should be kept before early March in Beijing, Shanghai, Guangzhou and Shenzhen, and before late March in Hubei. The model can also be useful to predict the trend of epidemic and provide quantitative guide for other countries at high risk of outbreak, such as South Korea, Japan, Italy and Iran. [Figure not available: see fulltext.]. © 2020, Higher Education Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Eurosurveillance Editorial Team

Updated rapid risk assessment from ECDC on the outbreak of COVID-19: increased transmission globally
(2020) Euro surveillance : bulletin Europeen sur les maladies transmissibles = European communicable disease bulletin, 25 (9)

Kumar, S., Maurya, V.K., Prasad, A.K., Bhatt, M.L.B., Saxena, S.K.
Structural, glycosylation and antigenic variation between 2019 novel coronavirus (2019-nCoV) and SARS coronavirus (SARS-CoV)

Abstract:
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. © 2020, Indian Virological Society.

Liu, Z., Magal, P., Seydi, O., Webb, G.
Understanding unreported cases in the COVID-19 epidemic outbreak in Wuhan, China, and the importance of major public health interventions
(2020) Biology, 9 (3), art. no. 50

Abstract:
We develop a mathematical model to provide epidemic predictions for the COVID-19 epidemic in Wuhan, China. We use reported case data up to 31 January 2020 from the Chinese Center for
Disease Control and Prevention and the Wuhan Municipal Health Commission to parameterize the model. From the parameterized model, we identify the number of unreported cases. We then use the model to project the epidemic forward with varying levels of public health interventions. The model predictions emphasize the importance of major public health interventions in controlling COVID-19 epidemics. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Gostic, K.M., Gomez, A.C.R., Mummah, R.O., Kucharski, A.J., Lloyd-Smith, J.O.

Estimated effectiveness of symptom and risk screening to prevent the spread of COVID-19
(2020) eLife, 9, art. no. e55570

Abstract:
Traveller screening is being used to limit further spread of COVID-19 following its recent emergence, and symptom screening has become a ubiquitous tool in the global response. Previously, we developed a mathematical model to understand factors governing the effectiveness of traveller screening to prevent spread of emerging pathogens (Gostic et al., 2015). Here, we estimate the impact of different screening programs given current knowledge of key COVID-19 life history and epidemiological parameters. Even under best-case assumptions, we estimate that screening will miss more than half of infected people. Breaking down the factors leading to screening successes and failures, we find that most cases missed by screening are fundamentally undetectable, because they have not yet developed symptoms and are unaware they were exposed. Our work underscores the need for measures to limit transmission by travellers who become ill after being missed by a screening program. These findings can support evidence-based policy to combat the spread of COVID-19, and prospective planning to mitigate future emerging pathogens. © 2020, eLife Sciences Publications Ltd. All rights reserved.

Eurosurveillance Editorial Team

Latest assessment on COVID-19 from the European Centre for Disease Prevention and Control (ECDC)

Eurosurveillance Editorial Team

Latest updates on COVID-19 from the European Centre for Disease Prevention and Control

Moreira, B.L., Brotto, M.P.D., Marchiori, E.

Chest radiography and computed tomography findings from a Brazilian patient with COVID-19 pneumonia

Helmich, R.C., Bloem, B.R.

The Impact of the COVID-19 Pandemic on Parkinson's Disease: Hidden Sorrows and Emerging Opportunities

Salomé, B., Magen, A.

Dysregulation of lung myeloid cells in COVID-19
(2020) Nature Reviews Immunology
Corona virus: A novel outbreak


Abstract:
In December 2019, a new pneumonia case emerged in the Wuhan, Hubei province of China which had an association with the novel Corona Virus (2019-nCoV). Most of the diagnosed cases had exposure to the Huanan seafood market. The present case is the successor of three earlier similar cases of Coronavirus known as SARS-Corona (Severe Acute Respiratory Syndrome) Virus and MERS-Corona Virus (Middle Eastern Respiratory Syndrome). The origin of the epidemic is still unknown and a lot of other uncertainties hinders the development of vaccines for the virus. As studies suggest that this virus is an evolution of SARS virus concerns are growing around the world as death toll has already surpassed that of SARS virus. This paper explores about the coronavirus, its relation to the similar SARS and MERS virus, its outreach and global impact according to the current scenario. Published by Oriental Scientific Publishing Company © 2020

Fighting COVID-19 exhausts T cells

(2020) Nature Reviews Immunology

Zhu, Y., Chen, Y.Q.
On a Statistical Transmission Model in Analysis of the Early Phase of COVID-19 Outbreak

(2020) Statistics in Biosciences

Abstract:
Since December 2019, a disease caused by a novel strain of coronavirus (COVID-19) had infected many people and the cumulative confirmed cases have reached almost 180,000 as of 17, March 2020. The COVID-19 outbreak was believed to have emerged from a seafood market in Wuhan, a metropolis city of more than 11 million population in Hubei province, China. We introduced a statistical disease transmission model using case symptom onset data to estimate the transmissibility of the early-phase outbreak in China, and provided sensitivity analyses with various assumptions of disease natural history of the COVID-19. We fitted the transmission model to several publicly available sources of the outbreak data until 11, February 2020, and estimated lock down intervention efficacy of Wuhan city. The estimated R was between 2.7 and 4.2 from plausible distribution assumptions of the incubation period and relative infectivity over the infectious period. 95% confidence interval of R were also reported. Potential issues such as data quality concerns and comparison of different modelling approaches were discussed. © 2020, International Chinese Statistical Association.

Li, Y., Yao, L., Li, J., Chen, L., Song, Y., Cai, Z., Yang, C.
Stability issues of RT-PCR testing of SARS-CoV-2 for hospitalized patients clinically diagnosed with COVID-19

(2020) Journal of Medical Virology

Abstract:
In this study, we collected a total of 610 hospitalized patients from Wuhan between February 2, 2020, and February 17, 2020. We reported a potentially high false negative rate of real-time reverse-transcriptase polymerase chain reaction (RT-PCR) testing for SARS-CoV-2 in the 610 hospitalized patients clinically diagnosed with COVID-19 during the 2019 outbreak. We also found that the RT-PCR results from several tests at different points were variable from the same patients during the course of diagnosis and treatment of these patients. Our results indicate that in addition to the emphasis on RT-PCR testing, clinical indicators such as computed tomography images should also be used not only for diagnosis and treatment but also for isolation, recovery/discharge, and
transferring for hospitalized patients clinically diagnosed with COVID-19 during the current epidemic. These results suggested the urgent needs for the standard of procedures of sampling from different anatomic sites, sample transportation, optimization of RT-PCR, serology diagnosis/screening for SARS-CoV-2 infection, and distinct diagnosis from other respiratory diseases such as flu mening infections as well. © 2020 Wiley Periodicals, Inc.

Szperka, C.L., Ailani, J., Barmherzig, R., Klein, B.C., Minen, M.T., Halker Singh, R.B., Shapiro, R.E.

Migraine Care in the Era of COVID-19: Clinical Pearls and Plea to Insurers
(2020) Headache

Abstract:
Objective: To outline strategies for the treatment of migraine which do not require in-person visits to clinic or the emergency department, and to describe ways that health insurance companies can remove barriers to quality care for migraine. Background: COVID-19 is a global pandemic causing widespread infections and death. To control the spread of infection we are called to observe “social distancing” and we have been asked to postpone any procedures which are not essential. Since procedural therapies are a mainstay of headache care, the inability to do procedures could negatively affect our patients with migraine. In this manuscript we review alternative therapies, with particular attention to those which may be contra-indicated in the setting of COVID-19 infection. Design/Results: The manuscript reviews the use of telemedicine visits and acute, bridge, and preventive therapies for migraine. We focus on evidence-based treatment where possible, but also describe “real world” strategies which may be tried. In each section we call out areas where changes to rules from commercial health insurance companies would facilitate better migraine care. Conclusions: Our common goal as health care providers is to maximize the health and safety of our patients. Successful management of migraine with avoidance of in-person clinic and emergency department visits further benefits the current urgent societal goal of maintaining social distance to contain the COVID-19 pandemic. © 2020 American Headache Society


Diabetes is a risk factor for the progression and prognosis of COVID-19
(2020) Diabetes/Metabolism Research and Reviews

Abstract:
Background: To figure out whether diabetes is a risk factor influencing the progression and prognosis of 2019 novel coronavirus disease (COVID-19). Methods: A total of 174 consecutive patients confirmed with COVID-19 were studied. Demographic data, medical history, symptoms and signs, laboratory findings, chest computed tomography (CT) as well the treatment measures were collected and analysed. Results: We found that COVID-19 patients without other comorbidities but with diabetes (n = 24) were at higher risk of severe pneumonia, release of tissue injury-related enzymes, excessive uncontrolled inflammation responses and hypercoagulable state associated with dysregulation of glucose metabolism. Furthermore, serum levels of inflammation-related biomarkers such as IL-6, C-reactive protein, serum ferritin and coagulation index, D-dimer, were significantly higher (P <.01) in diabetic patients compared with those without, suggesting that patients with diabetes are more susceptible to an inflammatory storm eventually leading to rapid deterioration of COVID-19. Conclusions: Our data support the notion that diabetes should be considered as a risk factor for a rapid progression and bad prognosis of COVID-19. More intensive attention should be paid to patients with diabetes, in case of rapid deterioration. © 2020 The Authors. Diabetes/Metabolism Research and Reviews published by John Wiley & Sons Ltd.

Dong, S., Sun, J., Mao, Z., Wang, L., Lu, Y.-L., Li, J.
A guideline for homology modeling of the proteins from newly discovered betacoronavirus, 2019 novel coronavirus (2019-nCoV)
(2020) Journal of Medical Virology

Abstract:
During an outbreak of respiratory diseases including atypical pneumonia in Wuhan, a previously unknown β-coronavirus was detected in patients. The newly discovered coronavirus is similar to some β-coronaviruses found in bats but different from previously known SARS-CoV and MERS-CoV. High sequence identities and similarities between 2019-nCoV and SARS-CoV were found. In this study, we searched the homologous templates of all nonstructural and structural proteins of 2019-nCoV. Among the nonstructural proteins, the leader protein (nsp1), the papain-like protease (nsp3), the nsp4, the 3C-like protease (nsp5), the nsp7, the nsp8, the nsp9, the nsp10, the RNA-directed RNA polymerase (nsp12), the helicase (nsp13), the guanine-N7 methyltransferase (nsp14), the uridylate-specific endoribonuclease (nsp15), the 2’-O-methyltransferase (nsp16), and the ORF7a protein could be built on the basis of homology templates. Among the structural proteins, the spike protein (S-protein), the envelope protein (E-protein), and the nucleocapsid protein (N-protein) can be constructed based on the crystal structures of the proteins from SARS-CoV. It is known that PL-Pro, 3CL-Pro, and RdRp are important targets for design antiviral drugs against 2019-nCoV. And S protein is a critical target candidate for inhibitor screening or vaccine design against 2019-nCoV because coronavirus replication is initiated by the binding of S protein to cell surface receptors. It is believed that these proteins should be useful for further structure-based virtual screening and related computer-aided drug development and vaccine design. © 2020 Wiley Periodicals, Inc.

Vaninov, N.

In the eye of the COVID-19 cytokine storm
(2020) Nature Reviews Immunology


Inhibition of SARS-CoV-2 (previously 2019-nCoV) infection by a highly potent pan-coronavirus fusion inhibitor targeting its spike protein that harbors a high capacity to mediate membrane fusion
(2020) Cell Research

Abstract:
The recent outbreak of coronavirus disease (COVID-19) caused by SARS-CoV-2 infection in Wuhan, China has posed a serious threat to global public health. To develop specific anti-coronavirus therapeutics and prophylactics, the molecular mechanism that underlies viral infection must first be defined. Therefore, we herein established a SARS-CoV-2 spike (S) protein-mediated cell–cell fusion assay and found that SARS-CoV-2 showed a superior plasma membrane fusion capacity compared to that of SARS-CoV. We solved the X-ray crystal structure of six-helical bundle (6-HB) core of the HR1 and HR2 domains in the SARS-CoV-2 S protein S2 subunit, revealing that several mutated amino acid residues in the HR1 domain may be associated with enhanced interactions with the HR2 domain. We previously developed a pan-coronavirus fusion inhibitor, EK1, which targeted the HR1 domain and could inhibit infection by divergent human coronaviruses tested, including SARS-CoV and MERS-CoV. Here we generated a series of lipopeptides derived from EK1 and found that EK1C4 was the most potent fusion inhibitor against SARS-CoV-2 S protein-mediated membrane fusion and pseudovirus infection with IC50s of 1.3 and 15.8 nM, about 241- and 149-fold more potent than the original EK1 peptide, respectively. EK1C4 was also highly effective against membrane fusion and infection of other human coronavirus pseudoviruses tested, including SARS-CoV and MERS-CoV, as well as SARSr-CoVs, and potently inhibited the replication of 5 live human coronaviruses examined, including SARS-
Intranasal application of EK1C4 before or after challenge with HCoV-OC43 protected mice from infection, suggesting that EK1C4 could be used for prevention and treatment of infection by the currently circulating SARS-CoV-2 and other emerging SARSr-CoVs. © 2020, The Author(s).

Amariles, P., Granados, J., Ceballos, M., Montoya, C.J.


Abstract:
The infection by the new coronavirus (SARS-CoV-2) has taken the dimension of a pandemic, affecting more than 160 countries in a few weeks. In Colombia, despite the implementation of the rules established by the national government, exists an elevate concern both for mortality and for the limited capacity of the health system to respond effectively to the needs of patients infected. For Colombia, assuming a case fatality rate among people infected with SARS-CoV-2 of 0.6% (average data from the information reported for Latin American countries for March 18) (Table 1), the number of deaths, in one or two weeks, could be 16 and 243, respectively. These estimates differ markedly from those documented in countries such as Spain and Italy, in which COVID-19 case fatality rates exceed 8% (case of Italy) and from the percentage of patients who have required intensive care, which has ranged from 9% to 11% of patients in Mediterranean European countries. These differences could be explained due to: a) the percentage of the population at risk (individuals older than 60 years); b) a higher epidemiological exposure to viral respiratory infections associated with more frequent exposure to them, due to geographic and climatic conditions; c) less spread of the virus by location in the tropical zone; and d) earlier preventive measures to contain the spread of SARS-CoV-2 infection. Therefore, it is possible to establish that the situation in this country will be different from in European Mediterranean and that Colombia could have different endpoints from Spain and Italy. © 2020


COVID-19 and people followed for breast cancer: French guidelines for clinical practice of Nice-St Paul de Vence, in collaboration with the Collège Nationale des Gynécologues et Obstétriciens Français (CNGOF), the Société d'Imagerie de la FEMme (SIFEM), the Société Française de Chirurgie Oncologique (SFCO), the Société Française de Sénologie et Pathologie Mammaire (SFSPM) and the French Breast Cancer Intergroup-UNICANCER (UCBG) [COVID-19 et personnes suivies pour un cancer du sein: recommandations françaises pour la pratique clinique de Nice-St Paul de Vence, en collaboration avec le Collège Nationale des Gynécologues et Obstétriciens Français (CNGOF), la Société d'Imagerie de la FEMme (SIFEM), la Société Française de Chirurgie Oncologique (SFCO), la Société Française de Sénologie et Pathologie Mammaire (SFSPM) et le French Breast Cancer Intergroup-UNICANCER (UCBG)] (2020) Bulletin du Cancer

Krishnakumar, B., Rana, S.

COVID 19 in INDIA: Strategies to combat from combination threat of life and livelihood
Abstract:
INDIA- As for reported in 360 COVID-19 cases (till March 22, 2020), seven people were died, and 23 people were treated successfully. This virus can easily affect who having respiratory problem and especially who all have been aged older than sixty. Most of the affected peoples had reached India from different part of the world, as like of carrier. Owing to this, India made several precautionary measures to mitigate/neglect the disease in beginning stage, however, the denser population of country will not be simple to control the same for long time (community spread), if government will not incorporate the visionary strategies. Since attacked several nations have been worried mostly for their people life (health), despite that developing country like India with huge population should consider about the livelihood (for Below Poverty Line (BPL) people), equally with the life. This article will give insights to make effective strategy to culminate the world threat COVID-19 in India. © 2020

Petropoulos, F., Makridakis, S.
Forecasting the novel coronavirus COVID-19
(2020) PLoS ONE, 15 (3), art. no. e0231236

Abstract:
What will be the global impact of the novel coronavirus (COVID-19)? Answering this question requires accurate forecasting the spread of confirmed cases as well as analysis of the number of deaths and recoveries. Forecasting, however, requires ample historical data. At the same time, no prediction is certain as the future rarely repeats itself in the same way as the past. Moreover, forecasts are influenced by the reliability of the data, vested interests, and what variables are being predicted. Also, psychological factors play a significant role in how people perceive and react to the danger from the disease and the fear that it may affect them personally. This paper introduces an objective approach to predicting the continuation of the COVID-19 using a simple, but powerful method to do so. Assuming that the data used is reliable and that the future will continue to follow the past pattern of the disease, our forecasts suggest a continuing increase in the confirmed COVID-19 cases with sizable associated uncertainty. The risks are far from symmetric as underestimating its spread like a pandemic and not doing enough to contain it is much more severe than overspending and being over careful when it will not be needed. This paper describes the timeline of a live forecasting exercise with massive potential implications for planning and decision making and provides objective forecasts for the confirmed cases of COVID-19. © 2020 Petropoulos, Makridakis. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Anastassopoulou, C., Russo, L., Tsakris, A., Siettos, C.
Data-based analysis, modelling and forecasting of the COVID-19 outbreak
(2020) PLoS ONE, 15 (3), art. no. e0230405

Abstract:
Since the first suspected case of coronavirus disease-2019 (COVID-19) on December 1st, 2019, in Wuhan, Hubei Province, China, a total of 40,235 confirmed cases and 909 deaths have been reported in China up to February 10, 2020, evoking fear locally and internationally. Here, based on the publicly available epidemiological data for Hubei, China from January 11 to February 10, 2020, we provide estimates of the main epidemiological parameters. In particular, we provide an estimation of the case fatality and case recovery ratios, along with their 90% confidence intervals as the outbreak evolves. On the basis of a Susceptible-Infectious-Recovered-Dead (SIRD) model, we provide estimations of the basic reproduction number (R0), and the per day infection mortality and recovery rates. By calibrating the parameters of the SIRD model to the reported data, we also attempt to forecast the evolution of the outbreak at the epicenter three weeks ahead, i.e. until February 29. As the number of infected individuals, especially of those with asymptomatic or mild
courses, is suspected to be much higher than the official numbers, which can be considered only as a subset of the actual numbers of infected and recovered cases in the total population, we have repeated the calculations under a second scenario that considers twenty times the number of confirmed infected cases and forty times the number of recovered, leaving the number of deaths unchanged. Based on the reported data, the expected value of R0 as computed considering the period from the 11th of January until the 18th of January, using the official counts of confirmed cases was found to be ~4.6, while the one computed under the second scenario was found to be ~3.2. Thus, based on the SIRD simulations, the estimated average value of R0 was found to be ~2.6 based on confirmed cases and ~2 based on the second scenario. Our forecasting flashes a note of caution for the presently unfolding outbreak in China. Based on the official counts for confirmed cases, the simulations suggest that the cumulative number of infected could reach 180,000 (with a lower bound of 45,000) by February 29. Regarding the number of deaths, simulations forecast that on the basis of the up to the 10th of February reported data, the death toll might exceed 2,700 (as a lower bound) by February 29. Our analysis further reveals a significant decline of the case fatality ratio from January 26 to which various factors may have contributed, such as the severe control measures taken in Hubei, China (e.g. quarantine and hospitalization of infected individuals), but mainly because of the fact that the actual cumulative numbers of infected and recovered cases in the population most likely are much higher than the reported ones. Thus, in a scenario where we have taken twenty times the confirmed number of infected and forty times the confirmed number of recovered cases, the case fatality ratio is around ~0.15% in the total population. Importantly, based on this scenario, simulations suggest a slow down of the outbreak in Hubei at the end of February. Copyright: © 2020 Anastassopoulou et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Functional exhaustion of antiviral lymphocytes in COVID-19 patients 
(2020) Cellular and Molecular Immunology

Contini, C., Nuzzo, M.D., Barp, N., Bonazza, A., de Giorgio, R., Tognon, M., Rubino, S. 
The novel zoonotic COVID-19 pandemic: An expected global health concern 

Abstract:
18 years ago, in 2002, the world was astonished by the appearance of Severe Acute Respiratory Syndrome (SARS), supported by a zoonotic coronavirus, called SARS-CoV, from the Guangdong Province of southern China. After about 10 years, in 2012, another similar coronavirus triggered the Middle East Respiratory Syndrome (MERS-CoV) in Saudi Arabia. Both caused severe pneumonia killing 774 and 858 people with 8700 cases of confirmed infection for the former, and 2494 for the latter, causing significant economic losses. 8 years later, despite the MERS outbreak remaining in certain parts of the world, at the end of 2019, a new zoonotic coronavirus (SARS-CoV-2) and responsible of coronavirus Disease (COVID-19), arose from Wuhan, Hubei Province, China. It spread rapidly and to date has killed 3,242 persons with more than 81,000 cases of infection in China and causing over 126,000 global cases and 5,414 deaths in 166 other countries around the world, especially Italy. SARS-CoV-2 would seem to have come from a bat, but the intermediate reservoir continues to be unknown. Nonetheless, as for SARS-CoV and MERS CoV, the Spillover effect linked to animal-human promiscuity, human activities including deforestation, illegal bush-trafficking and bushmeat, cannot be excluded. Recently, however, evidence of inter-human only transmission of SARS-CoV-2 has been accumulated and thus, the outbreak seems to be spreading by human-to-human transmission throughout a large part of the world. Herein we will provide with an update on the main features of COVID-19 and suggest possible solutions how to halt the expansion of this novel pandemic. Copyright © 2020 Contini et al.
Huang, R., Liu, M., Ding, Y.

**Spatial-temporal distribution of COVID-19 in China and its prediction: A data-driven modeling analysis**

**Abstract:**
Currently, the outbreak of COVID-19 is rapidly spreading especially in Wuhan city, and threatens 14 million people in central China. In the present study we applied the Moran index, a strong statistical tool, to the spatial panel to show that COVID-19 infection is spatially dependent and mainly spread from Hubei Province in Central China to neighbouring areas. Logistic model was employed according to the trend of available data, which shows the difference between Hubei Province and outside of it. We also calculated the reproduction number R0 for the range of [2.23, 2.51] via SEIR model. The measures to reduce or prevent the virus spread should be implemented, and we expect our data-driven modeling analysis providing some insights to identify and prepare for the future virus control. Copyright © 2020 Huang et al.

Hormati, A., Shahhamzeh, A., Afifian, M., Khodadust, F., Ahmadpour, S.

**Can COVID-19 present unusual GI symptoms?**
(2020) Journal of Microbiology, Immunology and Infection

Rubino, S., Kelvin, N., Bermejo-Martin, J.F., Kelvin, D.J.

**As COVID-19 cases, deaths and fatality rates surge in Italy, underlying causes require investigation**

**Abstract:**
COVID-19 case fatalities surged during the month of March 2020 in Italy, reaching over 10,000 by 28 March 2020. This number exceeds the number of fatalities in China (3,301) recorded from January to March, even though the number of diagnosed cases was similar (85,000 Italy vs. 80,000 China). Case Fatality Rates (CFR) could be somewhat unreliable because the estimation of total case numbers is limited by several factors, including insufficient testing and limitations in test kits and materials, such as NP swabs and PPE for testers. Sero prevalence of SARS-CoV-2 antibodies may help in more accurate estimations of the total number of cases. Nevertheless, the disparity in the differences in the total number of fatalities between Italy and China suggests that investigation into several factors, such as demographics, sociological interactions, availability of medical equipment (ICU beds and PPE), variants in immune proteins (e.g., HLA, IFNs), past immunity to related CoVs, and mutations in SARS-CoV-2, could impact survival of severe COVID-19 illness survival and the number of case fatalities. Copyright © 2020 Rubino et al.

van Staden, C.

**COVID-19 and the crisis of national development**

Cossarizza, A., De Biasi, S., Guaraldi, G., Girardis, M., Mussini, C., for the Modena Covid-19 Working Group (MoCo19)#

**SARS-CoV-2, the Virus that Causes COVID-19: Cytometry and the New Challenge for Global Health**
(2020) Cytometry Part A


**Evaluation of SARS-CoV-2 RNA shedding in clinical specimens and clinical characteristics of 10 patients with COVID-19 in Macau**
Abstract:
As a city famous for tourism, the public healthcare system of Macau SAR has been under great pressure during the outbreak of the Coronavirus Disease 2019 (COVID-19). In this study, we report clinical and microbiological features of ten COVID-19 patients enrolled in the Centro Hospitalar Conde de São Januário (CHCSJ) between January 21 to February 16, 2020. Clinical samples from all patients including nasopharyngeal swab (NPS)/sputum, urine, and feces were collected for serial virus RNA testing by standard qRT-PCR assay. In total, seven were imported cases and three were local cases. The median duration from Macau arrival to admission in imported cases was 3 days. Four patients required oxygen therapy but none of them needed machinal ventilation. No fatal cases were noted. The most common symptoms were fever (80%) and diarrhea (80%). In the "Severe" group, there was significantly more elderly patients (p=0.045), higher lactate dehydrogenase levels (p=0.002), and elevated C-Reactive protein levels compared to the "Mild to Moderate" group (p<0.001). There were positive SARS-CoV-2 RNA signals in all patients' NPS and stool specimens but negative in all urine specimens. Based on our data on SARS-CoV-2 RNA shedding in stool and the possibility of a lag in viral detection in NPS specimens, the assessment of both fecal and respiratory specimen is recommended to enhance diagnostic sensitivity, and also to aid discharge decision before the role of viral RNA shedding in stool is clarified. © The author(s).


Abstract:
The outbreak of the novel coronavirus in China (SARS-CoV-2) that began in December 2019 presents a significant and urgent threat to global health. This study was conducted to provide the international community with a deeper understanding of this new infectious disease. Epidemiological, clinical features, laboratory findings, radiological characteristics, treatment, and clinical outcomes of 135 patients in northeast Chongqing were collected and analyzed in this study. A total of 135 hospitalized patients with COVID-19 were enrolled. The median age was 47 years (interquartile range, 36-55), and there was no significant gender difference (53.3% men). The majority of patients had contact with people from the Wuhan area. Forty-three (31.9%) patients had underlying disease, primarily hypertension (13 [9.6%]), diabetes (12 [8.9%]), cardiovascular disease (7 [5.2%]), and malignancy (4 [3.0%]). Common symptoms included fever (120 [88.9%]), cough (102 [76.5%]), and fatigue (44 [32.5%]). Chest computed tomography scans showed bilateral patchy shadows or ground glass opacity in the lungs of all the patients. All patients received antiviral therapy (135 [100%]) (Kaletra and interferon were both used), antibacterial therapy (59 [43.7%]), and corticosteroids (36 [26.7%]). In addition, many patients received traditional Chinese medicine (TCM) (124 [91.8%]). It is suggested that patients should receive Kaletra early and should be treated by a combination of Western and Chinese medicines. Compared to the mild cases, the severe ones had lower lymphocyte counts and higher plasma levels of Pt, APTT, d-dimer, lactate dehydrogenase, PCT, ALB, C-reactive protein, and aspartate aminotransferase. This study demonstrates the clinic features and therapies of 135 COVID-19 patients. Kaletra and TCM played an important role in the treatment of the viral pneumonia. Further studies are required to explore the role of Kaletra and TCM in the treatment of COVID-19. © 2020 Wiley Periodicals, Inc.


Abstract:
Unprecedented measures have been adopted to control the rapid spread of the ongoing COVID-19 epidemic in China. People's adherence to control measures is affected by their knowledge, attitudes, and practices (KAP) towards COVID-19. In this study, we investigated Chinese residents' KAP towards COVID-19 during the rapid rise period of the outbreak. An online sample of Chinese residents was successfully recruited via the authors' networks with residents and popular media in Hubei, China. A self-developed online KAP questionnaire was completed by the participants. The knowledge questionnaire consisted of 12 questions regarding the clinical characteristics and prevention of COVID-19. Assessments on residents' attitudes and practices towards COVID-19 included questions on confidence in winning the battle against COVID-19 and wearing masks when going out in recent days. Among the survey completers (n=6910), 65.7% were women, 63.5% held a bachelor degree or above, and 56.2% engaged in mental labor. The overall correct rate of the knowledge questionnaire was 90%. The majority of the respondents (97.1%) had confidence that China can win the battle against COVID-19. Nearly all of the participants (98.0%) wore masks when going out in recent days. In multiple logistic regression analyses, the COVID-19 knowledge score (OR: 0.75-0.90, P<0.001) was significantly associated with a lower likelihood of negative attitudes and preventive practices towards COVID-19. Most Chinese residents of a relatively high socioeconomic status, in particular women, are knowledgeable about COVID-19, hold optimistic attitudes, and have appropriate practices towards COVID-19. Health education programs aimed at improving COVID-19 knowledge are helpful for Chinese residents to hold optimistic attitudes and maintain appropriate practices. Due to the limited sample representativeness, we must be cautious when generalizing these findings to populations of a low socioeconomic status. © The author(s).


Transcriptomic characteristics of bronchoalveolar lavage fluid and peripheral blood mononuclear cells in COVID-19 patients

Abstract:
Circulating in China and 158 other countries and areas, the ongoing COVID-19 outbreak has caused devastating mortality and posed a great threat to public health. However, efforts to identify effectively supportive therapeutic drugs and treatments has been hampered by our limited understanding of host immune response for this fatal disease. To characterize the transcriptional signatures of host inflammatory response to SARS-CoV-2 (HCoV-19) infection, we carried out transcriptome sequencing of the RNAs isolated from the bronchoalveolar lavage fluid (BALF) and peripheral blood mononuclear cells (PBMC) specimens of COVID-19 patients. Our results reveal distinct host inflammatory cytokine profiles to SARS-CoV-2 infection in patients, and highlight the association between COVID-19 pathogenesis and excessive cytokine release such as CCL2/MCP-1, CXCL10/IP-10, CCL3/MIP-1A, and CCL4/MIP1B. Furthermore, SARS-CoV-2 induced activation of apoptosis and P53 signalling pathway in lymphocytes may be the cause of patients' lymphopenia. The transcriptome dataset of COVID-19 patients would be a valuable resource for clinical guidance on anti-inflammatory medication and understanding the molecular mechanisms of host response. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.

Huang, Y.-C., Lee, P.-I., Hsueh, P.-R.
Evolving reporting criteria of COVID-19 in Taiwan during the epidemic
(2020) Journal of Microbiology, Immunology and Infection

**The correlation between viral clearance and biochemical outcomes of 94 COVID-19 infected discharged patients**

(2020) Inflammation Research

**Abstract:**

Objective: This study aims to evaluate the correlation between viral clearance and blood biochemical index of 94 discharged patients with COVID-19 infection in Shenzhen Third People’s Hospital, enrolled from Jan 5 to Feb 13, 2020. Methods: The clinical and laboratory findings were extracted from the electronic medical records of the patients. The data were analysed and reviewed by a trained team of physicians. Information on clinical signs and symptoms, medical treatment, virus clearance, and laboratory parameters including interleukin 6 (IL-6) and C-reactive protein were collected. Results: COVID-19 mRNA clearance ratio was identified significantly correlated with the decline of serum creatine kinase (CK) and lactate dehydrogenase (LDH) levels. Furthermore, COVID-19 mRNA clearance time was positively correlated with the length of hospital stay in patients treated with either IFN-α + lopinavir/ritonavir or IFN-α + lopinavir/ritonavir + ribavirin. Conclusions: Therapeutic regimens of IFN-α + lopinavir/ritonavir and IFN-α + lopinavir/ritonavir + ribavirin might be beneficial for treatment of COVID-19. Serum LDH or CK decline may predict a favorable response to treatment of COVID-19 infection. © 2020, Springer Nature Switzerland AG.


**Featuring COVID-19 cases via screening symptomatic patients with epidemiologic link during flu season in a medical center of central Taiwan**

(2020) Journal of Microbiology, Immunology and Infection

**Abstract:**

Background: Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), was first reported in Wuhan, Hubei province, China has now rapidly spread over 50 countries. For the prevention and control of infection, Taiwan Centers for Disease Control initiated testing of SARS-CoV-2 on January 24th 2020 for persons suspected with this disease. Until February 28th, 43 flu-like symptomatic patients were screened in China Medical University Hospital. Methods: Two patients were confirmed positive for SARS-CoV-2 infection by rRT-PCR as COVID-19 patients A and B. Causative pathogens for included patients were detected using FilmArray™ Respiratory Panel. We retrospectively analyzed the clinical presentations, laboratory data, radiologic findings, and travel and exposure contact histories, of the COVID-19 patients in comparison to those with other respiratory infections. Results: Through contact with Taiwan No. 19 case patient on 27th January, COVID-19 patients A and B were infected. Both patients had no identified comorbidities and developed mild illness with temporal fever, persistent cough, and lung interstitial infiltrates. Owing to the persistence of positive SARS-CoV-2 in respiratory specimen, the two COVID-19 patients are still in the isolation rooms despite recovery until 10th of March. The results of FilmArray™ Respiratory Panel revealed 22 of the 41 non-COVID-19 patients were infected by particular pathogens. In general, seasonal respiratory pathogens are more prevalent than SARS-CoV-2 in symptomatic patients in non-COVID-19 endemic area during the flu season. Since all patients shared similar clinical and laboratory findings, expanded surveillance of detailed exposure history for suspected patients and application of rapid detection tools are highly recommended. © 2020

Song, P., Karako, T.

**COVID-19: Real-time dissemination of scientific information to fight a public health emergency of international concern**
Abstract:
Rapidly sharing scientific information is an effective way to reduce public panic about COVID-19, and doing so is the key to providing real-time guidance to epidemiologists working to contain the outbreak, clinicians managing patients, and modelers helping to understand future developments and the possible effectiveness of various interventions. This issue has rapidly reviewed and published articles describing COVID-19, including the drug treatment options for SARS-CoV-2, its clinical characteristics, and therapies involving a combination of Chinese and Western medicine, the efficacy of chloroquine phosphate in the treatment of COVID-19 associated pneumonia according to clinical studies, and reflections on the system of reserve medical supplies for public health emergencies. As an academic journal, we will continue to quickly and transparently share data with frontline healthcare workers who need to know the epidemiological and clinical features of COVID-19. © 2020 International Advancement Center for Medicine and Health Research Co., Ltd.

Chen, Y.W., Yiu, C.-P.B., Wong, K.-Y.
Prediction of the SARS-CoV-2 (2019-nCoV) 3C-like protease (3CL pro) structure: virtual screening reveals velpatasvir, ledipasvir, and other drug repurposing candidates
Abstract:
We prepared the three-dimensional model of the SARS-CoV-2 (aka 2019-nCoV) 3C-like protease (3CL pro) using the crystal structure of the highly similar (96% identity) ortholog from the SARS-CoV. All residues involved in the catalysis, substrate binding and dimerisation are 100% conserved. Comparison of the polyprotein PP1AB sequences showed 86% identity. The 3C-like cleavage sites on the coronaviral polyproteins are highly conserved. Based on the near-identical substrate specificities and high sequence identities, we are of the opinion that some of the previous progress of specific inhibitors development for the SARS-CoV enzyme can be conferred on its SARS-CoV-2 counterpart. With the 3CL pro molecular model, we performed virtual screening for purchasable drugs and proposed 16 candidates for consideration. Among these, the antivirals ledipasvir or velpatasvir are particularly attractive as therapeutics to combat the new coronavirus with minimal side effects, commonly fatigue and headache. The drugs Epclusa (velpatasvir/sofosbuvir) and Harvoni (ledipasvir/sofosbuvir) could be very effective owing to their dual inhibitory actions on two viral enzymes. Copyright: © 2020 Chen YW et al.

Weston, S., Frieman, M.B.
COVID-19: Knowns, unknowns, and questions
(2020) mSphere, 5 (2), art. no. e00203
Abstract:
The recent emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) from the Hubei province in China in late 2019 demonstrates the epidemic potential of coronaviruses. The rapid spread of this virus across the world in only 2 months highlights the transmissibility of this family of viruses and the significant morbidity and mortality that they can cause. We highlight the current state of knowledge of coronavirus biology while answering questions concerning the current outbreak of SARS-CoV-2. © 2020 Weston and Frieman.

Internationally lost COVID-19 cases
(2020) Journal of Microbiology, Immunology and Infection
Abstract:
Background: With its epicenter in Wuhan, China, the COVID-19 outbreak was declared a pandemic by the World Health Organization (WHO). While many countries have implemented flight restrictions to China, an increasing number of cases with or without travel background to China are confirmed daily. These developments support concerns on possible unidentified and unreported international COVID-19 cases, which could lead to new local disease epicenters. Methods: We have analyzed all available data on the development of international COVID-19 cases from January 20th, 2020 until February 18th, 2020. COVID-19 cases with and without travel history to China were divided into cohorts according to the Healthcare Access and Quality Index (HAQ-Index) of each country. Chi-square and Post-hoc testing were performed. Results: While COVID-19 cases with travel history to China seem to peak for each HAQ-cohort, the number of non-travel related COVID-19 cases seem to continuously increase in the HAQ-cohort of countries with higher medical standards. Further analyses demonstrate a significantly lower proportion of reported COVID-19 cases without travel history to China in countries with lower HAQ (HAQ I vs. HAQ II, posthoc p < 0.01). Conclusions: Our data indicate that countries with lower HAQ-index may either underreport COVID-19 cases or are unable to adequately detect them. Although our data may be incomplete and must be interpreted with caution, inconsistencies in reporting COVID-19 cases is a serious problem which might sabotage efforts to contain the virus. © 2020

Fang, Y., Nie, Y., Penny, M.
Abstract:
Using the parameterized susceptible-exposed-infectious-recovered model, we simulated the spread dynamics of coronavirus disease 2019 (COVID-19) outbreak and impact of different control measures, conducted the sensitivity analysis to identify the key factor, plotted the trend curve of effective reproductive number (R), and performed data fitting after the simulation. By simulation and data fitting, the model showed the peak existing confirmed cases of 59 769 arriving on 15 February 2020, with the coefficient of determination close to 1 and the fitting bias 3.02%, suggesting high precision of the data-fitting results. More rigorous government control policies were associated with a slower increase in the infected population. Isolation and protective procedures would be less effective as more cases accrue, so the optimization of the treatment plan and the development of specific drugs would be of more importance. There was an upward trend of R in the beginning, followed by a downward trend, a temporary rebound, and another continuous decline. The feature of high infectiousness for severe acute respiratory syndrome coronavirus 2(SARS-CoV-2) led to an upward trend, and government measures contributed to the temporary rebound and declines. The declines of R could be exploited as strong evidence for the effectiveness of the interventions. Evidence from the four-phase stringent measures showed that it was significant to ensure early detection, early isolation, early treatment, adequate medical supplies, patients’ being admitted to designated hospitals, and comprehensive therapeutic strategy. Collaborative efforts are required to combat the novel coronavirus, focusing on both persistent strict domestic interventions and vigilance against exogenous imported cases. © 2020 Wiley Periodicals, Inc.

Yethindra, V.
Abstract:
Coronaviruses (CoVs) are enveloped RNA viruses related to the family Coro-naviridae, the order Nirdovales, and observed in humans and other mammals. In December 2019, many pneumonia cases reported by patients with unknown causes, mainly associated with seafood and wet animal
market in Wuhan, China, and where clinically resembled viral pneumonia. At present, there is no existence of antiviral drugs for the treatment of CoV infections. The results of our study are GS-5734 strongly inhibits SARS-CoV and MERS-CoV in HAE cells, GS-5734 inhibits CoVs at early stages in replication by inhibiting viral RNA synthesis, the absence of ExoN-mediated proofreading in viruses sensitive to treatment with GS-5734. Protease inhibitors can show improved outcomes in some coronaviruses, but mostly 99% of protease inhibitors bind to proteins present in the human body, and only 1% attacks on existed viruses. The expected role of GS-5734 (Remdesivir) in COVID-19 (2019-nCoV)-VYTR hypothesis explained. As broad-spectrum drugs are capable of inhibiting CoV infections, GS-5734 is a broad-spectrum drug and may show inhibition on CoV infections and COVID-19. GS-5734 will show desired results regarding antiviral activity against 2019-nCoV as it showed potent antiviral activity in other CoVs. More clinical trials and experiments needed to prove that GS-5734 (Remdesivir) is a potential and effective drug to treat COVID-19. © 2020 International Journal of Research in Pharmaceutical Sciences. All rights reserved.

Yang, C.-W., Chen, M.-F. Composition of human-specific slow codons and slow di-codons in SARS-CoV and 2019-nCoV are lower than other coronaviruses suggesting a faster protein synthesis rate of SARS-CoV and 2019-nCoV (2020) Journal of Microbiology, Immunology and Infection

Abstract:
Translation of a genetic codon without a cognate tRNA gene is affected by both the cognate tRNA availability and the interaction with non-cognate isoacceptor tRNAs. Moreover, two consecutive slow codons (slow di-codons) lead to a much slower translation rate. Calculating the composition of host specific slow codons and slow di-codons in the viral protein coding sequences can predict the order of viral protein synthesis rates between different virus strains. Comparison of human-specific slow codon and slow di-codon compositions in the genomes of 590 coronaviruses infect humans revealed that the protein synthetic rates of 2019 novel coronavirus (2019-nCoV) and severe acute respiratory syndrome-related coronavirus (SARS-CoV) may be much faster than other coronaviruses infect humans. Analysis of host-specific slow codon and di-codon compositions provides links between viral genomic sequences and capability of virus replication in host cells that may be useful for surveillance of the transmission potential of novel viruses. © 2020

Zhang, T., He, Y., Xu, W., Ma, A., Yang, Y., Xu, K.-F. Clinical trials for the treatment of Coronavirus disease 2019 (COVID-19): A rapid response to urgent need (2020) Science China Life Sciences


Abstract:
The current outbreak of a novel severe acute respiratory syndrome-like coronavirus, 2019_nCoV (now named SARS-CoV-2), illustrated difficulties in identifying a novel coronavirus and its natural host, as the coding sequences of various Betacoronavirus species can be highly diverse. By means of whole-genome sequence comparisons, we demonstrate that the noncoding flanks of the viral genome can be used to correctly separate the recognized four betacoronavirus subspecies. The conservation would be sufficient to define target sequences that could, in theory, classify novel virus species into their subspecies. Only 253 upstream noncoding sequences of Sarbecovirus are
sufficient to identify genetic similarities between species of this subgenus. Furthermore, it was investigated which bat species have commercial value in China, and would thus likely be handled for trading purposes. A number of coronavirus genomes have been published that were obtained from such bat species. These bats are used in Traditional Chinese Medicine, and their handling poses a potential risk to cause zoonotic coronavirus epidemics. Significance and Impact of the Study: The noncoding upstream and downstream flanks of coronavirus genomes allow for rapid classification of novel Betacoronavirus species and correct identification of genetic relationships. Although bats are the likely natural host of 2019_nCoV, the exact bat species that serves as the natural host of the virus remains as yet unknown. Chinese bat species with commercial value were identified as natural reservoirs of coronaviruses and are used in Traditional Chinese Medicine. Since their trading provides a potential risk for spreading zoonoses, a change in these practices is highly recommended. © 2020 The Authors. Letters in Applied Microbiology published by John Wiley & Sons Ltd on behalf of Society for Applied Microbiology.

Zhang, J.-J., Dong, X., Cao, Y.-Y., Yuan, Y.-D., Yang, Y.-B., Yan, Y.-Q., Akdis, C.A., Gao, Y.-D.

Clinical characteristics of 140 patients infected with SARS-CoV-2 in Wuhan, China

(2020) Allergy: European Journal of Allergy and Clinical Immunology

Abstract:
Background: Coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has been widely spread. We aim to investigate the clinical characteristic and allergy status of patients infected with SARS-CoV-2. Methods: Electronic medical records including demographics, clinical manifestation, comorbidities, laboratory data, and radiological materials of 140 hospitalized COVID-19 patients, with confirmed result of SARS-CoV-2 viral infection, were extracted and analyzed. Results: An approximately 1:1 ratio of male (50.7%) and female COVID-19 patients was found, with an overall median age of 57.0 years. All patients were community-acquired cases. Fever (91.7%), cough (75.0%), fatigue (75.0%), and gastrointestinal symptoms (39.6%) were the most common clinical manifestations, whereas hypertension (30.0%) and diabetes mellitus (12.1%) were the most common comorbidities. Drug hypersensitivity (11.4%) and urticaria (1.4%) were self-reported by several patients. Asthma or other allergic diseases were not reported by any of the patients. Chronic obstructive pulmonary disease (COPD, 1.4%) patients and current smokers (1.4%) were rare. Bilateral ground-glass or patchy opacity (89.6%) was the most common sign of radiological finding. Lymphopenia (75.4%) and eosinopenia (52.9%) were observed in most patients. Blood eosinophil counts correlate positively with lymphocyte counts in severe (r =.486, P <.001) and nonsevere (r =.469, P <.001) patients after hospital admission. Significantly higher levels of D-dimer, C-reactive protein, and procalcitonin were associated with severe patients compared to nonsevere patients (all P <.001). Conclusion: Detailed clinical investigation of 140 hospitalized COVID-19 cases suggests eosinopenia together with lymphopenia may be a potential indicator for diagnosis. Allergic diseases, asthma, and COPD are not risk factors for SARS-CoV-2 infection. Older age, high number of comorbidities, and more prominent laboratory abnormalities were associated with severe patients. © 2020 EAACI and John Wiley and Sons A/S. Published by John Wiley and Sons Ltd.


SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is Blocked by a Clinically Proven Protease Inhibitor


Abstract:
The emerging SARS-coronavirus 2 (SARS-CoV-2) threatens public health. Hoffmann and coworkers show that SARS-CoV-2 infection depends on the host cell factors ACE2 and TMPRSS2
and can be blocked by a clinically proven protease inhibitor. These findings might help to establish options for prevention and treatment. © 2020 Elsevier Inc.

The recent emergence of the novel, pathogenic SARS-coronavirus 2 (SARS-CoV-2) in China and its rapid national and international spread pose a global health emergency. Cell entry of coronaviruses depends on binding of the viral spike (S) proteins to cellular receptors and on S protein priming by host cell proteases. Unravelling which cellular factors are used by SARS-CoV-2 for entry might provide insights into viral transmission and reveal therapeutic targets. Here, we demonstrate that SARS-CoV-2 uses the SARS-CoV receptor ACE2 for entry and the serine protease TMPRSS2 for S protein priming. A TMPRSS2 inhibitor approved for clinical use blocked entry and might constitute a treatment option. Finally, we show that the sera from convalescent SARS patients cross-neutralized SARS-2-S-driven entry. Our results reveal important commonalities between SARS-CoV-2 and SARS-CoV infection and identify a potential target for antiviral intervention. © 2020 Elsevier Inc.

Xia, J., Tong, J., Liu, M., Shen, Y., Guo, D.

Evaluation of coronavirus in tears and conjunctival secretions of patients with SARS-CoV-2 infection
(2020) Journal of Medical Virology

Abstract:
Objective: This study aimed to assess the presence of novel coronavirus in tears and conjunctival secretions of SARS–CoV-2-infected patients. Methods: A prospective interventional case series study was performed, and 30 confirmed novel coronavirus pneumonia (NCP) patients were selected at the First Affiliated Hospital of Zhejiang University from 26 January 2020 to 9 February 2020. At an interval of 2 to 3 days, tear and conjunctival secretions were collected twice with disposable sampling swabs for reverse-transcription polymerase chain reaction (RT-PCR) assay. Results: Twenty-one common-type and nine severe-type NCP patients were enrolled. Two samples of tear and conjunctival secretions were obtained from the only one patient with conjunctivitis yielded positive RT-PCR results. Fifty-eight samples from other patents were all negative. Conclusion: We speculate that SARS-CoV-2 may be detected in the tears and conjunctival secretions in NCP patients with conjunctivitis. © 2020 Wiley Periodicals, Inc.

Letko, M., Marzi, A., Munster, V.

Functional assessment of cell entry and receptor usage for SARS-CoV-2 and other lineage B betacoronaviruses

Abstract:
Over the past 20 years, several coronaviruses have crossed the species barrier into humans, causing outbreaks of severe, and often fatal, respiratory illness. Since SARS-CoV was first identified in animal markets, global viromics projects have discovered thousands of coronavirus sequences in diverse animals and geographic regions. Unfortunately, there are few tools available to functionally test these viruses for their ability to infect humans, which has severely hampered efforts to predict the next zoonotic viral outbreak. Here, we developed an approach to rapidly screen lineage B betacoronaviruses, such as SARS-CoV and the recent SARS-CoV-2, for receptor usage and their ability to infect cell types from different species. We show that host protease processing during viral entry is a significant barrier for several lineage B viruses and that bypassing this barrier allows several lineage B viruses to enter human cells through an unknown receptor. We also demonstrate how different lineage B viruses can recombine to gain entry into human cells, and confirm that human ACE2 is the receptor for the recently emerging SARS-CoV-2. © 2020, The Author(s), under exclusive licence to Springer Nature Limited.

Composition and divergence of coronavirus spike proteins and host ACE2 receptors predict potential intermediate hosts of SARS-CoV-2

(2020) Journal of Medical Virology

Abstract:
From the beginning of 2002 and 2012, severe respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV) crossed the species barriers to infect humans, causing thousands of infections and hundreds of deaths, respectively. Currently, a novel coronavirus (SARS-CoV-2), which has become the cause of the outbreak of Coronavirus Disease 2019 (COVID-19), was discovered. Until 18 February 2020, there were 72 533 confirmed COVID-19 cases (including 10 644 severe cases) and 1872 deaths in China. SARS-CoV-2 is spreading among the public and causing substantial burden due to its human-to-human transmission. However, the intermediate host of SARS-CoV-2 is still unclear. Finding the possible intermediate host of SARS-CoV-2 is imperative to prevent further spread of the epidemic. In this study, we used systematic comparison and analysis to predict the interaction between the receptor-binding domain (RBD) of coronavirus spike protein and the host receptor, angiotensin-converting enzyme 2 (ACE2). The interaction between the key amino acids of S protein RBD and ACE2 indicated that, other than pangolins and snakes, as previously suggested, turtles (Chrysemys picta bellii, Chelonia mydas, and Pelodiscus sinensis) may act as the potential intermediate hosts transmitting SARS-CoV-2 to humans. © 2020 Wiley Periodicals, Inc.

Li, X., Zai, J., Zhao, Q., Nie, Q., Li, Y., Foley, B.T., Chaillon, A.

Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2

(2020) Journal of Medical Virology

Abstract:
To investigate the evolutionary history of the recent outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in China, a total of 70 genomes of virus strains from China and elsewhere with sampling dates between 24 December 2019 and 3 February 2020 were analyzed. To explore the potential intermediate animal host of the SARS-CoV-2 virus, we reanalyzed virome data sets from pangolins and representative SARS-related coronaviruses isolates from bats, with particular attention paid to the spike glycoprotein gene. We performed phylogenetic, split network, transmission network, likelihood-mapping, and comparative analyses of the genomes. Based on Bayesian time-scaled phylogenetic analysis using the tip-dating method, we estimated the time to the most recent common ancestor and evolutionary rate of SARS-CoV-2, which ranged from 22 to 24 November 2019 and 1.19 to 1.31 × 10−3 substitutions per site per year, respectively. Our results also revealed that the BetaCoV/bat/Yunnan/RaTG13/2013 virus was more similar to the SARS-CoV-2 virus than the coronavirus obtained from the two pangolin samples (SRR10168377 and SRR10168378). We also identified a unique peptide (PRRA) insertion in the human SARS-CoV-2 virus, which may be involved in the proteolytic cleavage of the spike protein by cellular proteases, and thus could impact host range and transmissibility. Interestingly, the coronavirus carried by pangolins did not have the RRAR motif. Therefore, we concluded that the human SARS-CoV-2 virus, which is responsible for the recent outbreak of COVID-19, did not come directly from pangolins. © 2020 Wiley Periodicals, Inc.

Lai, A., Bergna, A., Acciarri, C., Galli, M., Zehender, G.

Early phylogenetic estimate of the effective reproduction number of SARS-CoV-2

(2020) Journal of Medical Virology

Abstract:
To reconstruct the evolutionary dynamics of the 2019 novel-coronavirus recently causing an outbreak in Wuhan, China, 52 SARS-CoV-2 genomes available on 4 February 2020 at Global
Initiative on Sharing All Influenza Data were analyzed. The two models used to estimate the reproduction number (coalescent-based exponential growth and a birth-death skyline method) indicated an estimated mean evolutionary rate of $7.8 \times 10^{-4}$ subs/site/year (range, $1.1 \times 10^{-4}$ to $15 \times 10^{-4}$) and a mean tMRCA of the tree root of 73 days. The estimated $R$ value was 2.6 (range, 2.1-5.1), and increased from 0.8 to 2.4 in December 2019. The estimated mean doubling time of the epidemic was between 3.6 and 4.1 days. This study proves the usefulness of phylogeny in supporting the surveillance of emerging new infections even as the epidemic is growing. © 2020 Wiley Periodicals, Inc.

Xu, J., Zhao, S., Teng, T., Abdalla, A.E., Zhu, W., Xie, L., Wang, Y., Guo, X.

**Systematic comparison of two animal-to-human transmitted human coronaviruses: SARS-CoV-2 and SARS-CoV**

(2020) Viruses, 12 (2), art. no. 244

**Abstract:**

After the outbreak of the severe acute respiratory syndrome (SARS) in the world in 2003, human coronaviruses (HCoVs) have been reported as pathogens that cause severe symptoms in respiratory tract infections. Recently, a new emerged HCoV isolated from the respiratory epithelium of unexplained pneumonia patients in the Wuhan seafood market caused a major disease outbreak and has been named the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). This virus causes acute lung symptoms, leading to a condition that has been named as "coronavirus disease 2019" (COVID-19). The emergence of SARS-CoV-2 and of SARS-CoV caused widespread fear and concern and has threatened global health security. There are some similarities and differences in the epidemiology and clinical features between these two viruses and diseases that are caused by these viruses. The goal of this work is to systematically review and compare between SARS-CoV and SARS-CoV-2 in the context of their virus incubation, originations, diagnosis and treatment methods, genomic and proteomic sequences, and pathogenic mechanisms. © 2020 by the authors.


**Characteristics of pediatric SARS-CoV-2 infection and potential evidence for persistent fecal viral shedding**

(2020) Nature Medicine

**Abstract:**

We report epidemiological and clinical investigations on ten pediatric SARS-CoV-2 infection cases confirmed by real-time reverse transcription PCR assay of SARS-CoV-2 RNA. Symptoms in these cases were nonspecific and no children required respiratory support or intensive care. Chest X-rays lacked definite signs of pneumonia, a defining feature of the infection in adult cases. Notably, eight children persistently tested positive on rectal swabs even after nasopharyngeal testing was negative, raising the possibility of fecal–oral transmission. © 2020, The Author(s), under exclusive licence to Springer Nature America, Inc.

Phan, T.

**Genetic diversity and evolution of SARS-CoV-2**

(2020) Infection, Genetics and Evolution, 81, art. no. 104260

**Abstract:**

COVID-19 is a viral respiratory illness caused by a new coronavirus called SARS-CoV-2. The World Health Organization declared the SARS-CoV-2 outbreak a global public health emergency. We performed genetic analyses of eighty-six complete or near-complete genomes of SARS-CoV-2 and revealed many mutations and deletions on coding and non-coding regions. These observations provided evidence of the genetic diversity and rapid evolution of this novel coronavirus. © 2020 Elsevier B.V.
Liu, R., Han, H., Liu, F., Lv, Z., Wu, K., Liu, Y., Feng, Y., Zhu, C.

Positive rate of RT-PCR detection of SARS-CoV-2 infection in 4880 cases from one hospital in Wuhan, China, from Jan to Feb 2020 (2020) Clinica Chimica Acta, 505, pp. 172-175.

Abstract:
Background: There's an outbreak of a novel coronavirus (SARS-CoV-2) infection since December 2019, first in China, and currently with more than 80 thousand confirmed infection globally in 29 countries till March 2, 2020. Identification, isolation and caring for patients early are essential to limit human-to-human transmission including reducing secondary infections among close contacts and health care workers, preventing transmission amplification events. The RT-PCR detection of viral nucleic acid test (NAT) was one of the most quickly established laboratory diagnosis method in a novel viral pandemic, just as in this COVID-19 outbreak. Methods: 4880 cases that had respiratory infection symptoms or close contact with COVID-19 patients in hospital in Wuhan, China, were tested for SARS-CoV-2 infection by use of quantitative RT-PCR (qRT-PCR) on samples from the respiratory tract. Positive rates were calculated in groups divided by genders or ages. Results: The positive rate was about 38% for the total 4880 specimens. Male and older population had a significant higher positive rates. However, 57% was positive among the specimens from the Fever Clinics. Binary logistic regression analysis showed that age, not gender, was the risk factor for SARS-CoV-2 infection in fever clinics. Conclusions: Therefore, we concluded that viral NAT played an important role in identifying SARS-CoV-2 infection. © 2020 Elsevier B.V.

Sigrist, C.J., Bridge, A., Le Mercier, P.

A potential role for integrins in host cell entry by SARS-CoV-2 (2020) Antiviral Research, 177, art. no. 104759

Walls, A.C., Park, Y.-J., Tortorici, M.A., Wall, A., McGuire, A.T., Veesler, D.


Abstract:
The emergence of SARS-CoV-2 has resulted in &gt;90,000 infections and &gt;3,000 deaths. Coronavirus spike (S) glycoproteins promote entry into cells and are the main target of antibodies. We show that SARS-CoV-2 S uses ACE2 to enter cells and that the receptor-binding domains of SARS-CoV-2 S and SARS-CoV S bind with similar affinities to human ACE2, correlating with the efficient spread of SARS-CoV-2 among humans. We found that the SARS-CoV-2 S glycoprotein harbors a furin cleavage site at the boundary between the S1/S2 subunits, which is processed during biogenesis and sets this virus apart from SARS-CoV and SARS-related CoVs. We determined cryo-EM structures of the SARS-CoV-2 S ectodomain trimer, providing a blueprint for the design of vaccines and inhibitors of viral entry. Finally, we demonstrate that SARS-CoV S murine polyclonal antibodies potently inhibited SARS-CoV-2 S mediated entry into cells, indicating that cross-neutralizing antibodies targeting conserved S epitopes can be elicited upon vaccination. © 2020 Elsevier Inc.

SARS-CoV-2, a newly emerged pathogen spreading worldwide, binds with high affinity to human ACE2 and uses it as an entry receptor to invade target cells. Cryo-EM structures of the SARS-CoV-2 spike glycoprotein in two distinct conformations, along with inhibition of spike-mediated entry by SARS-CoV polyclonal antibodies, provide a blueprint for the design of vaccines and therapeutics. © 2020 Elsevier Inc.


Abstract:
Effective countermeasures against the recent emergence and rapid expansion of the 2019 novel coronavirus (SARS-CoV-2) require the development of data and tools to understand and monitor its spread and immune responses to it. However, little information is available about the targets of immune responses to SARS-CoV-2. We used the Immune Epitope Database and Analysis Resource (IEDB) to catalog available data related to other coronaviruses. This includes SARS-CoV, which has high sequence similarity to SARS-CoV-2 and is the best-characterized coronavirus in terms of epitope responses. We identified multiple specific regions in SARS-CoV-2 that have high homology to the SARS-CoV virus. Parallel bioinformatic predictions identified a priori potential B and T cell epitopes for SARS-CoV-2. The independent identification of the same regions using two approaches reflects the high probability that these regions are promising targets for immune recognition of SARS-CoV-2. These predictions can facilitate effective vaccine design against this virus of high priority. © 2020 Elsevier Inc.

Grifoni et al. identify potential targets for immune responses to the 2019 novel coronavirus (SARS-CoV-2) by sequence homology with closely related SARS-CoV and by a priori epitope prediction using bioinformatics approaches. This analysis provides essential information for understanding human immune responses to this virus and for evaluating diagnostic and vaccine candidates. © 2020 Elsevier Inc.

Pfefferle, S., Reucher, S., Nörz, D., Lütgehetmann, M.
Evaluation of a quantitative RT-PCR assay for the detection of the emerging coronavirus SARS-CoV-2 using a high throughput system
(2020) Eurosurveillance, 25 (9), art. no. 2000152

Abstract:
Facing the emergence of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), high-volume respiratory testing is demanded in laboratories worldwide. We evaluated the performance of a molecular assay for the detection of SARS-CoV-2 on a high-throughput platform, the cobas 6800, using the 'open channel' for integration of a laboratory-developed assay. We observed good analytical performance in clinical specimens. The fully automated workflow enables highthroughput testing with minimal hands-on time, while offering fast and reliable results. © 2020 European Centre for Disease Prevention and Control (ECDC). All rights reserved.

Predicting the angiotensin converting enzyme 2 (ACE2) utilizing capability as the receptor of SARS-CoV-2
(2020) Microbes and Infection

Abstract:
SARS-CoV-2, the newly identified human coronavirus causing severe pneumonia pandemic, was probably originated from Chinese horseshoe bats. However, direct transmission of the virus from bats to humans is unlikely due to lack of direct contact, implying the existence of unknown intermediate hosts. Angiotensin converting enzyme 2 (ACE2) is the receptor of SARS-CoV-2, but only ACE2s of certain species can be utilized by SARS-CoV-2. Here, we evaluated and ranked the receptor-utilizing capability of ACE2s from various species by phylogenetic clustering and sequence alignment with the currently known ACE2s utilized by SARS-CoV-2. As a result, we predicted that SARS-CoV-2 tends to utilize ACE2s of various mammals, except murines, and some birds, such as pigeon. This prediction may help to screen the intermediate hosts of SARS-CoV-2. © 2020 Institut Pasteur

Giovanetti, M., Angeletti, S., Benvenuto, D., Ciccozzi, M.
A doubt of multiple introduction of SARS-CoV-2 in Italy: A preliminary overview
(2020) Journal of Medical Virology
Abstract:
The emergence of the novel betacoronavirus, recently renamed as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has raised serious concerns due to the virus's rapid dissemination worldwide. Nevertheless, there is limited information about the genomic epidemiology of SARS-CoV-2 circulating in Italy from surveillance studies. The shortage of complete genomic sequences available impairs our understanding of the SARS-CoV-2 introduction and establishment in the country. To better understand its dynamics in Italy, we analyzed complete genomes of SARS-CoV-2 isolates, obtained directly from clinical samples. Our phylogenetic reconstructions suggest possible multiple introduction of SARS-CoV-2. Continued genomic surveillance strategies are needed to improve monitoring and understanding of the current SARS-CoV-2 epidemics, which might help to attenuate public health impact of infectious diseases. © 2020 Wiley Periodicals, Inc.

Ma, X., Su, L., Zhang, Y., Zhang, X., Gai, Z., Zhang, Z.

Do children need a longer time to shed SARS-CoV-2 in stool than adults?
(2020) Journal of Microbiology, Immunology and Infection
Abstract:
SARS-CoV-2 can be shed in the stool of patients in the recovery phase. Children show a longer shedding time than adults. We analyzed the possible causes of this finding and recommend that a negative stool sample be included in a patient's discharge criteria. © 2020

Wang, X., Zhang, X., He, J.

Challenges to the system of reserve medical supplies for public health emergencies: Reflections on the outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic in China
(2020) BioScience Trends, 14 (1), art. no. 1043
Abstract:
On December 31, 2019, the Wuhan Municipal Health Commission announced an outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), China is now at a critical period in the control of the epidemic. The Chinese Government has been taking a series of rapid, comprehensive, and effective prevention and control measures. As the pandemic has developed, a fact has become apparent: there is a serious dearth of emergency medical supplies, and especially an extreme shortage of personal protective equipment such as masks and medical protective clothing. This is one of the major factors affecting the progress of epidemic prevention and control. Although China has made great efforts to strengthen the ability to quickly respond to public health emergencies since the SARS outbreak in 2003 and it has clarified requirements for emergency supplies through legislation, the emergency reserve supplies program has not been effectively implemented, and there are also deficiencies in the types, quantity, and availability of emergency medical supplies. A sound system of emergency reserve supplies is crucial to the management of public health emergencies. Based on international experiences with pandemic control, the world should emphasize improving the system of emergency reserve medical supplies in the process of establishing and improving public health emergency response systems, and it should promote the establishment of international cooperative programs to jointly deal with public health emergencies of international concern in the future. © 2020 International Advancement Center for Medicine and Health Research Co., Ltd.

Luan, J., Lu, Y., Jin, X., Zhang, L.
Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection
(2020) Biochemical and Biophysical Research Communications

Abstract:
SARS-CoV-2 causes the recent global COVID-19 public health emergency. ACE2 is the receptor for both SARS-CoV-2 and SARS-CoV. To predict the potential host range of SARS-CoV-2, we analyzed the key residues of ACE2 for recognizing S protein. We found that most of the selected mammals including pets (dog and cat), pangolin and Circetidae mammals remained the most of key residues for association with S protein from SARS-CoV and SARS-CoV-2. The interaction interface between cat/dog/pangolin/Chinese hamster ACE2 and SARS-CoV/SARS-CoV-2 S protein was simulated through homology modeling. We identified that N82 in ACE2 showed a closer contact with SARS-CoV-2 S protein than M82 in human ACE2. Our finding will provide important insights into the host range of SARS-CoV-2 and a new strategy to design an optimized ACE2 for SARS-CoV-2 infection. © 2020 Elsevier Inc.

Zheng, M., Song, L.

Novel antibody epitopes dominate the antigenicity of spike glycoprotein in SARS-CoV-2 compared to SARS-CoV
(2020) Cellular and Molecular Immunology


Development of epitope-based peptide vaccine against novel coronavirus 2019 (SARS-COV-2): Immunoinformatics approach
(2020) Journal of Medical Virology

Abstract:
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. © 2020 Wiley Periodicals, Inc.


Characterization of spike glycoprotein of SARS-CoV-2 on virus entry and its immune cross-reactivity with SARS-CoV
(2020) Nature Communications, 11 (1), art. no. 1620

Abstract:
Since 2002, beta coronaviruses (CoV) have caused three zoonotic outbreaks, SARS-CoV in 2002–2003, MERS-CoV in 2012, and the newly emerged SARS-CoV-2 in late 2019. However, little is currently known about the biology of SARS-CoV-2. Here, using SARS-CoV-2 S protein pseudovirus system, we confirm that human angiotensin converting enzyme 2 (hACE2) is the receptor for SARS-CoV-2, find that SARS-CoV-2 enters 293/hACE2 cells mainly through endocytosis, that PIKfyve, TPC2, and cathepsin L are critical for entry, and that SARS-CoV-2 S protein is less stable than SARS-CoV S. Polyclonal anti-SARS S1 antibodies T62 inhibit entry of SARS-CoV S but not SARS-CoV-2 S pseudovirions. Further studies using recovered SARS and
COVID-19 patients’ sera show limited cross-neutralization, suggesting that recovery from one infection might not protect against the other. Our results present potential targets for development of drugs and vaccines for SARS-CoV-2. © 2020, The Author(s).

Zhang, Y.-Z., Holmes, E.C.  
**A Genomic Perspective on the Origin and Emergence of SARS-CoV-2**  
**Abstract:**  
The ongoing pandemic of a new human coronavirus, SARS-CoV-2, has generated enormous global concern. We and others in China were involved in the initial genome sequencing of the virus. Herein, we describe what genomic data reveal about the emergence SARS-CoV-2 and discuss the gaps in our understanding of its origins. © 2020 Elsevier Inc.

Zhang, J., Zeng, H., Gu, J., Li, H., Zheng, L., Zou, Q.  
**Progress and prospects on vaccine development against sars-cov-2**  
(2020) Vaccines, 8 (2), art. no. 153  
**Abstract:**  
In December 2019, the outbreak of pneumonia caused by a novel coronavirus, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has led to a serious pandemic in China and other countries worldwide. So far, more than 460,000 confirmed cases were diagnosed in nearly 190 countries, causing globally over 20,000 deaths. Currently, the epidemic is still spreading and there is no effective means to prevent the infection. Vaccines are proved to be the most effective and economical means to prevent and control infectious diseases. Several countries, companies, and institutions announced their programs and progress on vaccine development against the virus. While most of the vaccines are under design and preparation, there are some that have entered efficacy evaluation in animals and initial clinical trials. This review mainly focused on the progress and our prospects on field of vaccine development against SARS-CoV-2. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

**Complete genome sequence of a 2019 novel coronavirus (SARS-COV-2) strain isolated in Nepal**  
(2020) Microbiology Resource Announcements, 9 (11), art. no. e00169-20  
**Abstract:**  
A complete genome sequence was obtained for a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) strain isolated from an oropharyngeal swab specimen of a Nepalese patient with coronavirus disease 2019 (COVID-19), who had returned to Nepal after traveling to Wuhan, China. Copyright © 2020 Sah et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Rehman, S.U., Shafique, L., Ihsan, A., Liu, Q.  
**Evolutionary trajectory for the emergence of novel coronavirus SARS-CoV-2**  
(2020) Pathogens, 9 (3), art. no. 240  
**Abstract:**  
Over the last two decades, the world experienced three outbreaks of coronaviruses with elevated morbidity rates. Currently, the global community is facing emerging virus SARS-CoV-2 belonging to Betacoronavirus, which appears to be more transmissible but less deadly than SARS-CoV. The current study aimed to track the evolutionary ancestors and different evolutionary strategies that were genetically adapted by SARS-CoV-2. Our whole-genome analysis revealed that SARS-CoV-2 was the descendant of Bat SARS/SARS-like CoVs and bats served as a natural reservoir. SARS-CoV-2 used mutations and recombination as crucial strategies in different genomic regions
including the envelope, membrane, nucleocapsid, and spike glycoproteins to become a novel infectious agent. We confirmed that mutations in different genomic regions of SARS-CoV-2 have specific influence on virus reproductive adaptability, allowing for genotype adjustment and adaptations in rapidly changing environments. Moreover, for the first time we identified nine putative recombination patterns in SARS-CoV-2, which encompass spike glycoprotein, RdRp, helicase and ORF3a. Six recombination regions were spotted in the S gene and are undoubtedly important for evolutionary survival, meanwhile this permitted the virus to modify superficial antigenicity to find a way from immune reconnaissance in animals and adapt to a human host. With these combined natural selected strategies, SARS-CoV-2 emerged as a novel virus in human society. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.


Genomic characterization and phylogenetic analysis of SARS-COV-2 in Italy (2020) Journal of Medical Virology

Abstract:
This report describes the isolation, molecular characterization, and phylogenetic analysis of the first three complete genomes of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) isolated from three patients involved in the first outbreak of COVID-19 in Lombardy, Italy. Early molecular epidemiological tracing suggests that SARS-CoV-2 was present in Italy weeks before the first reported cases of infection. © 2020 Wiley Periodicals, Inc.

Ma, Q.-X., Shan, H., Zhang, H.-L., Li, G.-M., Yang, R.-M., Chen, J.-M.

Potential utilities of mask-wearing and instant hand hygiene for fighting SARS-CoV-2 (2020) Journal of Medical Virology

Abstract:
The surge of patients in the pandemic of COVID-19 caused by the novel coronavirus SARS-CoV-2 may overwhelm the medical systems of many countries. Mask-wearing and handwashing can slow the spread of the virus, but currently, masks are in shortage in many countries, and timely handwashing is often impossible. In this study, the efficacy of three types of masks and instant hand wiping was evaluated using the avian influenza virus to mock the coronavirus. Virus quantification was performed using real-time reverse transcription-polymerase chain reaction. Previous studies on mask-wearing were reviewed. The results showed that instant hand wiping using a wet towel soaked in water containing 1.00% soap powder, 0.05% active chlorine, or 0.25% active chlorine from sodium hypochlorite removed 98.36%, 96.62%, and 99.98% of the virus from hands, respectively. N95 masks, medical masks, and homemade masks made of four-layer kitchen paper and one-layer cloth could block 99.98%, 97.14%, and 95.15% of the virus in aerosols. Medical mask-wearing which was supported by many studies was opposed by other studies possibly due to erroneous judgment. With these data, we propose the approach of mask-wearing plus instant hand hygiene (MIH) to slow the exponential spread of the virus. This MIH approach has been supported by the experiences of seven countries in fighting against COVID-19. Collectively, a simple approach to slow the exponential spread of SARS-CoV-2 was proposed with the support of experiments, literature review, and control experiences. © 2020 Wiley Periodicals, Inc.


Phylogenetic analysis of the first four SARS-CoV-2 cases in Chile (2020) Journal of Medical Virology

Abstract:
The current pandemic caused by the new coronavirus is a worldwide public health concern. To aboard this emergency, and like never before, scientific groups around the world have been working in a fast and coordinated way to get the maximum of information about this virus when it has been almost 3 months since the first cases were detected in Wuhan province in China. The complete genome sequences of around 450 isolates are available, and studies about similarities and differences among them and with the close related viruses that caused similar epidemics in this century. In this work, we studied the complete genome of the first four cases of the new coronavirus disease in Chile, from patients who traveled to Europe and Southeast Asia. Our findings reveal at least two different viral variants entries to Chilean territory, coming from Europe and Asia. We also sub-classified the isolates into variants according to punctual mutations in the genome. Our work contributes to global information about transmission dynamics and the importance to take control measures to stop the spread of the infection. © 2020 Wiley Periodicals, Inc.


Predicting commercially available antiviral drugs that may act on the novel coronavirus (SARS-CoV-2) through a drug-target interaction deep learning model

Abstract:
The infection of a novel coronavirus found in Wuhan of China (SARS-CoV-2) is rapidly spreading, and the incidence rate is increasing worldwide. Due to the lack of effective treatment options for SARS-CoV-2, various strategies are being tested in China, including drug repurposing. In this study, we used our pre-trained deep learning-based drug-target interaction model called Molecule Transformer-Drug Target Interaction (MT-DTI) to identify commercially available drugs that could act on viral proteins of SARS-CoV-2. The result showed that atazanavir, an antiretroviral medication used to treat and prevent the human immunodeficiency virus (HIV), is the best chemical compound, showing an inhibitory potency with Kd of 94.94 nM against the SARS-CoV-2 3C-like proteinase, followed by remdesivir (113.13 nM), efavirenz (199.17 nM), ritonavir (204.05 nM), and dolutegravir (336.91 nM). Interestingly, lopinavir, ritonavir, and darunavir are all designed to target viral proteinases. However, in our prediction, they may also bind to the replication complex components of SARS-CoV-2 with an inhibitory potency with Kd &lt; 1000 nM. In addition, we also found that several antiviral agents, such as Kaletra (lopinavir/ritonavir), could be used for the treatment of SARS-CoV-2. Overall, we suggest that the list of antiviral drugs identified by the MT-DTI model should be considered, when establishing effective treatment strategies for SARS-CoV-2. © 2020 The Authors

Ton, A.-T., Gentile, F., Hsing, M., Ban, F., Cherkasov, A.

Rapid Identification of Potential Inhibitors of SARS-CoV-2 Main Protease by Deep Docking of 1.3 Billion Compounds
(2020) Molecular Informatics

Abstract:
The recently emerged 2019 Novel Coronavirus (SARS-CoV-2) and associated COVID-19 disease cause serious or even fatal respiratory tract infection and yet no approved therapeutics or effective treatment is currently available to effectively combat the outbreak. This urgent situation is pressing the world to respond with the development of novel vaccine or a small molecule therapeutics for SARS-CoV-2. Along these efforts, the structure of SARS-CoV-2 main protease (Mpro) has been rapidly resolved and made publicly available to facilitate global efforts to develop novel drug candidates. Recently, our group has developed a novel deep learning platform – Deep Docking (DD) which provides fast prediction of docking scores of Glide (or any other docking program) and, hence, enables structure-based virtual screening of billions of purchasable molecules in a short time. In the current study we applied DD to all 1.3 billion compounds from ZINC15 library to
identify top 1,000 potential ligands for SARS-CoV-2 Mpro protein. The compounds are made publicly available for further characterization and development by scientific community. © 2020 Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim

Srinivasan, S., Cui, H., Gao, Z., Liu, M., Lu, S., Mkandawire, W., Narykov, O., Sun, M., Korkin, D.

**Structural genomics of SARS-COV-2 indicates evolutionary conserved functional regions of viral proteins**
(2020) Viruses, 12 (4), art. no. 360

**Abstract:**
During its first two and a half months, the recently emerged 2019 novel coronavirus, SARS-CoV-2, has already infected over one-hundred thousand people worldwide and has taken more than four thousand lives. However, the swiftly spreading virus also caused an unprecedentedly rapid response from the research community facing the unknown health challenge of potentially enormous proportions. Unfortunately, the experimental research to understand the molecular mechanisms behind the viral infection and to design a vaccine or antivirals is costly and takes months to develop. To expedite the advancement of our knowledge, we leveraged data about the related coronaviruses that is readily available in public databases and integrated these data into a single computational pipeline. As a result, we provide comprehensive structural genomics and interactomics roadmaps of SARS-CoV-2 and use this information to infer the possible functional differences and similarities with the related SARS coronavirus. All data are made publicly available to the research community. © 2020 by the authors.


**Establishment and validation of a pseudovirus neutralization assay for SARS-CoV-2**

**Abstract:**
Pseudoviruses are useful virological tools because of their safety and versatility, especially for emerging and re-emerging viruses. Due to its high pathogenicity and infectivity and the lack of effective vaccines and therapeutics, live SARS-CoV-2 has to be handled under biosafety level 3 conditions, which has hindered the development of vaccines and therapeutics. Based on a VSV pseudovirus production system, a pseudovirus-based neutralization assay has been developed for evaluating neutralizing antibodies against SARS-CoV-2 in biosafety level 2 facilities. The key parameters for this assay were optimized, including cell types, cell numbers, virus inoculum. When tested against the SARS-CoV-2 pseudovirus, SARS-CoV-2 convalescent patient sera showed high neutralizing potency, which underscore its potential as therapeutics. The limit of detection for this assay was determined as 22.1 and 43.2 for human and mouse serum samples respectively using a panel of 120 negative samples. The cutoff values were set as 30 and 50 for human and mouse serum samples, respectively. This assay showed relatively low coefficient of variations with 15.9% and 16.2% for the intra- and inter-assay analyses respectively. Taken together, we established a robust pseudovirus-based neutralization assay for SARS-CoV-2 and are glad to share pseudoviruses and related protocols with the developers of vaccines or therapeutics to fight against this lethal virus. © 2020, © 2020 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group, on behalf of Shanghai Shangyixun Cultural Communication Co., Ltd.

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)
(2020) Journal of Medical Virology

Abstract:
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. © 2020 Wiley Periodicals, Inc.

Wang, C., Liu, Z., Chen, Z., Huang, X., Xu, M., He, T., Zhang, Z.
The establishment of reference sequence for SARS-CoV-2 and variation analysis
(2020) Journal of Medical Virology

Abstract:
Starting around December 2019, an epidemic of pneumonia, which was named COVID-19 by the World Health Organization, broke out in Wuhan, China, and is spreading throughout the world. A new coronavirus, named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) by the Coronavirus Study Group of the International Committee on Taxonomy of Viruses was soon found to be the cause. At present, the sensitivity of clinical nucleic acid detection is limited, and it is still unclear whether it is related to genetic variation. In this study, we retrieved 95 full-length genomic sequences of SARS-CoV-2 strains from the National Center for Biotechnology Information and GISAID databases, established the reference sequence by conducting multiple sequence alignment and phylogenetic analyses, and analyzed sequence variations along the SARS-CoV-2 genome. The homology among all viral strains was generally high, among them, 99.99% (99.91%-100%) at the nucleotide level and 99.99% (99.79%-100%) at the amino acid level. Although overall variation in open-reading frame (ORF) regions is low, 13 variation sites in 1a, 1b, S, 3a, M, 8, and N regions were identified, among which positions nt28144 in ORF 8 and nt8782 in ORF 1a showed mutation rate of 30.53% (29/95) and 29.47% (28/95), respectively. These findings suggested that there may be selective mutations in SARS-COV-2, and it is necessary to avoid certain regions when designing primers and probes. Establishment of the reference sequence for SARS-CoV-2 could benefit not only biological study of this virus but also diagnosis, clinical monitoring and intervention of SARS-CoV-2 infection in the future. © 2020 Wiley Periodicals, Inc.

Lung, J., Lin, Y.-S., Yang, Y.-H., Chou, Y.-L., Shu, L.-H., Cheng, Y.-C., Liu, H.T., Wu, C.-Y.
The potential chemical structure of anti-SARS-CoV-2 RNA-dependent RNA polymerase
(2020) Journal of Medical Virology

Abstract:
An outbreak of coronavirus disease 2019 (COVID-19) occurred in Wuhan and it has rapidly spread to almost all parts of the world. For coronaviruses, RNA-dependent RNA polymerase (RdRp) is an important protease that catalyzes the replication of RNA from RNA template and is an attractive therapeutic target. In this study, we screened these chemical structures from traditional Chinese medicinal compounds proven to show antiviral activity in severe acute respiratory syndrome coronavirus (SARS-CoV) and the similar chemical structures through a molecular docking study to target RdRp of SARS-CoV-2, SARS-CoV, and Middle East respiratory syndrome coronavirus (MERS-CoV). We found that theaflavin has a lower idock score in the catalytic pocket of RdRp in SARS-CoV-2 (−9.11 kcal/mol), SARS-CoV (−8.03 kcal/mol), and MERS-CoV (−8.26 kcal/mol) from idock. To confirm the result, we discovered that theaflavin has lower binding energy of −8.8 kcal/mol when it docks in the catalytic pocket of SARS-CoV-2 RdRp by using the Blind Docking server. Regarding contact modes, hydrophobic interactions contribute significantly in binding and additional hydrogen bonds were found between theaflavin and RdRp. Moreover, one π-cation interaction was formed between theaflavin and Arg553 from the Blind Docking server. Our results suggest that theaflavin could be a potential SARS-CoV-2 RdRp inhibitor for further study. © 2020 Wiley Periodicals, Inc.

Kandeel, M., Ibrahim, A., Fayez, M., Al-Nazawi, M. From SARS and MERS CoVs to SARS-CoV-2: Moving toward more biased codon usage in viral structural and nonstructural genes (2020) Journal of Medical Virology

Abstract:
Background: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an emerging disease with fatal outcomes. In this study, a fundamental knowledge gap question is to be resolved by evaluating the differences in biological and pathogenic aspects of SARS-CoV-2 and the changes in SARS-CoV-2 in comparison with the two prior major COV epidemics, SARS and Middle East respiratory syndrome (MERS) coronaviruses. Methods: The genome composition, nucleotide analysis, codon usage indices, relative synonymous codons usage, and effective number of codons (ENC) were analyzed in the four structural genes; Spike (S), Envelope (E), membrane (M), and Nucleocapsid (N) genes, and two of the most important nonstructural genes comprising RNA-dependent RNA polymerase and main protease (Mpro) of SARS-CoV-2, Beta-CoV from pangolins, bat SARS, MERS, and SARS CoVs. Results: SARS-CoV-2 prefers pyrimidine rich codons to purines. Most high-frequency codons were ending with A or T, while the low frequency and rare codons were ending with G or C. SARS-CoV-2 structural proteins showed 5 to 20 lower ENC values, compared with SARS, bat SARS, and MERS CoVs. This implies higher codon bias and higher gene expression efficiency of SARS-CoV-2 structural proteins. SARS-CoV-2 encoded the highest number of over-biased and negatively biased codons. Pangolin Beta-CoV showed little differences with SARS-CoV-2 ENC values, compared with SARS, bat SARS, and MERS CoV. Conclusion: Extreme bias and lower ENC values of SARS-CoV-2, especially in Spike, Envelope, and Mpro genes, are suggestive for higher gene expression efficiency, compared with SARS, bat SARS, and MERS CoVs.
Physical Sciences :

- Chemical Engineering
- Chemistry
- Computer Science
- Earth and Planetary Sciences
- Energy
- Engineering
- Environmental Science
- Materials Science
- Mathematics
- Physics and Astronomy

Clinical and biochemical indexes from 2019-nCoV infected patients linked to viral loads and lung injury

Abstract:
The outbreak of the 2019-nCoV infection began in December 2019 in Wuhan, Hubei province, and rapidly spread to many provinces in China as well as other countries. Here we report the epidemiological, clinical, laboratory, and radiological characteristics, as well as potential biomarkers for predicting disease severity in 2019-nCoV-infected patients in Shenzhen, China. All 12 cases of the 2019-nCoV-infected patients developed pneumonia and half of them developed acute respiratory distress syndrome (ARDS). The most common laboratory abnormalities were hypoalbuminemia, lymphopenia, decreased percentage of lymphocytes (LYM) and neutrophils (NEU), elevated C-reactive protein (CRP) and lactate dehydrogenase (LDH), and decreased CD8 count. The viral load of 2019-nCoV detected from patient respiratory tracts was positively linked to lung disease severity. ALB, LYM, LYM (%), LDH, NEU (%), and CRP were highly correlated to the acute lung injury. Age, viral load, lung injury score, and blood biochemistry indexes, albumin (ALB), CRP, LDH, LYM (%), LYM, and NEU (%), may be predictors of disease severity. Moreover, the Angiotensin II level in the plasma sample from 2019-nCoV infected patients was markedly elevated and linearly associated to viral load and lung injury. Our results suggest a number of potential diagnosis biomarkers and angiotensin receptor blocker (ARB) drugs for potential repurposing treatment of 2019-nCoV infection. © 2020, Science China Press and Springer-Verlag GmbH Germany, part of Springer Nature.


Clinical characteristics of 24 asymptomatic infections with COVID-19 screened among close contacts in Nanjing, China
(2020) Science China Life Sciences

Abstract:
Previous studies have showed clinical characteristics of patients with the 2019 novel coronavirus disease (COVID-19) and the evidence of person-to-person transmission. Limited data are available for asymptomatic infections. This study aims to present the clinical characteristics of 24 cases with asymptomatic infection screened from close contacts and to show the transmission potential of asymptomatic COVID-19 virus carriers. Epidemiological investigations were conducted among all close contacts of COVID-19 patients (or suspected patients) in Nanjing, Jiangsu Province, China, from Jan 28 to Feb 9, 2020, both in clinic and in community. Asymptomatic carriers were laboratory-confirmed positive for the COVID-19 virus by testing the nucleic acid of the pharyngeal swab samples. Their clinical records, laboratory assessments, and chest CT scans were reviewed. As a result, none of the 24 asymptomatic cases presented any obvious symptoms while nucleic acid screening. Five cases (20.8%) developed symptoms (fever, cough, fatigue, etc.) during hospitalization. Twelve (50.0%) cases showed typical CT images of ground-glass chest and 5 (20.8%) presented stripe shadowing in the lungs. The remaining 7 (29.2%) cases showed normal CT image and had no symptoms during hospitalization. These 7 cases were younger (median age: 14.0 years; P=0.012) than the rest. None of the 24 cases developed severe COVID-19 pneumonia or died. The median communicable period, defined as the interval from the first day of positive nucleic acid tests to the first day of continuous negative tests, was 9.5 days (up to 21 days among the 24 asymptomatic cases). Through epidemiological investigation, we observed a typical asymptomatic transmission to the cohabiting family members, which even caused severe COVID-19 pneumonia. Overall, the asymptomatic carriers identified from close contacts were prone to be mildly ill during hospitalization. However, the communicable period could be up to three weeks
and the communicated patients could develop severe illness. These results highlighted the importance of close contact tracing and longitudinally surveillance via virus nucleic acid tests. Further isolation recommendation and continuous nucleic acid tests may also be recommended to the patients discharged. © 2020, Science China Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Morse, J.S., Lalonde, T., Xu, S., Liu, W.R.
Learning from the Past: Possible Urgent Prevention and Treatment Options for Severe Acute Respiratory Infections Caused by 2019-nCoV
Abstract:
With the current trajectory of the 2019-nCoV outbreak unknown, public health and medicinal measures will both be needed to contain spreading of the virus and to optimize patient outcomes. Although little is known about the virus, an examination of the genome sequence shows strong homology with its better-studied cousin, SARS-CoV. The spike protein used for host cell infection shows key nonsynonymous mutations that might hamper the efficacy of previously developed therapeutics but remains a viable target for the development of biologics and macrocyclic peptides. Other key drug targets, including RNA-dependent RNA polymerase and coronavirus main proteinase (3CLpro), share a strikingly high (>95%) homology to SARS-CoV. Herein, we suggest four potential drug candidates (an ACE2-based peptide, remdesivir, 3CLpro-1 and a novel vinylsulfone protease inhibitor) that could be used to treat patients suffering with the 2019-nCoV. We also summarize previous efforts into drugging these targets and hope to help in the development of broad-spectrum anti-coronaviral agents for future epidemics. © 2020 Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim

Tang, B., Bragazzi, N.L., Li, Q., Tang, S., Xiao, Y., Wu, J.
An updated estimation of the risk of transmission of the novel coronavirus (2019-nCov)
(2020) Infectious Disease Modelling, 5, pp. 248-255.
Abstract:
The basic reproduction number of an infectious agent is the average number of infections one case can generate over the course of the infectious period, in a naïve, uninfected population. It is well-known that the estimation of this number may vary due to several methodological issues, including different assumptions and choice of parameters, utilized models, used datasets and estimation period. With the spreading of the novel coronavirus (2019-nCoV) infection, the reproduction number has been found to vary, reflecting the dynamics of transmission of the coronavirus outbreak as well as the case reporting rate. Due to significant variations in the control strategies, which have been changing over time, and thanks to the introduction of detection technologies that have been rapidly improved, enabling to shorten the time from infection/symptoms onset to diagnosis, leading to faster confirmation of the new coronavirus cases, our previous estimations on the transmission risk of the 2019-nCoV need to be revised. By using time-dependent contact and diagnose rates, we refit our previously proposed dynamics transmission model to the data available until January 29th, 2020 and re-estimated the effective daily reproduction ratio that better quantifies the evolution of the interventions. We estimated when the effective daily reproduction ratio has fallen below 1 and when the epidemics will peak. Our updated findings suggest that the best measure is persistent and strict self-isolation. The epidemics will continue to grow, and can peak soon with the peak time depending highly on the public health interventions practically implemented. © 2020 The Authors
CDC COVID-19 Response Team

Severe Outcomes Among Patients with Coronavirus Disease 2019 (COVID-19) - United States, February 12-March 16, 2020


Abstract:
Globally, approximately 170,000 confirmed cases of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) have been reported, including an estimated 7,000 deaths in approximately 150 countries (1). On March 11, 2020, the World Health Organization declared the COVID-19 outbreak a pandemic (2). Data from China have indicated that older adults, particularly those with serious underlying health conditions, are at higher risk for severe COVID-19-associated illness and death than are younger persons (3). Although the majority of reported COVID-19 cases in China were mild (81%), approximately 80% of deaths occurred among adults aged ≥60 years; only one (0.1%) death occurred in a person aged ≤19 years (3). In this report, COVID-19 cases in the United States that occurred during February 12-March 16, 2020 and severity of disease (hospitalization, admission to intensive care unit [ICU], and death) were analyzed by age group. As of March 16, a total of 4,226 COVID-19 cases in the United States had been reported to CDC, with multiple cases reported among older adults living in long-term care facilities (4). Overall, 31% of cases, 45% of hospitalizations, 53% of ICU admissions, and 80% of deaths associated with COVID-19 were among adults aged ≥65 years with the highest percentage of severe outcomes among persons aged ≥85 years. In contrast, no ICU admissions or deaths were reported among persons aged ≤19 years. Similar to reports from other countries, this finding suggests that the risk for serious disease and death from COVID-19 is higher in older age groups.

Layqah, L.A., Eissa, S.

An electrochemical immunosensor for the coronavirus associated with the Middle East respiratory syndrome using an array of gold nanoparticle-modified carbon electrodes

(2019) Microchimica Acta, 186 (4), art. no. 224

Abstract:
The Middle East respiratory syndrome coronavirus (MERS-CoV) is highly pathogenic. An immunosensor for the determination of MERS-CoV is described here. It is based on a competitive assay carried out on an array of carbon electrodes (DEP) modified with gold nanoparticles. Recombinant spike protein S1 was used as a biomarker for MERS-CoV. The electrode array enables multiplexed detection of different CoVs. The biosensor is based on indirect competition between free virus in the sample and immobilized MERS-CoV protein for a fixed concentration of antibody added to the sample. Voltammetric response is detected by monitoring the change in the peak current (typically acquired at a working potential of −0.05 V vs. Ag/AgCl) after addition of different concentrations of antigen against MERS-CoV. Electrochemical measurements using ferrocyanide/ferricyanide as a probe were recorded using square wave voltammetry (SWV). Good linear response between the sensor response and the concentrations from 0.001 to 100 ng.mL−1 and 0.01 to 10,000 ng.mL−1 were observed for MERS-CoV and HCoV, respectively. The assay was performed in 20 min with detection limit as low as 0.4 and 1.0 pg.mL−1 for HCoV and MERS-CoV, respectively. The method is highly selective over non-specific proteins such as Influenza A and B. The method is single-step, sensitive and accurate. It was successfully applied to spiked nasal samples. © 2019, Springer-Verlag GmbH Austria, part of Springer Nature.


Research and Development on Therapeutic Agents and Vaccines for COVID-19 and Related Human Coronavirus Diseases

Abstract:
Since the outbreak of the novel coronavirus disease COVID-19, caused by the SARS-CoV-2 virus, this disease has spread rapidly around the globe. Considering the potential threat of a pandemic, scientists and physicians have been racing to understand this new virus and the pathophysiology of this disease to uncover possible treatment regimens and discover effective therapeutic agents and vaccines. To support the current research and development, CAS has produced a special report to provide an overview of published scientific information with an emphasis on patents in the CAS content collection. It highlights antiviral strategies involving small molecules and biologics targeting complex molecular interactions involved in coronavirus infection and replication. The drug-repurposing effort documented herein focuses primarily on agents known to be effective against other RNA viruses including SARS-CoV and MERS-CoV. The patent analysis of coronavirus-related biologics includes therapeutic antibodies, cytokines, and nucleic acid-based therapies targeting virus gene expression as well as various types of vaccines. More than 500 patents disclose methodologies of these four biologics with the potential for treating and preventing coronavirus infections, which may be applicable to COVID-19. The information included in this report provides a strong intellectual groundwork for the ongoing development of therapeutic agents and vaccines. © 2020 American Chemical Society.

Mizumoto, K., Chowell, G.
Transmission potential of the novel coronavirus (COVID-19) onboard the diamond Princess Cruises Ship, 2020
(2020) Infectious Disease Modelling, 5, pp. 264-270.
Abstract:
An outbreak of COVID-19 developed aboard the Princess Cruises Ship during January–February 2020. Using mathematical modeling and time-series incidence data describing the trajectory of the outbreak among passengers and crew members, we characterize how the transmission potential varied over the course of the outbreak. Our estimate of the mean reproduction number in the confined setting reached values as high as ~11, which is higher than mean estimates reported from community-level transmission dynamics in China and Singapore (approximate range: 1.1–7). Our findings suggest that Rt decreased substantially compared to values during the early phase after the Japanese government implemented an enhanced quarantine control. Most recent estimates of Rt reached values largely below the epidemic threshold, indicating that a secondary outbreak of the novel coronavirus was unlikely to occur aboard the Diamond Princess Ship. © 2020 The Authors

Fanelli, D., Piazza, F.
Analysis and forecast of COVID-19 spreading in China, Italy and France
(2020) Chaos, Solitons and Fractals, 134, art. no. 109761
Abstract:
In this note we analyze the temporal dynamics of the coronavirus disease 2019 outbreak in China, Italy and France in the time window 22/01–15/03/2020. A first analysis of simple day-lag maps points to some universality in the epidemic spreading, suggesting that simple mean-field models can be meaningfully used to gather a quantitative picture of the epidemic spreading, and notably the height and time of the peak of confirmed infected individuals. The analysis of the same data within a simple susceptible-infected-recovered-deaths model indicates that the kinetic parameter that describes the rate of recovery seems to be the same, irrespective of the country, while the infection and death rates appear to be more variable. The model places the peak in Italy around March 21st 2020, with a peak number of infected individuals of about 26000 (not including recovered and dead) and a number of deaths at the end of the epidemics of about 18,000. Since the confirmed cases are believed to be between 10 and 20% of the real number of individuals who eventually get infected, the apparent mortality rate of COVID-19 falls between 4% and 8% in Italy,
while it appears substantially lower, between 1% and 3% in China. Based on our calculations, we estimate that 2500 ventilation units should represent a fair figure for the peak requirement to be considered by health authorities in Italy for their strategic planning. Finally, a simulation of the effects of drastic containment measures on the outbreak in Italy indicates that a reduction of the infection rate indeed causes a quench of the epidemic peak. However, it is also seen that the infection rate needs to be cut down drastically and quickly to observe an appreciable decrease of the epidemic peak and mortality rate. This appears only possible through a concerted and disciplined, albeit painful, effort of the population as a whole. © 2020 Elsevier Ltd


Abstract:
Epidemic outbreaks are a special case of supply chain (SC) risks which is distinctively characterized by a long-term disruption existence, disruption propagations (i.e., the ripple effect), and high uncertainty. We present the results of a simulation study that opens some new research tensions on the impact of COVID-19 (SARS-CoV-2) on the global SCs. First, we articulate the specific features that frame epidemic outbreaks as a unique type of SC disruption risks. Second, we demonstrate how simulation-based methodology can be used to examine and predict the impacts of epidemic outbreaks on the SC performance using the example of coronavirus COVID-19 and anyLogistix simulation and optimization software. We offer an analysis for observing and predicting both short-term and long-term impacts of epidemic outbreaks on the SCs along with managerial insights. A set of sensitivity experiments for different scenarios allows illustrating the model's behavior and its value for decision-makers. The major observation from the simulation experiments is that the timing of the closing and opening of the facilities at different echelons might become a major factor that determines the epidemic outbreak impact on the SC performance rather than an upstream disruption duration or the speed of epidemic propagation. Other important factors are lead-time, speed of epidemic propagation, and the upstream and downstream disruption durations in the SC. The outcomes of this research can be used by decision-makers to predict the operative and long-term impacts of epidemic outbreaks on the SCs and develop pandemic SC plans. Our approach can also help to identify the successful and wrong elements of risk mitigation/preparedness and recovery policies in case of epidemic outbreaks. The paper is concluded by summarizing the most important insights and outlining future research agenda. © 2020 Elsevier Ltd


Abstract:
What is already known about this topic? First detected in China in late 2019, coronavirus disease 2019 (COVID-19) transmission has spread globally. What is added by this report? Singapore implemented a multipronged surveillance and containment strategy that contributed to enhanced case ascertainment and slowing of the outbreak. Based on review of the first 100 cases, the mean interval from symptom onset to isolation was 5.6 days and declined after approximately 1 month. What are the implications for public health practice? A multipronged surveillance strategy could lead to enhanced case detection and reduced transmission of highly infectious diseases such as COVID-19. © 2020 Department of Health and Human Services. All rights reserved.
Active Monitoring of Persons Exposed to Patients with Confirmed COVID-19 - United States, January-February 2020 

Abstract:
In December 2019, an outbreak of coronavirus disease 2019 (COVID-19), caused by the virus SARS-CoV-2, began in Wuhan, China (1). The disease spread widely in China, and, as of February 26, 2020, COVID-19 cases had been identified in 36 other countries and territories, including the United States. Person-to-person transmission has been widely documented, and a limited number of countries have reported sustained person-to-person spread.* On January 20, state and local health departments in the United States, in collaboration with teams deployed from CDC, began identifying and monitoring all persons considered to have had close contact† with patients with confirmed COVID-19 (2). The aims of these efforts were to ensure rapid evaluation and care of patients, limit further transmission, and better understand risk factors for transmission.

Yu, H., Sun, X., Solvang, W.D., Zhao, X. 
Reverse logistics network design for effective management of medical waste in epidemic outbreaks: Insights from the coronavirus disease 2019 (COVID-19) outbreak in Wuhan (China) 
Abstract:
The outbreak of an epidemic disease may pose significant treats to human beings and may further lead to a global crisis. In order to control the spread of an epidemic, the effective management of rapidly increased medical waste through establishing a temporary reverse logistics system is of vital importance. However, no research has been conducted with the focus on the design of an epidemic reverse logistics network for dealing with medical waste during epidemic outbreaks, which, if improperly treated, may accelerate disease spread and pose a significant risk for both medical staffs and patients. Therefore, this paper proposes a novel multi-objective multi-period mixed integer program for reverse logistics network design in epidemic outbreaks, which aims at determining the best locations of temporary facilities and the transportation strategies for effective management of the exponentially increased medical waste within a very short period. The application of the model is illustrated with a case study based on the outbreak of the coronavirus disease 2019 (COVID-19) in Wuhan, China. Even though the uncertainty of the future COVID-19 spread tendency is very high at the time of this research, several general policy recommendations can still be obtained based on computational experiments and quantitative analyses. Among other insights, the results suggest installing temporary incinerators may be an effective solution for managing the tremendous increase of medical waste during the COVID-19 outbreak in Wuhan, but the location selection of these temporary incinerators is of significant importance. Due to the limitation on available data and knowledge at present stage, more real-world information are needed to assess the effectiveness of the current solution. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Wang, C., Pan, R., Wan, X., Tan, Y., Xu, L., Ho, C.S., Ho, R.C. 
Immediate psychological responses and associated factors during the initial stage of the 2019 coronavirus disease (COVID-19) epidemic among the general population in China 
Abstract:
Background: The 2019 coronavirus disease (COVID-19) epidemic is a public health emergency of international concern and poses a challenge to psychological resilience. Research data are needed to develop evidence-driven strategies to reduce adverse psychological impacts and psychiatric symptoms during the epidemic. The aim of this study was to survey the general public in China to better understand their levels of psychological impact, anxiety, depression, and stress during the initial stage of the COVID-19 outbreak. The data will be used for future reference. Methods: From 31 January to 2 February 2020, we conducted an online survey using snowball sampling techniques. The online survey collected information on demographic data, physical symptoms in the past 14 days, contact history with COVID-19, knowledge and concerns about COVID-19, precautionary measures against COVID-19, and additional information required with respect to COVID-19. Psychological impact was assessed by the Impact of Event Scale-Revised (IES-R), and mental health status was assessed by the Depression, Anxiety and Stress Scale (DASS-21). Results: This study included 1210 respondents from 194 cities in China. In total, 53.8% of respondents rated the psychological impact of the outbreak as moderate or severe; 16.5% reported moderate to severe depressive symptoms; 28.8% reported moderate to severe anxiety symptoms; and 8.1% reported moderate to severe stress levels. Most respondents spent 20–24 h per day at home (84.7%); were worried about their family members contracting COVID-19 (75.2%); and were satisfied with the amount of health information available (75.1%). Female gender, student status, specific physical symptoms (e.g., myalgia, dizziness, coryza), and poor self-rated health status were significantly associated with a greater psychological impact of the outbreak and higher levels of stress, anxiety, and depression (p < 0.05). Specific up-to-date and accurate health information (e.g., treatment, local outbreak situation) and particular precautionary measures (e.g., hand hygiene, wearing a mask) were associated with a lower psychological impact of the outbreak and lower levels of stress, anxiety, and depression (p < 0.05). Conclusions: During the initial phase of the COVID-19 outbreak in China, more than half of the respondents rated the psychological impact as moderate to severe, and about one-third reported moderate-to-severe anxiety. Our findings identify factors associated with a lower level of psychological impact and better mental health status that can be used to formulate psychological interventions to improve the mental health of vulnerable groups during the COVID-19 epidemic. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.


Experimental Treatment with Favipiravir for COVID-19: An Open-Label Control Study
(2020) Engineering

Abstract:
An outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection and its caused coronavirus disease 2019 (COVID-19) has been reported in China since December 2019. More than 16% of patients developed acute respiratory distress syndrome, and the fatality ratio was about 1%–2%. No specific treatment has been reported. Herein, we examine the effects of Favipiravir (FPV) versus Lopinavir (LPV)/ritonavir (RTV) for the treatment of COVID-19. Patients with laboratory-confirmed COVID-19 who received oral FPV (Day 1: 1600 mg twice daily; Days 2–14: 600 mg twice daily) plus interferon (IFN)-α by aerosol inhalation (5 million U twice daily) were included in the FPV arm of this study, whereas patients who were treated with LPV/RTV (Days 1–14: 400 mg/100 mg twice daily) plus IFN-α by aerosol inhalation (5 million U twice daily) were included in the control arm. Changes in chest computed tomography (CT), viral clearance, and drug safety were compared between the two groups. For the 35 patients enrolled in the FPV arm and the 45 patients in the control arm, all baseline characteristics were comparable between the two arms. A shorter viral clearance time was found for the FPV arm versus the control...
arm (median (interquartile range, IQR), 4 (2.5–9) d versus 11 (8–13) d, P < 0.001). The FPV arm also showed significant improvement in chest imaging compared with the control arm, with an improvement rate of 91.43% versus 62.22% (P = 0.004). After adjustment for potential confounders, the FPV arm also showed a significantly higher improvement rate in chest imaging. Multivariable Cox regression showed that FPV was independently associated with faster viral clearance. In addition, fewer adverse reactions were found in the FPV arm than in the control arm. In this open-label nonrandomized control study, FPV showed significantly better treatment effects on COVID-19 in terms of disease progression and viral clearance; if causal, these results should be important information for establishing standard treatment guidelines to combat the SARS-CoV-2 infection. © 2020


Real-time forecasts of the COVID-19 epidemic in China from February 5th to February 24th, 2020
(2020) Infectious Disease Modelling, 5, pp. 256-263.

Abstract:
The initial cluster of severe pneumonia cases that triggered the COVID-19 epidemic was identified in Wuhan, China in December 2019. While early cases of the disease were linked to a wet market, human-to-human transmission has driven the rapid spread of the virus throughout China. The Chinese government has implemented containment strategies of city-wide lockdowns, screening at airports and train stations, and isolation of suspected patients; however, the cumulative case count keeps growing every day. The ongoing outbreak presents a challenge for modelers, as limited data are available on the early growth trajectory, and the epidemiological characteristics of the novel coronavirus are yet to be fully elucidated. We use phenomenological models that have been validated during previous outbreaks to generate and assess short-term forecasts of the cumulative number of confirmed reported cases in Hubei province, the epicenter of the epidemic, and for the overall trajectory in China, excluding the province of Hubei. We collect daily reported cumulative confirmed cases for the 2019-nCoV outbreak for each Chinese province from the National Health Commission of China. Here, we provide 5, 10, and 15 day forecasts for five consecutive days, February 5th through February 9th, with quantified uncertainty based on a generalized logistic growth model, the Richards growth model, and a sub-epidemic wave model. Our most recent forecasts reported here, based on data up until February 9, 2020, largely agree across the three models presented and suggest an average range of 7409–7496 additional confirmed cases in Hubei and 1128–1929 additional cases in other provinces within the next five days. Models also predict an average total cumulative case count between 37,415 and 38,028 in Hubei and 11,588–13,499 in other provinces by February 24, 2020. Mean estimates and uncertainty bounds for both Hubei and other provinces have remained relatively stable in the last three reporting dates (February 7th – 9th). We also observe that each of the models predicts that the epidemic has reached saturation in both Hubei and other provinces. Our findings suggest that the containment strategies implemented in China are successfully reducing transmission and that the epidemic growth has slowed in recent days. © 2020 The Authors

Xie, J., Zhu, Y.

Association between ambient temperature and COVID-19 infection in 122 cities from China
(2020) Science of the Total Environment, 724, art. no. 138201

Abstract:
Background: Coronavirus disease 2019 (COVID-19) has become a severe public health problem globally. Both epidemiological and laboratory studies have shown that ambient temperature could affect the transmission and survival of coronaviruses. This study aimed to determine whether the temperature is an essential factor in the infection caused by this novel coronavirus. Methods: Daily confirmed cases and meteorological factors in 122 cities were collected between January 23, 2020,
to February 29, 2020. A generalized additive model (GAM) was applied to explore the nonlinear relationship between mean temperature and COVID-19 confirmed cases. We also used a piecewise linear regression to determine the relationship in detail. Results: The exposure-response curves suggested that the relationship between mean temperature and COVID-19 confirmed cases was approximately linear in the range of <3 °C and became flat above 3 °C. When mean temperature (lag0–14) was below 3 °C, each 1 °C rise was associated with a 4.861% (95% CI: 3.209–6.513) increase in the daily number of COVID-19 confirmed cases. These findings were robust in our sensitivity analyses. Conclusions: Our results indicate that mean temperature has a positive linear relationship with the number of COVID-19 cases with a threshold of 3 °C. There is no evidence supporting that case counts of COVID-19 could decline when the weather becomes warmer, which provides useful implications for policymakers and the public. © 2020 Elsevier B.V.

Wang, P., Chen, K., Zhu, S., Wang, P., Zhang, H.

**Severe air pollution events not avoided by reduced anthropogenic activities during COVID-19 outbreak**

(2020) Resources, Conservation and Recycling, 158, art. no. 104814

**Abstract:**

Due to the pandemic of coronavirus disease 2019 in China, almost all avoidable activities in China are prohibited since Wuhan announced lockdown on January 23, 2020. With reduced activities, severe air pollution events still occurred in the North China Plain, causing discussions regarding why severe air pollution was not avoided. The Community Multi-scale Air Quality model was applied during January 01 to February 12, 2020 to study PM2.5 changes under emission reduction scenarios. The estimated emission reduction case (Case 3) better reproduced PM2.5. Compared with the case without emission change (Case 1), Case 3 predicted that PM2.5 concentrations decreased by up to 20% with absolute decreases of 5.35, 6.37, 9.23, 10.25, 10.30, 12.14, 12.75, 14.41, 18.00 and 30.79 μg/m³ in Guangzhou, Shanghai, Beijing, Shijiazhuang, Tianjin, Jinan, Taiyuan, Xi’an, Zhengzhou, Wuhan, respectively. In high-pollution days with PM2.5 greater than 75 μg/m³, the reductions of PM2.5 in Case 3 were 7.78, 9.51, 11.38, 13.42, 13.64, 14.15, 14.42, 16.95 and 22.08 μg/m³ in Shanghai, Jinan, Shijiazhuang, Beijing, Taiyuan, Xi’an, Tianjin, Zhengzhou and Wuhan, respectively. The reductions in emissions of PM2.5 precursors were ~2 times of that in concentrations, indicating that meteorology was unfavorable during simulation episode. A further analysis shows that benefits of emission reductions were overwhelmed by adverse meteorology and severe air pollution events were not avoided. This study highlights that large emissions reduction in transportation and slight reduction in industrial would not help avoid severe air pollution in China, especially when meteorology is unfavorable. More efforts should be made to completely avoid severe air pollution. © 2020 Elsevier B.V.

Dargaville, T., Spann, K., Celina, M.

**Opinion to address the personal protective equipment shortage in the global community during the COVID-19 outbreak**

(2020) Polymer Degradation and Stability, 176, art. no. 109162

**Abstract:**

The current COVID-19 pandemic is stretching both the global supply for face masks and personal protective equipment (PPE). Production capacity is severely limited in many countries. This is a call for the R&D community, particularly to those in the polymer degradation and stability field. We have not only an opportunity but an obligation to engage and collaborate with virology and bio-medical experts. We require comparative R&D for extended, reuse and recyclability options. There is urgent need for large scale institutional approaches and methods that can be quickly applied locally by non-experts with limited resources. © 2020
Desjardins, M.R., Hohl, A., Delmelle, E.M.

Rapid surveillance of COVID-19 in the United States using a prospective space-time scan statistic: Detecting and evaluating emerging clusters
(2020) Applied Geography, 118, art. no. 102202

Abstract:
Coronavirus disease 2019 (COVID-19) was first identified in Wuhan, China in December 2019, and is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). COVID-19 is a pandemic with an estimated death rate between 1% and 5%; and an estimated R0 between 2.2 and 6.7 according to various sources. As of March 28th, 2020, there were over 649,000 confirmed cases and 30,249 total deaths, globally. In the United States, there were over 115,500 cases and 1891 deaths and this number is likely to increase rapidly. It is critical to detect clusters of COVID-19 to better allocate resources and improve decision-making as the outbreaks continue to grow. Using daily case data at the county level provided by Johns Hopkins University, we conducted a prospective spatial-temporal analysis with SaTScan. We detect statistically significant space-time clusters of COVID-19 at the county level in the U.S. between January 22nd-March 9th, 2020, and January 22nd-March 27th, 2020. The space-time prospective scan statistic detected “active” and emerging clusters that are present at the end of our study periods – notably, 18 more clusters were detected when adding the updated case data. These timely results can inform public health officials and decision makers about where to improve the allocation of resources, testing sites; also, where to implement stricter quarantines and travel bans. As more data becomes available, the statistic can be rerun to support timely surveillance of COVID-19, demonstrated here. Our research is the first geographic study that utilizes space-time statistics to monitor COVID-19 in the U.S. © 2020 The Authors

Zhang, C., Zheng, W., Huang, X., Bell, E.W., Zhou, X., Zhang, Y.
Protein Structure and Sequence Reanalysis of 2019-nCoV Genome Refutes Snakes as Its Intermediate Host and the Unique Similarity between Its Spike Protein Insertions and HIV-1

Abstract:
As the infection of 2019-nCoV coronavirus is quickly developing into a global pneumonia epidemic, the careful analysis of its transmission and cellular mechanisms is sorely needed. In this Communication, we first analyzed two recent studies that concluded that snakes are the intermediate hosts of 2019-nCoV and that the 2019-nCoV spike protein insertions share a unique similarity to HIV-1. However, the reimplementation of the analyses, built on larger scale data sets using state-of-the-art bioinformatics methods and databases, presents clear evidence that rebuts these conclusions. Next, using metagenomic samples from Manis javanica, we assembled a draft genome of the 2019-nCoV-like coronavirus, which shows 73% coverage and 91% sequence identity to the 2019-nCoV genome. In particular, the alignments of the spike surface glycoprotein receptor binding domain revealed four times more variations in the bat coronavirus RaTG13 than in the Manis coronavirus compared with 2019-nCoV, suggesting the pangolin as a missing link in the transmission of 2019-nCoV from bats to human.

Baker, E.N.
Visualizing an unseen enemy; mobilizing structural biology to counter COVID-19
Hua, J., Shaw, R.

Coronavirus (Covid-19) “infodemic” and emerging issues through a data lens: The case of China
(2020) International Journal of Environmental Research and Public Health, 17 (7), art. no. 2309

Abstract:
Coronavirus (COVID-19) is a humanitarian emergency, which started in Wuhan in China in early December 2019, brought into the notice of the authorities in late December, early January 2020, and, after investigation, was declared as an emergency in the third week of January 2020. The WHO declared this as Public Health Emergency of International Concern (PHEIC) on 31th of January 2020, and finally a pandemic on 11th March 2020. As of March 24th, 2020, the virus has caused a casualty of over 16,600 people worldwide with more than 380,000 people confirmed as infected by it, of which more than 10,000 cases are serious. Mainly based on Chinese newspapers, social media and other digital platform data, this paper analyzes the timeline of the key actions taken by the government and people over three months in five different phases. It found that although there was an initial delay in responding, a unique combination of strong governance, strict regulation, strong community vigilance and citizen participation, and wise use of big data and digital technologies, were some of the key factors in China’s efforts to combat this virus. Being inviable and non-measurable (unlike radioactive exposure), appropriate and timely information is very important to form the basic foundation of mitigation and curative measures. Infodemic, as it is termed by WHO, is a key word, where different stakeholder’s participation, along with stricter regulation, is required to reduce the impact of fake news in this information age and social media. Although different countries will need different approaches, focusing on its humanitarian nature and addressing infodemic issues are the two critical factors for future global mitigation efforts. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Khurstid, Z., Asiri, F.Y.I., Al Wadaani, H.

Human saliva: Non-invasive fluid for detecting novel coronavirus (2019-nCoV)
(2020) International Journal of Environmental Research and Public Health, 17 (7), art. no. 2225

Abstract:
The breakthrough of novel coronavirus (2019-nCoV) in Wuhan, a city of China, has damaged the status of health and quality of life. In the sequel of this epidemic or contagious disease, the patient experiences fever, chest paint, chills, a rapid heartbeat, breathing difficulties, pneumonia, and kidney failure. It has been suggested that this disease can spread through human-to-human transmission or by super spreading. By the help of the non-invasive fluid “saliva”, it is easy to detect the virus. This can help with the comfort of the patient as well as healthcare personnel. Under this perspective, we discuss the epidemic situation of 2019-nCOV and its relationship with human saliva. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Robson, B.

Computers and viral diseases. Preliminary bioinformatics studies on the design of a synthetic vaccine and a preventative peptidomimetic antagonist against the SARS-CoV-2 (2019-nCoV, COVID-19) coronavirus
(2020) Computers in Biology and Medicine, 119, art. no. 103670

Abstract:
This paper concerns study of the genome of the Wuhan Seafood Market isolate believed to represent the causative agent of the disease COVID-19. This is to find a short section or sections of viral protein sequence suitable for preliminary design proposal for a peptide synthetic vaccine and a peptidomimetic therapeutic, and to explore some design possibilities. The project was originally directed towards a use case for the Q-UEL language and its implementation in a knowledge management and automated inference system for medicine called the BioIngine, but
focus here remains mostly on the virus itself. However, using Q-UEL systems to access relevant and emerging literature, and to interact with standard publicly available bioinformatics tools on the Internet, did help quickly identify sequences of amino acids that are well conserved across many coronaviruses including 2019-nCoV. KRSFIEDLLFNKV was found to be particularly well conserved in this study and corresponds to the region around one of the known cleavage sites of the SARS virus that are believed to be required for virus activation for cell entry. This sequence motif and surrounding variations formed the basis for proposing a specific synthetic vaccine epitope and peptidomimetic agent. The work can, nonetheless, be described in traditional bioinformatics terms, and readily reproduced by others, albeit with the caveat that new data and research into 2019-nCoV is emerging and evolving at an explosive pace. Preliminary studies using molecular modeling and docking, and in that context the potential value of certain known herbal extracts, are also described. © 2020 Elsevier Ltd

Zhang, Y., Ma, Z.F.

**Impact of the COVID-19 Pandemic on Mental Health and Quality of Life among Local Residents in Liaoning Province, China: A Cross-Sectional Study**

(2020) International journal of environmental research and public health, 17 (7)

**Abstract:**

Our study aimed to investigate the immediate impact of the COVID-19 pandemic on mental health and quality of life among local Chinese residents aged ≥18 years in Liaoning Province, mainland China. An online survey was distributed through a social media platform between January and February 2020. Participants completed a modified validated questionnaire that assessed the Impact of Event Scale (IES), indicators of negative mental health impacts, social and family support, and mental health-related lifestyle changes. A total of 263 participants (106 males and 157 females) completed the study. The mean age of the participants was 37.7 ± 14.0 years, and 74.9% had a high level of education. The mean IES score in the participants was 13.6 ± 7.7, reflecting a mild stressful impact. Only 7.6% of participants had an IES score ≥26. The majority of participants (53.3%) did not feel helpless due to the pandemic. On the other hand, 52.1% of participants felt horrified and apprehensive due to the pandemic. Additionally, the majority of participants (57.8-77.9%) received increased support from friends and family members, increased shared feeling and caring with family members and others. In conclusion, the COVID-19 pandemic was associated with mild stressful impact in our sample, even though the COVID-19 pandemic is still ongoing. These findings would need to be verified in larger population studies.

Qin, L., Sun, Q., Wang, Y., Wu, K.-F., Chen, M., Shia, B.-C., Wu, S.-Y.

**Prediction of Number of Cases of 2019 Novel Coronavirus (COVID-19) Using Social Media Search Index**

(2020) International journal of environmental research and public health, 17 (7)

**Abstract:**

Predicting the number of new suspected or confirmed cases of novel coronavirus disease 2019 (COVID-19) is crucial in the prevention and control of the COVID-19 outbreak. Social media search indexes (SMXI) for dry cough, fever, chest distress, coronavirus, and pneumonia were collected from 31 December 2019 to 9 February 2020. The new suspected cases of COVID-19 data were collected from 20 January 2020 to 9 February 2020. We used the lagged series of SMXI to predict new suspected COVID-19 case numbers during this period. To avoid overfitting, five methods, namely subset selection, forward selection, lasso regression, ridge regression, and elastic net, were used to estimate coefficients. We selected the optimal method to predict new suspected COVID-19 case numbers from 20 January 2020 to 9 February 2020. We further validated the optimal method for new confirmed cases of COVID-19 from 31 December 2019 to 17 February 2020. The new suspected COVID-19 case numbers correlated significantly with the lagged series of SMXI. SMXI could be detected 6-9 days earlier than new suspected cases of COVID-19. The optimal method was the subset selection method, which had the lowest estimation error and a
The subset selection method also significantly correlated with the new confirmed COVID-19 cases after validation. SMSI findings on lag day 10 were significantly correlated with new confirmed COVID-19 cases. SMSI could be a significant predictor of the number of COVID-19 infections. SMSI could be an effective early predictor, which would enable governments' health departments to locate potential and high-risk outbreak areas.


Public Health Responses to COVID-19 Outbreaks on Cruise Ships - Worldwide, February-March 2020


Abstract:
An estimated 30 million passengers are transported on 272 cruise ships worldwide each year* (1). Cruise ships bring diverse populations into proximity for many days, facilitating transmission of respiratory illness (2). SARS-CoV-2, the virus that causes coronavirus disease (COVID-19) was first identified in Wuhan, China, in December 2019 and has since spread worldwide to at least 187 countries and territories. Widespread COVID-19 transmission on cruise ships has been reported as well (3). Passengers on certain cruise ship voyages might be aged ≥65 years, which places them at greater risk for severe consequences of SARS-CoV-2 infection (4). During February-March 2020, COVID-19 outbreaks associated with three cruise ship voyages have caused more than 800 laboratory-confirmed cases among passengers and crew, including 10 deaths. Transmission occurred across multiple voyages of several ships. This report describes public health responses to COVID-19 outbreaks on these ships. COVID-19 on cruise ships poses a risk for rapid spread of disease, causing outbreaks in a vulnerable population, and aggressive efforts are required to contain spread. All persons should defer all cruise travel worldwide during the COVID-19 pandemic.

Rong, X., Yang, L., Chu, H., Fan, M.

Effect of delay in diagnosis on transmission of COVID-19


Abstract:
The outbreak of COVID-19 caused by SARS-CoV-2 in Wuhan and other cities of China is a growing global concern. Delay in diagnosis and limited hospital resources lead to a rapid spread of COVID-19. In this study, we investigate the effect of delay in diagnosis on the disease transmission with a new formulated dynamic model. Sensitivity analyses and numerical simulations reveal that, improving the proportion of timely diagnosis and shortening the waiting time for diagnosis can not eliminate COVID-19 but can effectively decrease the basic reproduction number, significantly reduce the transmission risk, and effectively prevent the endemic of COVID-19, e.g., shorten the peak time and reduce the peak value of new confirmed cases and new infection, decrease the cumulative number of confirmed cases and total infection. More rigorous prevention measures and better treatment of patients are needed to control its further spread, e.g., increasing available hospital beds, shortening the period from symptom onset to isolation of patients, quarantining and isolating the suspected cases as well as all confirmed patients. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)
Zhou, W., Wang, A., Xia, F., Xiao, Y., Tang, S.

Effects of media reporting on mitigating spread of COVID-19 in the early phase of the outbreak

Abstract:
The 2019 novel coronavirus disease (COVID-19) is running rampant in China and is swiftly spreading to other countries in the world, which causes a great concern on the global public health. The absence of specific therapeutic treatment or effective vaccine against COVID-19 call for other avenues of the prevention and control measures. Media reporting is thought to be effective to curb the spreading of an emergency disease in the early stage. Cross-correlation analysis based on our collected data demonstrated a strong correlation between media data and the infection case data. Thus we proposed a deterministic dynamical model to examine the interaction of the disease progression and the media reports and to investigate the effectiveness of media reporting on mitigating the spread of COVID-19. The basic reproduction number was estimated as 5.3167 through parameterization of the model with the number of cumulative confirmed cases, the number of cumulative deaths and the daily number of media items. Sensitivity analysis suggested that, during the early phase of the COVID-19 outbreak, enhancing the response rate of the media reporting to the severity of COVID-19, and enhancing the response rate of the public awareness to the media reports, both can bring forward the peak time and reduce the peak size of the infection significantly. These findings suggested that besides improving the medical levels, media coverage can be considered as an effective way to mitigate the disease spreading during the initial stage of an outbreak. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)

Yin, F., Lv, J., Zhang, X., Xia, X., Wu, J.

COVID-19 information propagation dynamics in the Chinese Sina-microblog

Abstract:
The outbreak of a novel coronavirus (COVID-19) generated an outbreak of public opinions in the Chinese Sina-microblog. To help in designing effective communication strategies during a major public health emergency, we propose a multiple-information susceptible-discussing-immune (M-SDI) model in order to understand the patterns of key information propagation on social networks. We develop the M-SDI model, based on the public discussion quantity and take into account of the behavior that users may re-enter another related topic or Weibo after discussing one. Data fitting using the real data of COVID-19 public opinion obtained from Chinese Sina-microblog can parameterize the model to make accurate prediction of the public opinion trend until the next major news item occurs. The reproduction ratio has fallen from 1.7769 and maintained around 0.97, which reflects the peak of public opinion has passed but it will continue for a period of time. © 2020 the Author(s), licensee AIMS Press. This is an open access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0)

Li, S., Wang, Y., Xue, J., Zhao, N., Zhu, T.

The impact of covid-19 epidemic declaration on psychological consequences: A study on active weibo users
(2020) International Journal of Environmental Research and Public Health, 17 (6), art. no. 2032

Abstract:
COVID-19 (Corona Virus Disease 2019) has significantly resulted in a large number of psychological consequences. The aim of this study is to explore the impacts of COVID-19 on people’s mental health, to assist policy makers to develop actionable policies, and help clinical
practitioners (e.g., social workers, psychiatrists, and psychologists) provide timely services to affected populations. We sample and analyze the Weibo posts from 17,865 active Weibo users using the approach of Online Ecological Recognition (OER) based on several machine-learning predictive models. We calculated word frequency, scores of emotional indicators (e.g., anxiety, depression, indignation, and Oxford happiness) and cognitive indicators (e.g., social risk judgment and life satisfaction) from the collected data. The sentiment analysis and the paired sample t-test were performed to examine the differences in the same group before and after the declaration of COVID-19 on 20 January, 2020. The results showed that negative emotions (e.g., anxiety, depression and indignation) and sensitivity to social risks increased, while the scores of positive emotions (e.g., Oxford happiness) and life satisfaction decreased. People were concerned more about their health and family, while less about leisure and friends. The results contribute to the knowledge gaps of short-term individual changes in psychological conditions after the outbreak. It may provide references for policy makers to plan and fight against COVID-19 effectively by improving stability of popular feelings and urgently prepare clinical practitioners to deliver corresponding therapy foundations for the risk groups and affected people. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.


Tabletop exercise to prepare institutions of higher education for an outbreak of COVID-19

Abstract:
Preparing for public health emergencies is an ongoing process and involves a variety of approaches and tools. Tabletop exercises are one of the tools designed to simulate the emergence of a public health emergency and address some or all of the phases of emergency management: mitigation, preparedness, response, and recovery. They typically are designed to include participation of stakeholders from diverse and complementary backgrounds, including command, operations, logistics, planning, and finance. Effective tabletop exercises provide a plausible scenario that require cooperation and communication from these functional areas. Tabletops also require forward thinking and planning in a variety of scenarios. When a public health emergency occurs, decision makers may be overwhelmed with decisions that need their immediate attention. Tabletop exercises can provide a framework to help decision makers anticipate future challenges, which may provide the mental model encompassing knowledge and insights that inform both current and future decisions.

Zhao, S., Chen, H.

Modeling the epidemic dynamics and control of COVID-19 outbreak in China

Abstract:
Background: The coronavirus disease 2019 (COVID-19) is rapidly spreading in China and more than 30 countries over last two months. COVID-19 has multiple characteristics distinct from other infectious diseases, including high infectivity during incubation, time delay between real dynamics and daily observed number of confirmed cases, and the intervention effects of implemented quarantine and control measures. Methods: We develop a Susceptible, Un-quarantined infected, Quarantined infected, Confirmed infected (SUQC) model to characterize the dynamics of COVID-19 and explicitly parameterize the intervention effects of control measures, which is more suitable for analysis than other existing epidemic models. Results: The SUQC model is applied to the daily released data of the confirmed infections to analyze the outbreak of COVID-19 in Wuhan, Hubei (excluding Wuhan), China (excluding Hubei) and four first-tier cities of China. We found that, before January 30, 2020, all these regions except Beijing had a reproductive number $R > 1$, and
after January 30, all regions had a reproductive number $R < 1$, indicating that the quarantine and control measures are effective in preventing the spread of COVID-19. The confirmation rate of Wuhan estimated by our model is 0.0643, substantially lower than that of Hubei excluding Wuhan (0.1914), and that of China excluding Hubei (0.2189), but it jumps to 0.3229 after February 12 when clinical evidence was adopted in new diagnosis guidelines. The number of unquarantined infected cases in Wuhan on February 12, 2020 is estimated to be 3,509 and declines to 334 on February 21, 2020. After fitting the model with data as of February 21, 2020, we predict that the end time of COVID-19 in Wuhan and Hubei is around late March, around mid March for China excluding Hubei, and before early March 2020 for the four tier-one cities. A total of 80,511 individuals are estimated to be infected in China, among which 49,510 are from Wuhan, 17,679 from Hubei (excluding Wuhan), and the rest 13,322 from other regions of China (excluding Hubei). Note that the estimates are from a deterministic ODE model and should be interpreted with some uncertainty. Conclusions: We suggest that rigorous quarantine and control measures should be kept before early March in Beijing, Shanghai, Guangzhou and Shenzhen, and before late March in Hubei. The model can also be useful to predict the trend of epidemic and provide quantitative guide for other countries at high risk of outbreak, such as South Korea, Japan, Italy and Iran. [Figure not available: see fulltext.]. © 2020, Higher Education Press and Springer-Verlag GmbH Germany, part of Springer Nature.

Bianconi, A., Marcelli, A., Campi, G., Perali, A.

**Ostwald growth rate in controlled covid-19 epidemic spreading as in arrested growth in quantum complex matter**

(2020) Condensed Matter, 5 (2), art. no. 23

**Abstract:**

Here, we focus on the data analysis of the growth of epidemic spread of Covid-19 in countries where different policies of containment were activated. It is known that the growth of pandemic spread at its threshold is exponential, but it is not known how to quantify the success of different containment policies. We identify that a successful approach gives an arrested phase regime following the Ostwald growth, where, over the course of time, one phase transforms into another metastable phase with a similar free energy as observed in oxygen interstitial diffusion in quantum complex matter and in crystallization of proteins. We introduce the $s$ factor which provides a quantitative measure of the efficiency and speed of the adopted containment policy, which is very helpful not only to monitor the Covid-19 pandemic spread but also for other countries to choose the best containment policy. The results show that a policy based on joint confinement, targeted tests, and tracking positive cases is the most rapid pandemic containment policy; in fact, we found values of 9, 5, and 31 for the success $s$ factor for China, South Korea, and Italy, respectively, where the lowest $s$ factor indicates the best containment policy. © 2020 by the authors. Licensee MDPI, Basel, Switzerland.

Zhu, Y., Chen, Y.Q.

**On a Statistical Transmission Model in Analysis of the Early Phase of COVID-19 Outbreak**

(2020) Statistics in Biosciences

**Abstract:**

Since December 2019, a disease caused by a novel strain of coronavirus (COVID-19) had infected many people and the cumulative confirmed cases have reached almost 180,000 as of 17, March 2020. The COVID-19 outbreak was believed to have emerged from a seafood market in Wuhan, a metropolis city of more than 11 million population in Hubei province, China. We introduced a statistical disease transmission model using case symptom onset data to estimate the transmissibility of the early-phase outbreak in China, and provided sensitivity analyses with various assumptions of disease natural history of the COVID-19. We fitted the transmission model to several publicly available sources of the outbreak data until 11, February 2020, and estimated lock
down intervention efficacy of Wuhan city. The estimated $R$ was between 2.7 and 4.2 from plausible distribution assumptions of the incubation period and relative infectivity over the infectious period. 95% confidence interval of $R$ were also reported. Potential issues such as data quality concerns and comparison of different modelling approaches were discussed. © 2020, International Chinese Statistical Association.

Schwartz, S.A.
Climate Change, Covid-19, Preparedness, and Consciousness (2020) Explore

Nguyen, T., Bang, D.D., Wolff, A.
Abstract:
We believe a point-of-care (PoC) device for the rapid detection of the 2019 novel Coronavirus (SARS-CoV-2) is crucial and urgently needed. With this perspective, we give suggestions regarding a potential candidate for the rapid detection of the coronavirus disease 2019 (COVID-19), as well as factors for the preparedness and response to the outbreak of the COVID-19. © 2019 by the authors.

Pirouz, B., Haghshenas, S.S., Haghshenas, S.S., Piro, P.
Investigating a serious challenge in the sustainable development process: Analysis of confirmed cases of COVID-19 (new type of Coronavirus) through a binary classification using artificial intelligence and regression analysis (2020) Sustainability (United States), 12 (6), art. no. 2427
Abstract:
Nowadays, sustainable development is considered a key concept and solution in creating a promising and prosperous future for human societies. Nevertheless, there are some predicted and unpredicted problems that epidemic diseases are real and complex problems. Hence, in this research work, a serious challenge in the sustainable development process was investigated using the classification of confirmed cases of COVID-19 (new version of Coronavirus) as one of the epidemic diseases. Hence, binary classification modeling was used by the group method of data handling (GMDH) type of neural network as one of the artificial intelligence methods. For this purpose, the Hubei province in China was selected as a case study to construct the proposed model, and some important factors, namely maximum, minimum, and average daily temperature, the density of a city, relative humidity, and wind speed, were considered as the input dataset, and the number of confirmed cases was selected as the output dataset for 30 days. The proposed binary classification model provides higher performance capacity in predicting the confirmed cases. In addition, regression analysis has been done and the trend of confirmed cases compared with the fluctuations of daily weather parameters (wind, humidity, and average temperature). The results demonstrated that the relative humidity and maximum daily temperature had the highest impact on the confirmed cases. The relative humidity in the main case study, with an average of 77.9%, affected positively, and maximum daily temperature, with an average of 15.4 °C, affected negatively, the confirmed cases. © 2020 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).


Core Outcome Set for Clinical Trials on Coronavirus Disease 2019 (COS-COVID)
(2020) Engineering

Abstract:
Since its outbreak in December 2019, a series of clinical trials on Coronavirus Disease 2019 (COVID-19) have been registered or carried out. However, the significant heterogeneity and less critical outcomes of such trials may be leading to a waste of research resources. This study aimed to develop a core outcome set (COS) for clinical trials on COVID-19 in order to tackle the outcome issues. The study was conducted according to the Core Outcome Measures in Effectiveness Trials (COMET) handbook (version 1.0), a guideline for COS development. A research group was set up that included experts in respiratory and critical medicine, traditional Chinese medicine, evidence-based medicine, clinical pharmacology, and statistics, in addition to medical journal editors. Clinical trial registry websites (chictr.org.cn and clinicaltrials.gov) were searched to retrieve clinical trial protocols and outcomes in order to form an outcome pool. A total of 78 clinical trial protocols on COVID-19 were included and 259 outcomes were collected. After standardization, 132 outcomes were identified within seven different categories, of which 58 were selected to develop a preliminary outcome list for further consensus. After two rounds of Delphi survey and one consensus meeting, the most important outcomes for the different clinical classifications of COVID-19 were identified and determined to constitute the COS for clinical trials on COVID-19 (COS-COVID). The COS-COVID includes one outcome for the mild type (time to 2019-nCoV reverse transcription-polymerase chain reaction (RT-PCR) negativity), four outcomes for the ordinary type (length of hospital stay, composite events, score of clinical symptoms, and time to 2019-nCoV RT-PCR negativity), five outcomes for the severe type (composite events, length of hospital stay, arterial oxygen partial pressure (PaO2)/fraction of inspired oxygen (FiO2), duration of mechanical ventilation, and time to 2019-nCoV RT-PCR negativity), one outcome for critical type (all-cause mortality), and one outcome for rehabilitation period (pulmonary function). The COS-COVID is currently the most valuable and practical clinical outcome set for the evaluation of intervention effect, and is useful for evidence assessment and decision-making. With a deepening understanding of COVID-19 and application feedback, the COS-COVID should be continuously updated. © 2020

Roda, W.C., Varughese, M.B., Han, D., Li, M.Y.

Why is it difficult to accurately predict the COVID-19 epidemic?
(2020) Infectious Disease Modelling, 5, pp. 271-281.

Abstract:
Since the COVID-19 outbreak in Wuhan City in December of 2019, numerous model predictions on the COVID-19 epidemics in Wuhan and other parts of China have been reported. These model predictions have shown a wide range of variations. In our study, we demonstrate that nonidentifiability in model calibrations using the confirmed-case data is the main reason for such wide variations. Using the Akaike Information Criterion (AIC) for model selection, we show that an SIR model performs much better than an SEIR model in representing the information contained in the confirmed-case data. This indicates that predictions using more complex models may not be more reliable compared to using a simpler model. We present our model predictions for the COVID-19 epidemic in Wuhan after the lockdown and quarantine of the city on January 23, 2020. We also report our results of modeling the impacts of the strict quarantine measures undertaken in the city after February 7 on the time course of the epidemic, and modeling the potential of a second outbreak after the return-to-work in the city. © 2020 The Authors
Khan, M.A., Atangana, A.

Modeling the dynamics of novel coronavirus (2019-nCoV) with fractional derivative
(2020) Alexandria Engineering Journal

Abstract:
The present paper describes the mathematical modeling and dynamics of a novel coronavirus (2019-nCoV). We describe the brief details of interactions among the bats and unknown hosts, then among the peoples and the infections reservoir (seafood market). The seafood market is considered the main source of infection when the bats and the unknown hosts (may be wild animals) leave the infection there. The purchasing of items from the seafood market by peoples have the ability to infect either asymptotically or symptomatically. We reduced the model with the assumptions that the seafood market has enough source of infection that can be effective to infect people. We present the mathematical results of the model and then formulate a fractional model. We consider the available infection cases for January 21, 2020, till January 28, 2020 and parameterized the model. We compute the basic reproduction number for the data is \( R_0 \approx 2.4829 \). The fractional model is then solved numerically by presenting many graphical results, which can be helpful for the infection minimization. © 2020 Faculty of Engineering, Alexandria University

Kamel Boulos, M.N., Geraghty, E.M.

Geographical tracking and mapping of coronavirus disease COVID-19/severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic and associated events around the world: How 21st century GIS technologies are supporting the global fight against outbreaks and epidemics
(2020) International Journal of Health Geographics, 19 (1), art. no. 8

Abstract:
In December 2019, a new virus (initially called ‘Novel Coronavirus 2019-nCoV’ and later renamed to SARS-CoV-2) causing severe acute respiratory syndrome (coronavirus disease COVID-19) emerged in Wuhan, Hubei Province, China, and rapidly spread to other parts of China and other countries around the world, despite China’s massive efforts to contain the disease within Hubei. As with the original SARS-CoV epidemic of 2002/2003 and with seasonal influenza, geographic information systems and methods, including, among other application possibilities, online real or near-real-time mapping of disease cases and of social media reactions to disease spread, predictive risk mapping using population travel data, and tracing and mapping super-spreader trajectories and contacts across space and time, are proving indispensable for timely and effective epidemic monitoring and response. This paper offers pointers to, and describes, a range of practical online/mobile GIS and mapping dashboards and applications for tracking the 2019/2020 coronavirus epidemic and associated events as they unfold around the world. Some of these dashboards and applications are receiving data updates in near-real-time (at the time of writing), and one of them is meant for individual users (in China) to check if the app user has had any close contact with a person confirmed or suspected to have been infected with SARS-CoV-2 in the recent past. We also discuss additional ways GIS can support the fight against infectious disease outbreaks and epidemics. © The Author(s) 2020.

Zhang, T., He, Y., Xu, W., Ma, A., Yang, Y., Xu, K.-F.

Clinical trials for the treatment of Coronavirus disease 2019 (COVID-19): A rapid response to urgent need
(2020) Science China Life Sciences
**Predicting commercially available antiviral drugs that may act on the novel coronavirus (SARS-CoV-2) through a drug-target interaction deep learning model**  
**Abstract:**  
The infection of a novel coronavirus found in Wuhan of China (SARS-CoV-2) is rapidly spreading, and the incidence rate is increasing worldwide. Due to the lack of effective treatment options for SARS-CoV-2, various strategies are being tested in China, including drug repurposing. In this study, we used our pre-trained deep learning-based drug-target interaction model called Molecule Transformer-Drug Target Interaction (MT-DTI) to identify commercially available drugs that could act on viral proteins of SARS-CoV-2. The result showed that atazanavir, an antiretroviral medication used to treat and prevent the human immunodeficiency virus (HIV), is the best chemical compound, showing an inhibitory potency with Kd of 94.94 nM against the SARS-CoV-2 3C-like proteinase, followed by remdesivir (113.13 nM), efavirenz (199.17 nM), ritonavir (204.05 nM), and dolutegravir (336.91 nM). Interestingly, lopinavir, ritonavir, and darunavir are all designed to target viral proteinases. However, in our prediction, they may also bind to the replication complex components of SARS-CoV-2 with an inhibitory potency with Kd $< 1000$ nM. In addition, we also found that several antiviral agents, such as Kaletra (lopinavir/ritonavir), could be used for the treatment of SARS-CoV-2. Overall, we suggest that the list of antiviral drugs identified by the MT-DTI model should be considered, when establishing effective treatment strategies for SARS-CoV-2. © 2020 The Authors

**Investigation into SARS-CoV-2 Resistance of Compounds in Garlic Essential Oil**  
(2020) ACS Omega  
**Abstract:**  
Eighteen active substances, including 17 organosulfur compounds found in garlic essential oil (T), were identified by GC-MS analysis. For the first time, using the molecular docking technique, we report the inhibitory effect of the considered compounds on the host receptor angiotensin-converting enzyme 2 (ACE2) protein in the human body that leads to a crucial foundation about coronavirus resistance of individual compounds on the main protease (PDB6LU7) protein of SARS-CoV-2. The results show that the 17 organosulfur compounds, accounting for 99.4% contents of the garlic essential oil, have strong interactions with the amino acids of the ACE2 protein and the main protease PDB6LU7 of SARS-CoV-2. The strongest antiviral activity is expressed in allyl disulfide and allyl trisulfide, which account for the highest content in the garlic essential oil (51.3%). Interestingly, docking results indicate the synergistic interactions of the 17 substances, which exhibit good inhibition of the ACE2 and PDB6LU7 proteins. The results suggest that the garlic essential oil is a valuable natural antivirus source, which contributes to preventing the invasion of coronavirus into the human body. Copyright © 2020 American Chemical Society.
Ton, A.-T., Gentile, F., Hsing, M., Ban, F., Cherkasov, A.

Rapid Identification of Potential Inhibitors of SARS-CoV-2 Main Protease by Deep Docking of 1.3 Billion Compounds
(2020) Molecular Informatics

Abstract:
The recently emerged 2019 Novel Coronavirus (SARS-CoV-2) and associated COVID-19 disease cause serious or even fatal respiratory tract infection and yet no approved therapeutics or effective treatment is currently available to effectively combat the outbreak. This urgent situation is pressing the world to respond with the development of novel vaccine or a small molecule therapeutics for SARS-CoV-2. Along these efforts, the structure of SARS-CoV-2 main protease (Mpro) has been rapidly resolved and made publicly available to facilitate global efforts to develop novel drug candidates. Recently, our group has developed a novel deep learning platform – Deep Docking (DD) which provides fast prediction of docking scores of Glide (or any other docking program) and, hence, enables structure-based virtual screening of billions of purchasable molecules in a short time. In the current study we applied DD to all 1.3 billion compounds from ZINC15 library to identify top 1,000 potential ligands for SARS-CoV-2 Mpro protein. The compounds are made publicly available for further characterization and development by scientific community. © 2020 Wiley-VCH Verlag GmbH & Co. KGaA, Weinheim
Social Sciences:

- Arts and Humanities
- Business, Management, and accounting
- Decision Sciences
- Economics, Econometrics, and Finance
- Psychology
Lu, H.

**Drug treatment options for the 2019-new coronavirus (2019-nCoV)**


**Abstract:**
As of January 22, 2020, a total of 571 cases of the 2019-new coronavirus (2019-nCoV) have been reported in 25 provinces (districts and cities) in China. At present, there is no vaccine or antiviral treatment for human and animal coronavirus, so that identifying the drug treatment options as soon as possible is critical for the response to the 2019-nCoV outbreak. Three general methods, which include existing broad-spectrum antiviral drugs using standard assays, screening of a chemical library containing many existing compounds or databases, and the redevelopment of new specific drugs based on the genome and biophysical understanding of individual coronaviruses, are used to discover the potential antiviral treatment of human pathogen coronavirus. Lopinavir /Ritonavir, Nucleoside analogues, Neuraminidase inhibitors, Remdesivir, Peptide (EK1), arbidol, RNA synthesis inhibitors (such as TDF, 3TC), anti-inflammatory drugs (such as hormones and other molecules), Chinese traditional medicine, such ShuFengJieDu Capsules and Lianhuaqingwen Capsule, could be the drug treatment options for 2019-nCoV. However, the efficacy and safety of these drugs for 2019-nCoV still need to be further confirmed by clinical experiments. © 2020 International Advancement Center for Medicine and Health Research Co., Ltd.

CDC COVID-19 Response Team

**Severe Outcomes Among Patients with Coronavirus Disease 2019 (COVID-19) - United States, February 12-March 16, 2020**


**Abstract:**
Globally, approximately 170,000 confirmed cases of coronavirus disease 2019 (COVID-19) caused by the 2019 novel coronavirus (SARS-CoV-2) have been reported, including an estimated 7,000 deaths in approximately 150 countries (1). On March 11, 2020, the World Health Organization declared the COVID-19 outbreak a pandemic (2). Data from China have indicated that older adults, particularly those with serious underlying health conditions, are at higher risk for severe COVID-19-associated illness and death than are younger persons (3). Although the majority of reported COVID-19 cases in China were mild (81%), approximately 80% of deaths occurred among adults aged ≥60 years; only one (0.1%) death occurred in a person aged ≤19 years (3). In this report, COVID-19 cases in the United States that occurred during February 12-March 16, 2020 and severity of disease (hospitalization, admission to intensive care unit [ICU], and death) were analyzed by age group. As of March 16, a total of 4,226 COVID-19 cases in the United States had been reported to CDC, with multiple cases reported among older adults living in long-term care facilities (4). Overall, 31% of cases, 45% of hospitalizations, 53% of ICU admissions, and 80% of deaths associated with COVID-19 were among adults aged ≥65 years with the highest percentage of severe outcomes among persons aged ≥85 years. In contrast, no ICU admissions or deaths were reported among persons aged ≤19 years. Similar to reports from other countries, this finding suggests that the risk for serious disease and death from COVID-19 is higher in older age groups.

Ivanov, D.

**Predicting the impacts of epidemic outbreaks on global supply chains: A simulation-based analysis on the coronavirus outbreak (COVID-19/SARS-CoV-2) case**

(2020) *Transportation Research Part E: Logistics and Transportation Review*, 136, art. no. 101922,
Abstract:
Epidemic outbreaks are a special case of supply chain (SC) risks which is distinctively characterized by a long-term disruption existence, disruption propagations (i.e., the ripple effect), and high uncertainty. We present the results of a simulation study that opens some new research tensions on the impact of COVID-19 (SARS-CoV-2) on the global SCs. First, we articulate the specific features that frame epidemic outbreaks as a unique type of SC disruption risks. Second, we demonstrate how simulation-based methodology can be used to examine and predict the impacts of epidemic outbreaks on the SC performance using the example of coronavirus COVID-19 and anyLogistix simulation and optimization software. We offer an analysis for observing and predicting both short-term and long-term impacts of epidemic outbreaks on the SCs along with managerial insights. A set of sensitivity experiments for different scenarios allows illustrating the model's behavior and its value for decision-makers. The major observation from the simulation experiments is that the timing of the closing and opening of the facilities at different echelons might become a major factor that determines the epidemic outbreak impact on the SC performance rather than an upstream disruption duration or the speed of epidemic propagation. Other important factors are lead-time, speed of epidemic propagation, and the upstream and downstream disruption durations in the SC. The outcomes of this research can be used by decision-makers to predict the operative and long-term impacts of epidemic outbreaks on the SCs and develop pandemic SC plans. Our approach can also help to identify the successful and wrong elements of risk mitigation/preparedness and recovery policies in case of epidemic outbreaks. The paper is concluded by summarizing the most important insights and outlining future research agenda. © 2020 Elsevier Ltd

Ng, Y., Li, Z., Chua, Y.X., Chaw, W.L., Zhao, Z., Er, B., Pung, R., Chiew, C.J., Lye, D.C., Heng, D., Lee, V.J.


Abstract:
What is already known about this topic? First detected in China in late 2019, coronavirus disease 2019 (COVID-19) transmission has spread globally. What is added by this report? Singapore implemented a multipronged surveillance and containment strategy that contributed to enhanced case ascertainment and slowing of the outbreak. Based on review of the first 100 cases, the mean interval from symptom onset to isolation was 5.6 days and declined after approximately 1 month. What are the implications for public health practice? A multipronged surveillance strategy could lead to enhanced case detection and reduced transmission of highly infectious diseases such as COVID-19. © 2020 Department of Health and Human Services. All rights reserved.


Abstract:
In December 2019, an outbreak of coronavirus disease 2019 (COVID-19), caused by the virus SARS-CoV-2, began in Wuhan, China (1). The disease spread widely in China, and, as of February 26, 2020, COVID-19 cases had been identified in 36 other countries and territories, including the United States. Person-to-person transmission has been widely documented, and a limited number of countries have reported sustained person-to-person spread.* On January 20, state and local health departments in the United States, in collaboration with teams deployed from CDC, began identifying and monitoring all persons considered to have had close contact† with patients with confirmed COVID-19 (2). The aims of these efforts were to ensure rapid evaluation and care of patients, limit further transmission, and better understand risk factors for transmission.
Wang, P., Chen, K., Zhu, S., Wang, P., Zhang, H.  
**Severe air pollution events not avoided by reduced anthropogenic activities during COVID-19 outbreak**  
(2020) *Resources, Conservation and Recycling*, 158, art. no. 104814  
*Abstract:*  
Due to the pandemic of coronavirus disease 2019 in China, almost all avoidable activities in China are prohibited since Wuhan announced lockdown on January 23, 2020. With reduced activities, severe air pollution events still occurred in the North China Plain, causing discussions regarding why severe air pollution was not avoided. The Community Multi-scale Air Quality model was applied during January 01 to February 12, 2020 to study PM2.5 changes under emission reduction scenarios. The estimated emission reduction case (Case 3) better reproduced PM2.5. Compared with the case without emission change (Case 1), Case 3 predicted that PM2.5 concentrations decreased by up to 20% with absolute decreases of 5.35, 6.37, 9.23, 10.25, 10.30, 12.14, 12.75, 14.41, 18.00 and 30.79 μg/m³ in Guangzhou, Shanghai, Beijing, Shijiazhuang, Tianjin, Jinan, Taiyuan, Xi'an, Zhengzhou, Wuhan, respectively. In high-pollution days with PM2.5 greater than 75 μg/m³, the reductions of PM2.5 in Case 3 were 7.78, 9.51, 11.38, 13.42, 13.64, 14.15, 14.42, 16.95 and 22.08 μg/m³ in Shanghai, Jinan, Shijiazhuang, Beijing, Taiyuan, Xi'an, Tianjin, Zhengzhou and Wuhan, respectively. The reductions in emissions of PM2.5 precursors were ~2 times of that in concentrations, indicating that meteorology was unfavorable during simulation episode. A further analysis shows that benefits of emission reductions were overwhelmed by adverse meteorology and severe air pollution events were not avoided. This study highlights that large emissions reduction in transportation and slight reduction in industrial would not help avoid severe air pollution in China, especially when meteorology is unfavorable. More efforts should be made to completely avoid severe air pollution. © 2020 Elsevier B.V.

**Study of knowledge, attitude, anxiety & perceived mental healthcare need in Indian population during COVID-19 pandemic**  
(2020) *Asian Journal of Psychiatry*, 51, art. no. 102083  
*Abstract:*  
Novel Corona Virus Disease (COVID-19) originating from China has rapidly crossed borders, infecting people throughout the whole world. This phenomenon has led to a massive public reaction; the media has been reporting continuously across borders to keep all informed about the pandemic situation. All these things are creating a lot of concern for people leading to heightened levels of anxiety. Pandemics can lead to heightened levels of stress; Anxiety is a common response to any stressful situation. This study attempted to assess the knowledge, attitude, anxiety experience, and perceived mental healthcare need among adult Indian population during the COVID-19 pandemic. An online survey was conducted using a semi-structured questionnaire using a non-probability snowball sampling technique. A total of 662 responses were received. The responders had a moderate level of knowledge about the COVID-19 infection and adequate knowledge about its preventive aspects. The attitude towards COVID-19 showed peoples' willingness to follow government guidelines on quarantine and social distancing. The anxiety levels identified in the study were high. More than 80 % of the people were preoccupied with the thoughts of COVID-19 and 72 % reported the need to use gloves, and sanitizers. In this study, sleep difficulties, paranoia about acquiring COVID-19 infection and distress related social media were reported in 12.5 %, 37.8 %, and 36.4 % participants respectively. The perceived mental healthcare need was seen in more than 80 % of participants. There is a need to intensify the awareness and address the mental health issues of people during this COVID-19 pandemic. © 2020 Elsevier B.V.
Desjardins, M.R., Hohl, A., Delmelle, E.M.

**Rapid surveillance of COVID-19 in the United States using a prospective space-time scan statistic: Detecting and evaluating emerging clusters**

*(2020) Applied Geography, 118, art. no. 102202*

**Abstract:**

Coronavirus disease 2019 (COVID-19) was first identified in Wuhan, China in December 2019, and is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). COVID-19 is a pandemic with an estimated death rate between 1% and 5%; and an estimated R0 between 2.2 and 6.7 according to various sources. As of March 28th, 2020, there were over 649,000 confirmed cases and 30,249 total deaths, globally. In the United States, there were over 115,500 cases and 1891 deaths and this number is likely to increase rapidly. It is critical to detect clusters of COVID-19 to better allocate resources and improve decision-making as the outbreaks continue to grow. Using daily case data at the county level provided by Johns Hopkins University, we conducted a prospective spatial-temporal analysis with SaTScan. We detect statistically significant space-time clusters of COVID-19 at the county level in the U.S. between January 22nd-March 9th, 2020, and January 22nd-March 27th, 2020. The space-time prospective scan statistic detected “active” and emerging clusters that are present at the end of our study periods – notably, 18 more clusters were detected when adding the updated case data. These timely results can inform public health officials and decision makers about where to improve the allocation of resources, testing sites; also, where to implement stricter quarantines and travel bans. As more data becomes available, the statistic can be rerun to support timely surveillance of COVID-19, demonstrated here. Our research is the first geographic study that utilizes space-time statistics to monitor COVID-19 in the U.S. © 2020 The Authors


**Public Health Responses to COVID-19 Outbreaks on Cruise Ships - Worldwide, February-March 2020**


**Abstract:**

An estimated 30 million passengers are transported on 272 cruise ships worldwide each year* (1). Cruise ships bring diverse populations into proximity for many days, facilitating transmission of respiratory illness (2). SARS-CoV-2, the virus that causes coronavirus disease (COVID-19) was first identified in Wuhan, China, in December 2019 and has since spread worldwide to at least 187 countries and territories. Widespread COVID-19 transmission on cruise ships has been reported as well (3). Passengers on certain cruise ship voyages might be aged ≥65 years, which places them at greater risk for severe consequences of SARS-CoV-2 infection (4). During February-March 2020, COVID-19 outbreaks associated with three cruise ship voyages have caused more than 800 laboratory-confirmed cases among passengers and crew, including 10 deaths. Transmission occurred across multiple voyages of several ships. This report describes public health responses to COVID-19 outbreaks on these ships. COVID-19 on cruise ships poses a risk for rapid spread of disease, causing outbreaks in a vulnerable population, and aggressive efforts are required to contain spread. All persons should defer all cruise travel worldwide during the COVID-19 pandemic.

**Tabletop exercise to prepare institutions of higher education for an outbreak of COVID-19**


**Abstract:**
Preparing for public health emergencies is an ongoing process and involves a variety of approaches and tools. Tabletop exercises are one of the tools designed to simulate the emergence of a public health emergency and address some or all of the phases of emergency management: mitigation, preparedness, response, and recovery. They typically are designed to include participation of stakeholders from diverse and complementary backgrounds, including command, operations, logistics, planning, and finance. Effective tabletop exercises provide a plausible scenario that require cooperation and communication from these functional areas. Tabletops also require forward thinking and planning in a variety of scenarios. When a public health emergency occurs, decision makers may be overwhelmed with decisions that need their immediate attention. Tabletop exercises can provide a framework to help decision makers anticipate future challenges, which may provide the mental model encompassing knowledge and insights that inform both current and future decisions.

Gostin, L.O., Friedman, E.A., Wetter, S.A.

**Responding to COVID-19: How to Navigate a Public Health Emergency Legally and Ethically**

(2020) *Hastings Center Report*

**Abstract:**
Few novel or emerging infectious diseases have posed such vital ethical challenges so quickly and dramatically as the novel coronavirus SARS-CoV-2. The World Health Organization declared a public health emergency of international concern and recently classified COVID-19 as a worldwide pandemic. As of this writing, the epidemic has not yet peaked in the United States, but community transmission is widespread. President Trump declared a national emergency as fifty governors declared state emergencies. In the coming weeks, hospitals will become overrun, stretched to their capacities. When the health system becomes stretched beyond capacity, how can we ethically allocate scarce health goods and services? How can we ensure that marginalized populations can access the care they need? What ethical duties do we owe to vulnerable people separated from their families and communities? And how do we ethically and legally balance public health with civil liberties?. © 2020 The Hastings Center

Ali, I.

**The COVID-19 Pandemic: Making Sense of Rumor and Fear: Op-Ed**

(2020) *Medical Anthropology: Cross Cultural Studies in Health and Illness*

Raffaeà, R.

**Another Day in Dystopia. Italy in the Time of COVID-19**

(2020) *Medical Anthropology: Cross Cultural Studies in Health and Illness*

van Staden, C.

**COVID-19 and the crisis of national development**

(2020) *Nature Human Behaviour*

Pirouz, B., Haghshenas, S.S., Haghshenas, S.S., Piro, P.

**Investigating a serious challenge in the sustainable development process: Analysis of confirmed cases of COVID-19 (new type of Coronavirus) through a binary classification using artificial intelligence and regression analysis**

(2020) *Sustainability (United States)*, 12 (6), art. no. 2427
Abstract:
Nowadays, sustainable development is considered a key concept and solution in creating a promising and prosperous future for human societies. Nevertheless, there are some predicted and unpredicted problems that epidemic diseases are real and complex problems. Hence, in this research work, a serious challenge in the sustainable development process was investigated using the classification of confirmed cases of COVID-19 (new version of Coronavirus) as one of the epidemic diseases. Hence, binary classification modeling was used by the group method of data handling (GMDH) type of neural network as one of the artificial intelligence methods. For this purpose, the Hubei province in China was selected as a case study to construct the proposed model, and some important factors, namely maximum, minimum, and average daily temperature, the density of a city, relative humidity, and wind speed, were considered as the input dataset, and the number of confirmed cases was selected as the output dataset for 30 days. The proposed binary classification model provides higher performance capacity in predicting the confirmed cases. In addition, regression analysis has been done and the trend of confirmed cases compared with the fluctuations of daily weather parameters (wind, humidity, and average temperature). The results demonstrated that the relative humidity and maximum daily temperature had the highest impact on the confirmed cases. The relative humidity in the main case study, with an average of 77.9%, affected positively, and maximum daily temperature, with an average of 15.4 °C, affected negatively, the confirmed cases. © 2020 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (http://creativecommons.org/licenses/by/4.0/).


Abstract:
Background: As COVID-19 occurs suddenly and is highly contagious, this will inevitably cause people anxiety, depression, etc. The study on the public psychological states and its related factors during the COVID-19 outbreak is of practical significance. Methods: 600 valid questionnaires were received. The Self-Rating Anxiety Scale (SAS) and the Self-Rating Depression Scale (SDS) were used. Results: Females’ anxiety risk was 3.01 times compared to males (95% CI 1.39–6.52). Compared with people below 40 years old, the anxiety risk of people above 40 years old was 0.40 times (95% CI 0.16–0.99). SDS results indicated that the difference between education level and occupation was statistically significant (p = 0.024, 0.005). Compared to people with a master’s degree or above, those with a bachelor’s degree group had a depression risk of 0.39 times (95% CI 0.17–0.87). Compared with professionals, industrial service workers and other staff had a depression risk of 0.31 times (95% CI 0.15–0.65) and 0.38 times (95% CI 0.15–0.93). Conclusions: 600 questionnaire participants were psychologically stable. Non-anxiety and non-depression rates were 93.67% and 82.83%, respectively, There were anxiety in 6.33% and depression in 17.17%. Therefore, we should pay attention to the psychological states of the public. © 2020, © 2020 Informa UK Limited, trading as Taylor & Francis Group.

Abstract:
We present the case of the outbreak and containment of COVID-19 in its early stage and analyze the causes for conservative judgment of the disease control experts who are blamed for delayed action and inadequate response by the government. We find that the disease control experts have a clear tendency and preference to make conservative judgment about the epidemic risk of a low probability and high impact new disease. This conservative preference may have been a major factor in the judging and communicating the risk of COVID-19 epidemic. The experts’ perception of the epidemic risk is affected by their habitual thinking facing a low probability event with uncertain progression. Their conservative preference is augmented by political concerns due to the high social and political impact of the event and the potential political consequence of a false judgment. Balancing personal payoffs of decision options, the experts’ rational choice would lean towards a conservative decision. We propose a three-factor decision model that integrates habitual thinking, political concerns and rational choice to explain the experts’ conservative judgment, and corroborate the model with evidences from the case. We conclude the paper with policy implications for improving experts’ role in public health emergency response. © 2020, © 2020 Zhejiang University.

French, M., Monahan, T.
Disease surveillance: how might surveillance studies address covid-19?
Abstract:
We are currently in the midst of a global pandemic with the spread of Coronavirus Disease 2019 (COVID-19). While we do not know how this situation will unfold or resolve, we do have insight into how it fits within existing patterns and relations, particularly those pertaining to sociocultural constructions of (in)security, vulnerability, and risk. We can see evidence of surveillance dynamics at play with how bodies and pathogens are being measured, tracked, predicted, and regulated. We can grasp how threat is being racialized, how and why institutions are flailing, and how social media might be fueling social divisions. There is, in other words, a lot that our scholarly community could add to the conversation. In this rapid-response editorial, we provide an introduction to the framing devices of disease surveillance and discuss how a surveillance studies orientation could help us think critically about the present crisis and its possible aftermath. © The author(s), 2020.

Song, P., Karako, T.
COVID-19: Real-time dissemination of scientific information to fight a public health emergency of international concern
(2020) BioScience Trends, 14 (1), art. no. 1056
Abstract:
Rapidly sharing scientific information is an effective way to reduce public panic about COVID-19, and doing so is the key to providing real-time guidance to epidemiologists working to contain the outbreak, clinicians managing patients, and modelers helping to understand future developments and the possible effectiveness of various interventions. This issue has rapidly reviewed and published articles describing COVID-19, including the drug treatment options for SARS-CoV-2, its clinical characteristics, and therapies involving a combination of Chinese and Western medicine, the efficacy of chloroquine phosphate in the treatment of COVID-19 associated pneumonia according to clinical studies, and reflections on the system of reserve medical supplies for public health emergencies. As an academic journal, we will continue to quickly and transparently share data with frontline healthcare workers who need to know the epidemiological and clinical features of COVID-19. © 2020 International Advancement Center for Medicine and Health Research Co., Ltd.

Kamel Boulos, M.N., Geraghty, E.M.
Geographical tracking and mapping of coronavirus disease COVID-19/severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic and
associated events around the world: How 21st century GIS technologies are supporting the global fight against outbreaks and epidemics

(2020) *International Journal of Health Geographics*, 19 (1), art. no. 8

**Abstract:**

In December 2019, a new virus (initially called ‘Novel Coronavirus 2019-nCoV’ and later renamed to SARS-CoV-2) causing severe acute respiratory syndrome (coronavirus disease COVID-19) emerged in Wuhan, Hubei Province, China, and rapidly spread to other parts of China and other countries around the world, despite China’s massive efforts to contain the disease within Hubei. As with the original SARS-CoV epidemic of 2002/2003 and with seasonal influenza, geographic information systems and methods, including, among other application possibilities, online real-or near-real-time mapping of disease cases and of social media reactions to disease spread, predictive risk mapping using population travel data, and tracing and mapping super-spreader trajectories and contacts across space and time, are proving indispensable for timely and effective epidemic monitoring and response. This paper offers pointers to, and describes, a range of practical online/mobile GIS and mapping dashboards and applications for tracking the 2019/2020 coronavirus epidemic and associated events as they unfold around the world. Some of these dashboards and applications are receiving data updates in near-real-time (at the time of writing), and one of them is meant for individual users (in China) to check if the app user has had any close contact with a person confirmed or suspected to have been infected with SARS-CoV-2 in the recent past. We also discuss additional ways GIS can support the fight against infectious disease outbreaks and epidemics. © The Author(s) 2020.

Wang, X., Zhang, X., He, J.

**Challenges to the system of reserve medical supplies for public health emergencies: Reflections on the outbreak of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) epidemic in China**


**Abstract:**

On December 31, 2019, the Wuhan Municipal Health Commission announced an outbreak of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), China is now at a critical period in the control of the epidemic. The Chinese Government has been taking a series of rapid, comprehensive, and effective prevention and control measures. As the pandemic has developed, a fact has become apparent: there is a serious dearth of emergency medical supplies, and especially an extreme shortage of personal protective equipment such as masks and medical protective clothing. This is one of the major factors affecting the progress of epidemic prevention and control. Although China has made great efforts to strengthen the ability to quickly respond to public health emergencies since the SARS outbreak in 2003 and it has clarified requirements for emergency supplies through legislation, the emergency reserve supplies program has not been effectively implemented, and there are also deficiencies in the types, quantity, and availability of emergency medical supplies. A sound system of emergency reserve supplies is crucial to the management of public health emergencies. Based on international experiences with pandemic control, the world should emphasize improving the system of emergency reserve medical supplies in the process of establishing and improving public health emergency response systems, and it should promote the establishment of international cooperative programs to jointly deal with public health emergencies of international concern in the future.