## EVIDENCE SEARCH REPORT

**RESEARCH QUESTION:**
What is the relationship between antibody development and viral shedding and infectiousness?

**UNIQUE IDENTIFIER:** LAB041601v2-01 ESR

**REQUESTED RESOURCES:**
- medRxiv
- CDC website/database
- Europe PMC
- Google
- Google Scholar
- Medline
- PubMed
- WHO Global Research on COVID-19
- PHAC COVID-19

**LIMITS/EXCLUSIONS/INCLUSIONS:**
- English, since 2020

**DATE:** May 22, 2020

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**CITE AS:**

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Updated May 22, 2020

Originally run on April 15th, 2020

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SUMMARIES, GUIDELINES & OTHER RESOURCES

Clinical Evidence

None

Recommendations


In December 2019 a novel coronavirus (2019-nCoV) was identified as the causative agent of a severe acute respiratory illness among people exposed in a seafood market in Wuhan, China. Human-to-human transmission has been documented, including in healthcare workers, and aerosol-generating procedures (AGP)† may play a role in the spread of the disease. There are uncertainties in the natural history of the 2019-nCoV, including source(s), transmissibility mechanisms, viral shedding, and persistence of the virus in the environment and on fomites. As of 6 February 2020, the following precautions are recommended for the care of patients with suspected or confirmed cases of 2019-nCoV: For any suspected or confirmed cases of 2019-nCoV: standard + contact + droplet precautions; for any suspected or confirmed cases of 2019-nCoV and AGP: standard + contact + airborne precautions. The use of personal protective equipment (PPE) by healthcare workers requires an evaluation of the risk related to healthcare-related activities. These recommendations are preliminary and subject to review as new evidence becomes available.

URL: https://iris.paho.org/handle/10665.2/51906

Grey Literature

None

ARTICLES FROM LIBRARY DATABASES

Note: References are sorted by year (newest to oldest)

Medline – May 15, 2020, 1:38pm

Journal articles


ABSTRACT: The "novel" coronavirus disease 2019 (abbreviated "COVID-19") is the third coronavirus outbreak emerging during the past two decades. This infectious disease, sustained by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), has been recently declared a global pandemic by the World Health Organization. Despite the concerning epidemiological burden, many people, including some policymakers, are underestimating this pandemic and are remaining enigmatically inactive against a human pathology which, for a combination of reasons, can be reasonably defined as a perfect storm.
(i.e., the "wrong virus" at the "wrong time"). These many paradigmatic aspects include SARS-CoV-2 structure and peculiar biology of infection, high risk of inter-human transmission, long incubation time combined with early and sustained viral load, existence of asymptomatic or mildly-symptomatic carriers, viral shedding for days after symptom relief, unfavorable progression towards respiratory distress and death in up to 5-10% of patients thus causing dramatic healthcare challenges, as well as environmental contamination. Last but not least, the combination of the current case fatality rate with the extraordinary number of people that could be potentially infected by SARS-CoV-2 would permit to estimate that the worldwide deaths for COVID-19 may even approximate those recorded during World War II if appropriate restrictive measures for preventing human-to-human transmission are not readily undertaken. Everybody should be inexcusably aware that this is not a drill, and that the consequences of inadequate action will be tragedy.

URL: http://atm.amegroups.com/article/view/38768/html

PubMed – May 8, 2020, 5:42am

Journal articles


ABSTRACT: BACKGROUND: Information regarding viral shedding in children with coronavirus disease 2019 (COVID-19) was limited. This study aims to investigate the clinical and laboratory characteristics associated with viral shedding in children with mild COVID-19. METHODS: The clinical and laboratory information of 110 children with COVID-19 at Wuhan Children's Hospital, Wuhan, China, from January 30 to March 10, 2020, were analyzed retrospectively. RESULTS: The median age was 6 years old. The median period of viral shedding of COVID-19 was 15 days (interquartile range [IQR], 11-20 days) as measured from illness onset to discharge. This period was shorter in asymptomatic patients (26.4%) compared with symptomatic patients (73.6%) (11 days vs. 17 days). Multivariable regression analysis showed increased odds of symptomatic infection was associated with age <6 years (odds ratio [OR] 8.94, 95% confidence interval [CI]: 2.55-31.35; P = 0.001), hypersensitive C-reactive protein >3.0 mg/L (OR 4.89; 95% CI: 1.10-21.75; P = 0.037) and presenting pneumonia in chest radiologic findings (OR 8.45; 95% CI: 2.69-26.61; P < 0.001). Kaplan-Meier analysis displayed symptomatic infection (P < 0.001), fever (P = 0.006), pneumonia (P = 0.003) and lymphocyte counts <2.0 x 10/L (P = 0.008) in children with COVID-19 were associated with prolonged duration of viral shedding in children with COVID-19. CONCLUSION: Prolonged duration of viral shedding in children with COVID-19 was associated with symptomatic infection, fever, pneumonia and lymphocyte count =2.0 x 10/L. Monitoring of symptoms could help to know the viral shedding in children with COVID-19.

URL: https://oce-ovid-com.shal.idm.oclc.org/article/0006454-900000000-96181/HTML
DOI: 10.1097/inf.0000000000002729

PubMed – May 1, 2020, 5:34am
Journal articles


ABSTRACT: A few studies have reported the long shedding of SARS-CoV-2 RNA. However, the duration of RNA shedding in Wuhan is rarely known and the meaning of the prolonged shedding is still under investigation. Almost 10% patients diagnosed of COVID-19 had a RNA shedding longer than 30 days even if the symptom elimination. The IgM was in a high level in the 9(th) week after symptom onset in these prolonged-RNA-shedding patients. Further study should be conducted to know the infectivity of the virus and the relationship between RNA shedding and antibody expression. This article is protected by copyright. All rights reserved.

DOI: 10.1002/jmv.25952


ABSTRACT: As an emerging infectious disease, the clinical course and virological course of SARS-CoV-2 infection remain to be further investigated. In this case report, we described a case of SARS-CoV-2 infection with clinical course more than two months. This patient had recovered from the pneumonia after treatment. The viral RNA of throat swabs became negative and the viral specific antibodies were produced during recovery period. However, the viral RNA reappeared and additionally persisted in throat swabs for more than 40 days. In addition, the viral RNA was detected in multiple types of specimens with extremely high titers in the saliva. In conclusion, these findings indicate that SARS-CoV-2 can cause a long clinical course. The coexistence of viral RNA and viral specific antibodies may imply an immune evasion of SARS-CoV-2 from host’s immune system. This article is protected by copyright. All rights reserved.

DOI: 10.1002/jmv.25940

April 15, 2020

Pre-printed articles


URL: https://ClinicalTrials.gov/show/NCT04333472


Background: Coronavirus disease 2019 (COVID-19), caused by the virus SARS-CoV-2, is spreading rapidly across the globe, with no proven effective therapy. Fever is seen in most cases of COVID-19, at least at the initial stages of illness. Although fever is typically treated (with antipyretics or directly with ice or other mechanical means), increasing data suggest that fever is a protective adaptive response that facilitates recovery from infectious illness. Objective: To describe a randomized controlled pilot study of core warming patients with COVID-19 undergoing mechanical ventilation. Methods: This prospective single-site randomized controlled pilot study will enroll 20 patients undergoing mechanical ventilation for respiratory failure due to COVID-19. Patients will be randomized 1:1 to standard-of-care or to receive
core warming via an esophageal heat exchanger commonly utilized in critical care and surgical patients. The primary outcome is the severity of acute respiratory distress syndrome (as measured by PaO2/FiO2 ratio) 24 hours after initiation of treatment. Secondary outcomes include hospital and intensive care unit length of stay, duration of mechanical ventilation, amount of viral shedding, and 30-day mortality.

Results: Resulting data will provide effect size estimates to guide a definitive multi-center randomized clinical trial. ClinicalTrials.gov registration number: pending. Conclusions: With growing data to support clinical benefits of elevated temperature in infectious illness, this study will provide data to guide further understanding of the role of active temperature management in COVID-19 treatment and provide effect size estimates to power larger studies.


Background: Controlling the transmission of respiratory infections such as influenza and COVID-19 is a critical public health priority. Non-pharmaceutical intervention policies such as community quarantines, closures and travel bans are often implemented in emergencies but many of them are disruptive and difficult to maintain for extended periods of time. A promising alternative recommended by the CDC for influenza is requiring individuals showing fever symptoms to remain isolated at home until they are fever-free for at least one day, but there is limited evidence to support the effectiveness of such symptom-based isolation policies. Methods: Here we introduce a computational model of symptom-based isolation that accounts for the timing of symptoms, viral shedding and the population structure. It was validated on outbreaks of influenza in schools and modified to account for COVID-19. It was then used to estimate the outbreak curves and the attack rates (the proportion of the population infected) under one or more days of fever-based isolation. Results: Using the model we find evidence that symptom-based isolation policies could reduce the attack rates of both influenza and COVID-19 outbreaks, and flatten the outbreak curves. Specifically, we found that across a range of influenza scenarios, a CDC-recommended policy of one day isolation following fever can reduce the attack rate from 27% of the population to 12%, and to 3% if the isolation is extended to two days. In COVID-19 transmission, we estimate that implementing one day post-fever isolation would reduce the attack rate from 79% to 71%, and there is possible benefit from isolation for six days. In both influenza and COVID-19, the policies are predicted to reduce the peak number of infected but not shorten the outbreak duration. Conclusions: Symptom-based isolation could be an important tool to control influenza and COVID-19 outbreaks in schools, and potentially other settings. We recommend that schools implement a post-fever isolation policy of two days for influenza and six days for COVID-19.
Statement
The authors have declared no competing interest. Funding Statement
AG was sponsored by US NIH grant R01GM121600. Author Declarations
All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes
All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes
I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes
I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes
Complete source code and data are available https://github.com/sashagutfraind/feverfighter/

URL: http://medrxiv.org/content/early/2020/03/30/2020.03.26.20044750.abstract
DOI: 10.1101/2020.03.26.20044750


Background: The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has progressed to a pandemic associated with substantial morbidity and mortality. The WHO and the United States Center for Disease Control and Prevention (CDC) have issued interim clinical guidance for management of patients with confirmed coronavirus disease (COVID-19), but there is limited data on the virologic and clinical characteristics for prognosis of severe COVID-19. Methods: A total of 50 patients with severe COVID-19 were divided into good and poor recovery groups. The dynamic viral shedding and serological characteristics of SARS-CoV-2 were explored. The risk factors associated with poor recovery and lung lesion resolutions were identified. In addition, the potential relationships among the viral shedding, the pro-inflammatory response, and lung lesion evolutions were characterized. Results: A total of 58% of the patients had poor recovery and were more likely to have a prolonged interval of viral shedding. The longest viral shedding was 57 days after symptom onset. Older age, hyperlipemia, hypoproteinemia, corticosteroid therapy, consolidation on chest computed-tomography (CT), and prolonged SARS-CoV-2 IgM positive were all associated with poor recovery. Additionally, the odds of impaired lung lesion resolutions were higher in patients with hypoproteinemia, hyperlipemia, and elevated levels of IL-4 and ferritin. Finally, viral shedding and proinflammatory responses were closely correlated with lung lesion evolutions on chest CT. Conclusions: Patients with severe COVID-19 have prolonged SARS-CoV-2 infection and delayed intermittent viral shedding. Older age, hyperlipemia, hypoproteinemia, corticosteroid usage, and prolonged SARS-CoV-2 IgM positive might be utilized as predicative factors for the patients with poor recovery.

Competing Interest Statement
The authors have declared no competing interest. Funding Statement
This work was supported by grants from the 13th Five-Year National Science and Technology Major Projects (grant number: 2016X10002003). Author Declarations
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I have followed all appropriate research reporting
guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes Availability of all data requests to Dr. Yi Ouyang at the Department of Infectious Diseases, Xiangya Hospital, Central South University, Xiangya Rd 87#. Changsha 410008, P.R.China, or at doctor-ouyang@csu.edu.cn

URL: http://medrxiv.org/content/early/2020/04/06/2020.04.03.20051763.abstract
DOI: 10.1101/2020.04.03.20051763


Treatments are desperately needed to lower the hospitalization and case fatality rates of SARS CoV-2 infection. In order to meaningfully impact the COVID-19 pandemic, promising antiviral therapies must be identified within the next several months. However, the number of clinical trials that can be performed in this timeframe is limited. We therefore developed a mathematical model which allows projection of all possible therapeutic approaches. Our model recapitulates off-treatment viral dynamics and predicts a three-phase immune response. Addition of treatment with remdesivir, hydroxychloroquine, neutralizing antibodies or cellular immunotherapy demonstrates that if in vivo drug potency is high, then rapid elimination of virus is possible. Potent therapies dosed soon after peak viral load when infected people typically develop symptoms, are predicted to decrease shedding duration and intensity of the effector immune response, but to have little effect on viral area under the curve, which is driven by high levels of early SARS CoV-2 replication. Potent therapy dosed prior to peak viral load, when infection is usually pre-symptomatic, is predicted to be the only option to lower viral area under the curve. We also identify that clinically meaningful drug resistance is less likely to emerge with a highly potent agent that is dosed after peak viral load. Our results support an early test and treat approach for COVID-19, but also demonstrate the need to identify early viral shedding kinetic features that are the most predictive surrogates of clinical severity and transmission risk. Competing Interest Statement The authors have declared no competing interest. Funding Statement This study was supported by Fred Hutchinson Cancer Research Center faculty discretionary funds. Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes All data and code will be made available upon request.

URL: http://medrxiv.org/content/early/2020/04/14/2020.04.10.20061325.abstract
DOI: 10.1101/2020.04.10.20061325


URL: https://ClinicalTrials.gov/show/NCT04333628
DOI:

We report temporal patterns of viral shedding in 94 laboratory-confirmed COVID-19 patients and modelled COVID-19 infectiousness profile from a separate sample of 77 infector-infectee transmission pairs. We observed the highest viral load in throat swabs at the time of symptom onset, and inferred that infectiousness peaked on or before symptom onset. We estimated that 44% of transmission could occur before first symptoms of the index. Disease control measures should be adjusted to account for probable substantial pre-symptomatic transmission. Competing Interest Statement The authors have declared no competing interest. Funding Statement This work was supported by Department of Science and Technology of Guangdong Province (Project No #2020B111108001) and a commissioned grant from the Health and Medical Research Fund from the Government of the Hong Kong Special Administrative Region. Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes Detailed transmission pairs data in this study are given in the supplementary information and viral shedding data will be available upon request and approval by a data access committee. The data access committee comprises leadership of the Guangzhou Eighth People’s Hospital and the Guangzhou Health Commission; there is no restriction to data access.

URL: http://medrxiv.org/content/early/2020/03/18/2020.03.15.20036707.1.abstract
DOI: 10.1101/2020.03.15.20036707


COVID-19, caused by SARS-CoV-2 infection, has recently been announced as a pandemic all over the world. Plenty of diagnostic, preventive and therapeutic knowledges have been enriched from clinical studies since December 2019. However, animal models, particularly non-human primate models, are urgently needed for critical questions that could not be answered in clinical patients, evaluations of anti-viral drugs and vaccines. In this study, two families of non-human primates, old world monkeys (12 Macaca mulatta, 6 Macaca fascicularis) and new world monkeys (6 Callithrix jacchus), were experimentally inoculated with SARS-CoV-2. Clinical signs were recorded. Samples were collected for analysis of viral shedding, viremia and histopathological examination. Increased body temperature was observed in 100% (12/12) M. mulatta, 33.3% (2/6) M. fascicularis and none (0/6) of C. jacchus post inoculation of SARS-CoV-2. All of M. mulatta and M. fascicularis showed chest radiographic abnormality. Viral genomes were detected in nasal swabs, throat swabs, anal swabs and blood from all 3 species of monkeys. Viral shedding from upper respiratory reached the peak between day 6 and day 8 post inoculation. From necropsied M. mulatta and M. fascicularis, tissues showing virus positive were mainly lung, weasand, bronchus and spleen. No viral genome was seen in any of tissues from 2 necropsied C. jacchus. Severe gross lesions and histopathological changes were observed in lung, heart and stomach of SARS-CoV-2 infected animals. In summary, we have established a NHP model for COVID-19, which could be used to evaluate drugs and vaccines, and investigate viral pathogenesis. M. mulatta is the most susceptible to SARS-CoV2 infection, followed by M. fascicularis and C. jacchus. Competing Interest Statement

The first cases of COVID-19 in France were detected on January 24, 2020. The number of screening tests carried out and the methodology used to target the patients tested do not allow for a direct computation of the actual number of cases and the mortality rate. In this note, we develop a 'mechanistic-statistical' approach coupling a SIR ODE model describing the unobserved epidemiological dynamics, a probabilistic model describing the data acquisition process and a statistical inference method. The objective of this model is not to make forecasts but to estimate the actual number of people infected with COVID-19 during the observation window in France and to deduce the mortality rate associated with the epidemic.

Main results. The actual number of infected cases in France is probably much higher than the observations: we find here a factor x15 (95%-CI: 4-33), which leads to a 5.2/1000 mortality rate (95%-CI: 1.5/1000-11.7/1000) at the end of the observation period. We find a R0 of 4.8, a high value which may be linked to the long viral shedding period of 20 days.

Competing Interest Statement
The authors have declared no competing interest.

Funding Statement
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Author Declarations
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All of the data in this manuscript are available from public sources: Johns Hopkins University Center for Systems Science and Engineering, Santé publique France, and Korean Center for Disease Control https://github.com/CSSEGISandData/COVID-19

URL: http://biorxiv.org/content/early/2020/04/12/2020.04.08.031807.abstract
DOI: 10.1101/2020.04.08.031807


URL: https://ClinicalTrials.gov/show/NCT04336332


Lack of evidence on SARS-CoV-2 transmission dynamics has led to shifting isolation guidelines between airborne and droplet isolation precautions. During the initial isolation of 13 individuals confirmed positive with COVID-19 infection, air and surface samples were collected in eleven isolation rooms to examine viral shedding from isolated individuals. While all individuals were confirmed positive for SARS-CoV-2, symptoms and viral shedding to the environment varied considerably. Many commonly used items,
toilet facilities, and air samples had evidence of viral contamination, indicating that SARS-CoV-2 is shed to the environment as expired particles, during toileting, and through contact with fomites. Disease spread through both direct (droplet and person-to-person) as well as indirect contact (contaminated objects and airborne transmission) are indicated, supporting the use of airborne isolation precautions. Competing Interest Statement The authors have declared no competing interest. Funding Statement Work was supported by University of Nebraska internal funding. Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes All data is included in manuscript materials.

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DOI: 10.1101/2020.03.23.20039446


Prolonged viral shedding is associated with severe status and poor prognosis of COVID-19 patients. Unexpectedly, here we report a non-severe patient with the longest duration of viral shedding. According to the investigation on the clinical and epidemiological information of this case, we concluded that this type of virus might have a low toxicity and transmissibility, but have a prolonged infective ability and was hardly to be eliminated in the body with regular therapy. However, infusion of plasma from recovered patients showed high efficiency in elimination of this virus. Our findings might shed light on the management of COVID-19. Competing Interest Statement The authors have declared no competing interest. Clinical Trial This is a descriptive study, not a trial. Funding Statement This work was supported in part by award numbers 81872028 and 81672693 (H.M.) from the National Natural Science Foundation of China, cstc2017jcyjBX0071 (H.M.) from the Foundation and Frontier Research Project of Chongqing and T04010019 (H.M.) from the Chongqing Youth Top Talent Project. Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes All data can be provided by the corresponding authors upon reasonable request.

URL: http://medrxiv.org/content/early/2020/03/27/2020.03.22.20040071.abstract
DOI: 10.1101/2020.03.22.20040071
The rapid spread of coronavirus disease 2019 (COVID-19) raises concern about a global pandemic. Knowledge about the duration of viral shedding remains important for patient management and infection control. We report the duration of viral detection in throat and rectum of a COVID-19 patient treated at the Hospital for Tropical Diseases in Ho Chi Minh City, Vietnam. Despite clinical recovery, SARS-CoV-2 RNA remained detectable by real time RT-PCR in throat and rectal swabs until day 11 and 18 of hospitalization, respectively. Because live SARS-CoV-2 has been successfully isolated from a stool sample from a COVID-19 patient in China, the results demonstrate that COVID-19 patients may remain infectious for long periods, and fecal-oral transmission may be possible. Therefore, our finding has important implications for infection control.

Competing Interest Statement
The authors have declared no competing interest.

Funding Statement
This study was funded by the Wellcome Trust of Great Britain (106680/B/14/Z and 204904/Z/16/Z). Author Declarations
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All data referred to in the manuscript have been presented either in the manuscript main text or in Supplementary Materials.

URL: http://medrxiv.org/content/early/2020/03/16/2020.03.07.20032052.abstract
DOI: 10.1101/2020.03.07.20032052


Background
A pandemic of coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been spreading over the world. However, the viral dynamics, host serologic responses, and their associations with clinical manifestations, have not been well described in prospective cohort. Methods
We conducted a prospective cohort and enrolled 67 COVID-19 patients admitting between Jan 26 and Feb 5, 2020. Clinical specimens including nasopharyngeal swab, sputum, blood, urine and stool were tested periodically according to standardized case report form with final follow-up on February 27. The routes and duration of viral shedding, antibody response, and their associations with disease severity and clinical manifestations were systematically evaluated. Coronaviral particles in clinical specimens were observed by transmission electron microscopy (TEM). Results
The median duration of SARS-CoV-2 RNA shedding were 12 (3-38), 19 (5-37), and 18 (7-26) days in nasopharyngeal swabs, sputum and stools, respectively. Only 13 urines (5.6%) and 12 plasmas (5.7%) were viral positive. Prolonged viral shedding was observed in severe patients than that of non-severe patients. Cough but not fever, aligned with viral shedding in clinical respiratory specimens, meanwhile the positive stool-RNA appeared to align with the proportion who concurrently had cough and sputum production, but not diarrhea. Typical coronaviral particles could be found directly in sputum by TEM. The anti-nucleocapsid-protein IgM started on day 7 and positive rate peaked on day 28, while that of IgG was on day 10 and day 49 after illness onset. IgM and IgG appear earlier, and their titers are significantly higher in severe patients than non-severe patients (p<0.05). The weak responders for IgG had a significantly higher viral clearance rate than that of strong responders (p= 0.011). Conclusions
Nasopharyngeal, sputum and stools rather than blood and urine, were the major shedding routes for SARS-CoV-2, and meanwhile sputum had a prolonged viral shedding. Symptom cough seems to be aligned with viral shedding in clinical respiratory and fecal specimens. Stronger antibody response was associated with delayed viral clearance and disease severity. Competing Interest Statement The authors have declared no competing interest. Funding Statement This work was partly supported by Chongqing Health Commission COVID-19 Project 2020NCPZX01, Youth Talent Medical Technology Program of PLA (17QNP010), the Chinese Key Project Specialized for Infectious Diseases (2018ZX10723203), the TMMU key project for medical research (2018XYY10), and the Southwest Hospital Medical Science Innovation Plan (SWH2018BJKJ-01, SWH2018QNLC-04). We thank for the supports the Youth Talent Program from Third Military Medical University (Tan W and Sun F) and the Academy of Medical Sciences Newton International Fellowship (Tan W). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript. Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes Relevant anonymized data will be made available on reasonable request from the corresponding author at gh_deng@hotmail.com or yaokaichen@hotmail.com.

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URL: https://ClinicalTrials.gov/show/NCT04334148

URL: https://ClinicalTrials.gov/show/NCT04331899

URL: https://ClinicalTrials.gov/show/NCT04342169

Background: Since there is little awareness of the consequences of coronavirus disease 2019 (COVID-19) in pregnancy, data on the safety of vaginal delivery and breastfeeding in pregnant women with COVID-19 are urgently needed. Methods: We studied COVID-19-infected pregnant women diagnosed at the Renmin Hospital of Wuhan University between January 31 and March 9, 2020, and collected clinical data, vaginal secretion, and stool specimens during different stages of pregnancy. We also collected breast milk samples, as well as throat and anal swabs from the corresponding infants to detect the presence of the virus. Results: Of the 13 women with COVID-19, 5 were in their first trimester, 3 in their
second trimester, and 5 in their third trimester. Clinical manifestations observed among the 13 women included fever (n = 8), cough (n = 5), increased leukocyte count (n = 3), lymphopenia (n = 2), impaired liver function (n = 3), dyspnea (n = 1), myalgia (n = 1), and diarrhea (n = 1). Of the 5 women during their third trimester who gave birth, all delivered live newborns. Among these 5 deliveries, the primary adverse perinatal outcomes included premature delivery (n = 2) and neonatal pneumonia (n = 2). One of the 5 women followed from the first trimester experienced a biochemical pregnancy. One of 9 stool samples was positive; and all 13 vaginal secretion samples, and 5 throat swabs and 4 anal swabs collected from newborns were negative for the novel coronavirus. However, 1 of 3 samples of breast milk was positive by viral nucleic acid testing. Conclusions: In this case series of 13 pregnant women with COVID-19, we observed negative viral test results in vaginal secretion specimens, suggesting that a vaginal delivery may be a safe delivery option. However, additional research is urgently needed to examine breast milk and the potential risk for viral contamination.

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Background: The duration of viral shedding is central to guide decisions around isolation precautions and antiviral treatment. However, studies about risk factors associated with prolonged SARS-CoV-2 shedding and the potential impact of Lopinavir/Ritonavir (LPV/r) treatment remain scarce. Methods: In this retrospective study, data were collected from all SARS-CoV-2 infected patients who were admitted to isolation wards and had RT-PCR conversion at the NO.3 People's hospital of Hubei province between 31 January and 09 March 2020. We compared clinical features and SARS-CoV-2 RNA shedding between patients with LPV/r treatment and those without. Logistic regression analysis was employed to evaluate risk factors associated with prolonged viral shedding. Results: Of 120 patients, the median age was 52 years, 54 (45%) were male and 78 (65%) received LPV/r treatment. The median duration of SARS-CoV-2 RNA detection from symptom onset was 23 days (IQR, 18-32 days). Older age (odd ratio OR 1.03, 95% confidence interval CI 1.00-1.05, p=0.03) and lack of LPV/r treatment (OR 2.42, 95% CI 1.10-5.36, p=0.029) were independent risk factors for prolonged SARS-CoV-2 RNA shedding in multivariate logistic regression analysis. The median duration of viral shedding was shorter in the LPV/r treatment group (n=78) than that in no LPV/r treatment group (n=42) (median, 22 days vs. 28.5 days, p=0.02). Only earlier administration of LPV/r treatment (≤10 days from symptom onset) could shorten the duration of viral shedding. Conclusions: Older age and lack of LPV/r treatment were independently associated with prolonged SARS-CoV-2 RNA shedding in patients with COVID-19. Earlier administration of LPV/r treatment could shorten viral shedding. Competing Interest StatementThe authors have declared no competing interest. Funding StatementNo funding. Author DeclarationsAll relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes We declare that all data are available.

**Background:** The outbreak of novel coronavirus pneumonia (NCP) caused by 2019-nCoV spread rapidly, and elucidation the diagnostic accuracy of different respiratory specimens is crucial for the control and treatment of this diseases. **Methods:** Respiratory samples including nasal swabs, throat swabs, sputum and bronchoalveolar lavage fluid (BALF) were collected from Guangdong CDC confirmed NCP patients, and viral RNAs were detected using a CFDA approved detection kit. Results were analyzed in combination with sample collection date and clinical information. **Finding:** Except for BALF, the sputum possessed the highest positive rate (74.4%~88.9%), followed by nasal swabs (53.6%~73.3%) for both severe and mild cases during the first 14 days after illness onset (d.a.o). For samples collected ≥ 15 d.a.o, sputum and nasal swabs still possessed a high positive rate ranging from 42.9%~61.1%. The positive rate of throat swabs collected ≥ 8 d.a.o was low, especially in samples from mild cases. Viral RNAs could be detected in all the lower respiratory tract of severe cases, but not the mild cases. CT scan of cases 02, 07 and 13 showed typical viral pneumonia with ground glass opacity, while no viral RNAs were detected in first three or all the upper respiratory samples. **Interpretation:** Sputum is most accurate for laboratory diagnosis of NCP, followed by nasal swabs. Detection of viral RNAs in BALF is necessary for diagnosis and monitoring of viruses in severe cases. CT scan could serve as an important make up for the diagnosis of NCP. **Funding** National Science and Technology Major Project, Sanming Project of Medicine and China Postdoctoral Science Foundation.

**Competing Interest Statement** The authors have declared no competing interest.

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**Author Declarations** All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes

All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes

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I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes

All data generated or used during the study have been presented in the submitted article.

**URL:** [http://medrxiv.org/content/early/2020/02/17/2020.02.11.20021493.abstract](http://medrxiv.org/content/early/2020/02/17/2020.02.11.20021493.abstract)

**DOI:** 10.1101/2020.02.11.20021493


**Background:** The outbreak of novel coronavirus pneumonia (NCP) caused by 2019-nCoV spread rapidly, and elucidation the diagnostic accuracy of different respiratory specimens is crucial for the control and treatment of this diseases. **Methods:** Respiratory samples including nasal swabs, throat swabs, sputum and bronchoalveolar lavage fluid (BALF) were collected from Guangdong CDC confirmed NCP patients, and viral RNAs were detected using a CFDA approved detection kit. Results were analyzed in combination with sample collection date and clinical information. **Finding:** Except for BALF, the sputum
possessed the highest positive rate (74.4%~88.9%), followed by nasal swabs (53.6%~73.3%) for both severe and mild cases during the first 14 days after illness onset (d.a.o). For samples collected ≥ 15 d.a.o, sputum and nasal swabs still possessed a high positive rate ranging from 42.9%~61.1%. The positive rate of throat swabs collected ≥ 8 d.a.o was low, especially in samples from mild cases. Viral RNAs could be detected in all the lower respiratory tract of severe cases, but not the mild cases. CT scan of cases 02, 07 and 13 showed typical viral pneumonia with ground glass opacity, while no viral RNAs were detected in first three or all the upper respiratory samples. Interpretation: Sputum is most accurate for laboratory diagnosis of NCP, followed by nasal swabs. Detection of viral RNAs in BLAF is necessary for diagnosis and monitoring of viruses in severe cases. CT scan could serve as an important make up for the diagnosis of NCP. Funding National Science and Technology Major Project, Sanming Project of Medicine and China Postdoctoral Science Foundation. Competing Interest Statement The authors have declared no competing interest. Funding Statement This work was supported by the National Science and Technology Major Project (2017ZX10103011, 2017ZX10204401, 2018ZX10711001), Sanming Project of Medicine in Shenzhen (SZSM201412003, SZSM201512005) and China Postdoctoral Science Foundation (2019T120147, 2019M660836). Author Declarations All relevant ethical guidelines have been followed; any necessary IRB and/or ethics committee approvals have been obtained and details of the IRB/oversight body are included in the manuscript. Yes All necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes All data generated or used during the study have been presented in the submitted article.

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DOI: 10.1101/2020.02.11.20021493

Journal Articles


Introduction: Middle East Respiratory Syndrome Coronavirus (MERS-CoV) infection is zoonotic infection that was first identified in 2012 with high mortality rate. It is linked to camel exposure or human-to-human transmission. Clinical presentation of MERS-CoV infection ranges from mild disease to septic shock with multi organ failure and death. Acute kidney injury (AKI) has been described in cohorts of MERS-CoV infected patients with variable degree of severity. We studied the clinical characteristics and outcomes of AKI in MERS-CoV infected patients. Method(s): Ethical approval was obtained to conduct a retrospective multicenter chart review study for MERS-CoV confirmed cases in Al Ain City over 7 years period (May 2012 - May 2019). We included patients who developed AKI and studied their outcomes. Demographic, clinical and laboratory data were collected and analyzed. Result(s): A total of 58 individuals with MERS-CoV infection were identified during the study period. Ten patients developed AKI and were included in the study. The mean age was 54.5 years and majority were males 8 (80%). The comorbid conditions were hypertension (5), chronic kidney disease (4), diabetes mellitus (3), ischemic heart disease (2), nephrotic syndrome (1) and dyslipidemia (2). Risk factors for MERS-CoV infection
included close contact with infected patient (3), camel exposure (2) and travel history to Oman (2) or Saudi Arabia (1). MERS CoV PCR was detected in nasopharyngeal aspirate (8) and sputum (2) with mean viral shedding of 13.5 days. Majority of patients 9 (90%) had severe MERS CoV infection and required critical care. AKI episodes were classified as severe stage 3 in 9 patients, and stage 2 in one patient. Mild proteinuria and hematuria were noted in urine analysis of some patients. Autoimmune workups and hepatitis serology were done for three patients and were negative. Provisional diagnosis of acute tubular necrosis due to severe sepsis and shock was considered. Imaging renal studies in all patients were negative for hydronephrosis or stones. Renal replacement therapy were needed in 7 (70%) patients and duration of range from 3 to 14 days. MERS CoV PCR was not done in urine sample. Other complications related to severe MERS CoV infection including septic shock 6 (60%), acute respiratory failure required intubation 7 (70%) or non-invasive ventilation 2 (20%), supraventricular tachycardia 2 (20%), Anemia 3 (30%), acute ischemic stroke 1 (10%), and secondary pulmonary infections (Influenza B, Klepseilla pneumonia, Staph aureus). Mortality rate was high 7 (70%) among patient with severe MERS CoV and AKI. Two patients recovered from AKI and one patient became hemodialysis dependent as he has advanced CKD at baseline. Conclusion(s): AKI is commonly associated with severe MERS CoV infection in old patients with comorbid conditions. The mortality is high with severe infection and multi organ failure. Copyright © 2020

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With the outbreak of unknown pneumonia in Wuhan, China, in December 2019, a new coronavirus, Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), aroused the attention of the entire world. The current outbreak of infections with SARS-CoV-2 is termed Coronavirus Disease 2019 (COVID-19). The World Health Organization declared COVID-19 in China as a Public Health Emergency of International Concern. Two other coronavirus infections: SARs in 2002-2003 and Middle East Respiratory Syndrome (MERS) in 2012-2014 both caused severe respiratory syndrome in humans. All 3 of these emerging infectious diseases leading to a global spread are caused by Î²-coronaviruses. Although coronaviruses usually infect the upper or lower respiratory tract, viral shedding in plasma or serum is common. Therefore, there is still a theoretical risk of transmission of coronaviruses through the transfusion of labile blood products. Because more and more asymptomatic infections are being found among COVID-19 cases, considerations of blood safety and coronaviruses have arisen especially in endemic areas. In this review, we detail current evidence and understanding of the transmission of SARS-CoV, MERSâ€”CoV, and SARS-CoV-2 through blood products as of February 10, 2020, and also discuss pathogen inactivation methods on coronaviruses.

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DOI: https://doi.org/10.1016/j.tmrv.2020.02.003


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, and has spread globally. However, the transmission route of SARS-CoV-2 has not been fully understood. In this study, we aimed to investigate the SARS-CoV-2 shedding in excreta of COVID-19 patients. Methods Electronical medical records, including demographics, clinical characteristics, laboratory and radiological findings, of enrolled patients were extracted and analyzed. Pharyngeal swab, stool and urine specimens were collected and tested for SARS-CoV-2 RNA by RT-PCR. Viral shedding at multiple time points in specimens was
recorded, and analyzed its correlation with clinical manifestations and the severity of illness. Results A total of 42 laboratory-confirmed patients were enrolled, 8 (19.05%) of whom had gastrointestinal symptoms. 28 (66.67%) patients tested positive for SARS-CoV-2 RNA in stool specimens, which was not associated with the presence of gastrointestinal symptoms and the severity of illness. Among them, 18 (64.29%) patients remained positive for viral RNA in feces after pharyngeal swabs turned negative. The duration of viral shedding from feces after negative conversion in pharyngeal swabs was 7 (6-10) days, regardless of COVID-19 severity. The demographics, clinical characteristics, laboratory and radiologic findings did no differ between patients tested positive and negative for SARS-CoV-2 RNA in feces. Viral RNA was not detectable in urine specimens from 10 patients. Conclusions Our results demonstrated the presence of SARS-CoV-2 RNA in feces of COVID-19 patients, and suggested the possibility of SARS-CoV-2 transmission via the fecal-oral route. This article is protected by copyright. All rights reserved.

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10.7326/M20-1301.

Diagnostic testing to identify persons infected with severe acute respiratory syndrome-related coronavirus-2 (SARS-CoV-2) infection is central to control the global pandemic of COVID-19 that began in late 2019. In a few countries, the use of diagnostic testing on a massive scale has been a cornerstone of successful containment strategies. In contrast, the United States, hampered by limited testing capacity, has prioritized testing for specific groups of persons. Real-time reverse transcriptase polymerase chain reaction-based assays performed in a laboratory on respiratory specimens are the reference standard for COVID-19 diagnostics. However, point-of-care technologies and serologic immunoassays are rapidly emerging. Although excellent tools exist for the diagnosis of symptomatic patients in well-equipped laboratories, important gaps remain in screening asymptomatic persons in the incubation phase, as well as in the accurate determination of live viral shedding during convalescence to inform decisions to end isolation. Many affluent countries have encountered challenges in test delivery and specimen collection that have inhibited rapid increases in testing capacity. These challenges may be even greater in low-resource settings. Urgent clinical and public health needs currently drive an unprecedented global effort to increase testing capacity for SARS-CoV-2 infection. Here, the authors review the current array of tests for SARS-CoV-2, highlight gaps in current diagnostic capacity, and propose potential solutions.

DOI: 10.7326/m20-1301


Severe infection involving the novel coronavirus 2019 (COVID-19) has been associated with acute respiratory distress syndrome that subsequently requires patients to be intubated and dependent on mechanical ventilation. In the setting of the recent pandemic, there is a greater need to perform tracheostomy for these patients. With the high transmissibility of the virus, there has been an increasing concern for the development of techniques to perform surgical intervention while mitigating the risk for infecting hospital staff. As more data emerge pertaining to viral shedding in various bodily fluids, it has become more important to give special attention to precautions. In this article, we submit a novel approach for better protection and thus reduced transmission for tracheostomy in a COVID-19 positive patient.
Importantly, this technique is functional, easy to set up, and can be used for additional operations that involve risk of aerosolization or droplet exposure to operating room staff.

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Porcine deltacoronavirus (PDCoV) is a novel swine enteropathogenic coronavirus that causes acute diarrhea, vomiting, dehydration and mortality in neonatal piglets, resulting in significant economic losses to the pig industry. However, there is currently little information on vaccine studies and commercially available vaccines for PDCoV. Hence, herein, a PDCoV strain, CH/XJYN/2016, was successfully isolated and serially propagated in vitro, and its biological characteristics were determined. Compared to that of previously reported and recently isolated PDCoV strains from China and the United States, the S gene of the CH/XJYN/2016 strain contains novel mutations. Infection studies revealed that CH/XJYN/2016 is pathogenic to suckling piglets and conventional weaned pigs. In addition, the median pig diarrhea dose (PDD50) of PDCoV in conventional weaned pigs was determined (2.0 log10PDD50/3 mL). Furthermore, an inactivated cell-adapted CH/XJYN/2016-based vaccine candidate was developed with different adjuvants. Compared with nonvaccinated pigs, conventional weaned pigs given the inactivated vaccine developed a potent humoral immune response and showed no clinical signs or viral shedding after challenge, indicating a potent protective effect of the vaccine against PDCoV infection. Therefore, the PDCoV vaccine developed in this study is a promising vaccine candidate that can be used for the control of PDCoV infection in pigs.

**URL: DOI:** 10.1016/j.virusres.2020.197955


Objective The ongoing pandemic of coronavirus disease (COVID-19), caused by the SARS-CoV-2 virus, is highly contagious with high morbidity and mortality. The role of the nasal and paranasal sinus cavities is increasingly recognized for COVID-19 symptomatology and transmission. We therefore conducted a systematic review, synthesizing existing scientific evidence about sinonasal pathophysiology in COVID-19. Study design Systematic review. Methods Systematic searches were performed of all indexed studies in PubMed/Medline and Cochrane databases through March 28, 2020 and studies searchable on preprints.com (including ArXiv and Scilit repositories) through March 30, 2020. Data extraction focused on sinonasal pathophysiology in COVID-19. Results A total 19 studies were identified. The sinonasal cavity may be a major site of infection by SARS-CoV-2, where susceptibility genes required for infection are expressed at high levels and may be modulated by environmental and host factors. Viral shedding appears to be highest from the nose, therefore reflecting a major source for transmission. This has been highlighted by multiple reports of healthcare-associated infection during rhinologic procedures, which are now consequently considered to be high risk for SARS-CoV-2 transmission to healthcare workers. While sinonasal symptomatology, such as rhinorrhea or congestion, appears to be a rarer symptom of COVID-19, anosmia without nasal obstruction is reported as highly specific predictor of COVID-19+ patients. Conclusion Sinonasal pathophysiology is increasingly important in our understanding of COVID-19. The sinonasal tract may be an important site of infection while sinonasal viral shedding may be an
important transmission mechanism? including healthcare-associated infection. Anosmia without nasal obstruction may be a highly specific indicator of COVID-19. This article is protected by copyright. All rights reserved.

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

DOI: 10.1002/jmv.25715


BACKGROUND: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-infected pneumonia emerged in Wuhan, China in December 2019. In this retrospective multicenter study, we investigated the clinical course and outcomes of novel coronavirus disease 2019 (COVID-19) from early cases in Republic of Korea. METHODS: All of the cases confirmed by real time polymerase chain reaction were enrolled from the 1st to the 28th patient nationwide. Clinical data were collected and analyzed for changes in clinical severity including laboratory, radiological, and virologic dynamics during the progression of illness. RESULTS: The median age was 40 years (range, 20-73 years) and 15 (53.6%) patients were male. The most common symptoms were cough (28.6%) and sore throat (28.6%), followed by fever (25.0%). Diarrhea was not common (10.7%). Two patients had no symptoms. Initial chest X-ray (CXR) showed infiltration in 46.4% of the patients, but computed tomography scan confirmed pneumonia in 88.9% (16/18) of the patients. Six patients (21.4%) required supplemental oxygen therapy, but no one needed mechanical ventilation. Lymphopenia was more common in severe cases. Higher level of C-reactive protein and worsening of chest radiographic score was observed during the 5-7 day period after symptom onset. Viral shedding was high from day 1 of illness, especially from the upper respiratory tract (URT). CONCLUSION: The prodromal symptoms of COVID-19 were mild and most patients did not have limitations of daily activity. Viral shedding from URT was high from the prodromal phase. Radiological
pneumonia was common from the early days of illness, but it was frequently not evident in simple CXR. These findings could be plausible explanations for the easy and rapid spread of SARS-CoV-2 in the community.

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10.3346/jkms.2020.35.e142


**BACKGROUND:** Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)-infected pneumonia emerged in Wuhan, China in December 2019. In this retrospective multicenter study, we investigated the clinical course and outcomes of novel coronavirus disease 2019 (COVID-19) from early cases in Republic of Korea.

**METHODS:** All of the cases confirmed by real time polymerase chain reaction were enrolled from the 1st to the 28th patient nationwide. Clinical data were collected and analyzed for changes in clinical severity including laboratory, radiological, and virologic dynamics during the progression of illness.

**RESULTS:** The median age was 40 years (range, 20-73 years) and 15 (53.6%) patients were male. The most common symptoms were cough (28.6%) and sore throat (28.6%), followed by fever (25.0%). Diarrhea was not common (10.7%). Two patients had no symptoms. Initial chest X-ray (CXR) showed infiltration in 46.4% of the patients, but computed tomography scan confirmed pneumonia in 88.9% (16/18) of the patients. Six patients (21.4%) required supplemental oxygen therapy, but no one needed mechanical ventilation. Lymphopenia was more common in severe cases. Higher level of C-reactive protein and worsening of chest radiographic score was observed during the 5-7 day period after symptom onset. Viral shedding was high from day 1 of illness, especially from the upper respiratory tract (URT). CONCLUSION: The prodromal symptoms of COVID-19 were mild and most patients did not have limitations of daily activity. Viral shedding from URT was high from the prodromal phase. Radiological pneumonia was common from the early days of illness, but it was frequently not evident in simple CXR. These findings could be plausible explanations for the easy and rapid spread of SARS-CoV-2 in the community.

DOI: https://dx.doi.org/10.3346/jkms.2020.35.e142


Introduction In 2012, MERS-CoV was identified in Saudi Arabia and resulted in more than 2442 confirmed cases worldwide by May 2019. MERS-CoV infection in children is less common. A review of MERS-CoV in children from 2012 to April 2016 summarized the clinical manifestation of 31 reported cases. Most children were asymptomatic or had mild respiratory symptoms, and severe infection reported in patients with comorbid conditions. We aimed to study the clinical characteristics of pediatric MERS CoV infected cases in UAE supported by literature review. Method A retrospective multicenter chart review study was conducted for MERS-CoV cases in Abu Dhabi Emirate (May 2012 - May 2019). Demographic, clinical and laboratory data were analyzed. We reviewed WHO outbreak surveillance reports published online to identify pediatric MERS-CoV cases from April 2016 to June 2019. Results We describe favorable outcomes of MERS-CoV infection in three children identified in UAE. Two patients had household contact with MERS-CoV infected family members and another patient travelled to Saudi Arabia. MERS-CoV was confirmed by PCR from nasopharyngeal aspirates and duration of viral shedding ranged from 4 to 11 days. One patient was asymptomatic and other two had mild respiratory symptoms. Laboratory
data and chest X rays were normal. We reviewed WHO surveillance data and identified 11 pediatric MERS-CoV cases from April 2016 to June 2019. Mean age of 14.9 years (6 females, 5 males). The majority of pediatric outbreak was in year 2017 (8 cases) and most cases identified in Saudi Arabia. The main risk factor was household infection. Two patients died due to severe MERS-CoV infection. There are an estimated 42 pediatric MERS-CoV cases reported globally, with a mortality rate of 9.5% (4 cases). Conclusion Pediatric MERS-CoV infection is acquired mainly through household contact. It has favorable outcomes and the mortality rate in children remains lower than adults. Copyright © 2020 DOI: http://dx.doi.org/10.1016/j.jiph.2020.01.181

12. Lau SKP, Li KSM, Luk HKH, et al. Middle East Respiratory Syndrome Coronavirus Antibodies in Bactrian and Hybrid Camels from Dubai. mSphere. 2020;5(1). DOI: 10.1128/mSphere.00898-19
So far, dromedary camels are the only known animal reservoir for Middle East respiratory syndrome (MERS) coronavirus (MERS-CoV). Previous published serological studies showed that sera of Bactrian camels were all negative for MERS-CoV antibodies. However, a recent study revealed that direct inoculation of Bactrian camels intranasally with MERS-CoV can lead to infection with abundant virus shedding and seroconversion. In this study, we examined the presence of MERS-CoV antibodies in Bactrian and hybrid camels in Dubai, the United Arab Emirates (where dromedaries are also present), and Bactrian camels in Xinjiang, China (where dromedaries are absent). For the 29 serum samples from Bactrian camels in Dubai tested by the MERS-CoV spike (S) protein-based enzyme-linked immunosorbent assay (S-ELISA) and neutralization antibody test, 14 (48%) and 12 (41%), respectively, were positive for MERS-CoV antibodies. All the 12 serum samples that were positive with the neutralization antibody test were also positive for the S-ELISA. For the 11 sera from hybrid camels in Dubai tested with the S-ELISA and neutralization antibody test, 6 (55%) and 9 (82%), respectively, were positive for MERS-CoV antibodies. All the 6 serum samples that were positive for the S-ELISA were also positive with the neutralization antibody test. There was a strong correlation between the antibody levels detected by S-ELISA and neutralizing antibody titers, with a Spearman coefficient of 0.6262 (P < 0.0001; 95% confidence interval, 0.5062 to 0.7225). All 92 Bactrian camel serum samples from Xinjiang were negative for MERS-CoV antibodies tested using both S-ELISA and the neutralization antibody test. Bactrian and hybrid camels are potential sources of MERS-CoV infection. IMPORTANCE Since its first appearance in 2012, Middle East respiratory syndrome (MERS) has affected >25 countries, with >2,400 cases and an extremely high fatality rate of >30%. The total number of mortalities due to MERS is already greater than that due to severe acute respiratory syndrome. MERS coronavirus (MERS-CoV) has been confirmed to be the etiological agent. So far, dromedaries are the only known animal reservoir for MERS-CoV. Previously published serological studies showed that sera of Bactrian camels were all negative for MERS-CoV antibodies. In this study, we observed that 41% of the Bactrian camel sera and 55% of the hybrid camel sera from Dubai (where dromedaries are also present), but none of the sera from Bactrian camels in Xinjiang (where dromedaries are absent), were positive for MERS-CoV antibodies. Based on these results, we conclude that in addition to dromedaries, Bactrian and hybrid camels are also potential sources of MERS-CoV infection.

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DOI: 10.1128/mSphere.00898-19

10.1007/s00592-020-01522-8
AIMS: Analyze the relationship between obesity and influenza. METHODS: Basal hormone milieu, defective response of both innate and adaptive immune system and sedentariness are major determinants in the
severity of influenza viral infection in obese patients. Being overweight not only increases the risk of infection and of complications for the single obese person, but a large prevalence of obese individuals within the population might increase the chance of appearance of more virulent viral strain, prolongs the virus shedding throughout the total population and eventually might increase overall mortality rate of an influenza pandemic. 

RESULTS: Waiting for the development of a vaccination against COVID-19, isolation of positive cases and social distancing are the primary interventions. Nonetheless, evidence from previous influenza pandemics suggests the following interventions aimed at improving immune response: (1) lose weight with a mild caloric restriction; (2) include AMPK activators and PPAR gamma activators in the drug treatment for obesity associated with diabetes; and (3) practice mild-to-moderate physical exercise. CONCLUSIONS: Due to prolonged viral shedding, quarantine in obese subjects should likely be longer than normal weight individuals.

URL: https://pubmed.ncbi.nlm.nih.gov/32249357/


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.

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DOI: https://dx.doi.org/10.1080/23744235.2020.1748705


Objective Comparing the benefit of Abidor, lopinavir/ritonavir and recombinant interferon &alpha;-2b triple combination antiviral therapy and lopinavir/ritonavir and interferon dual combination antiviral therapy to hospitalized novel coronavirus pneumonia 2019 in Zhejiang province. Methods A multi-center prospective study was carried out to compare the effect of triple combination antiviral therapy with dual combination antiviral therapy in 15 medical institutions of Zhejiang Province. All patients were treated with recombinant interferon &alpha;-2b (5 million U, 2 times/d) aerosol inhalation. 196 patients were treated with abidol (200 mg, 3 times/d) + lopinavir / ritonavir (2 tablets, 1 time/12 h) as the triple combination antiviral treatment group. 41 patients were treated with lopinavir / ritonavir (2 tablets, 1 time/12 h) as the dual combination antiviral treatment group. The patients who received triple combination antiviral therapy were divided into three groups: within 48 hours, 3-5 days and > 5 days after the symptom onset. To explore the therapeutic effects of triple combination antiviral drugs and dual combination antiviral drugs, as well as triple combination antiviral drugs with different antiviral initiate time. SPSS17.0 software was used to analyze the data. Results The time of virus nucleic acid turning negative was (12.2 &plusmn; 4.7) days in the triple combination antiviral drug group, which was...
shorter than that in the dual combination antiviral drug group [(15.0 ± 5.0) days] (t = 6.159, P < 0.01). The length of hospital stay [12 (9, 17) d] in the triple combination antiviral drug group was also shorter than that in the dual combination antiviral drug group [15 (10, 18) d] (H = 2.073, P < 0.05).

Comparing the antiviral treatment which was started within 48 hours, 3-5 days and > 5 days after the symptom onset of triple combination antiviral drug group, the time from the symptom onset to the negative of viral shedding was 13 (10,16.8), 17 (13,22) and 21 (18-24) days respectively (Z = 32.983, P < 0.01), and the time from antiviral therapy to the negative of viral shedding was (11.8±3.9), (13.5±5.1) and (11.2±4.3) d. The differences among the three groups were statistically significant (Z=32.983 and 6.722, P <0.01 or<0.05). Conclusions The triple combination antiviral therapy of Abidor, Lopinavir/Litonavir and recombinant interferon α-2b showed shorter viral shedding time and hospitalization time compared with the dual combination antiviral therapy. The earlier the time to initiate triple antiviral treatment, the shorter the time of virus shedding.


Background: Hainan Island, a popular tourist destination, had received many imported cases of Coronavirus disease 2019 (COVID-19), but successfully contained the epidemics in one month. We described epidemiological and clinical characteristics of COVID-19 cases in Hainan and compared these features between imported and local cases to provide information for other international epidemic areas.

Methods: We included 91 patients (56 imported and 35 local cases) from two designed hospitals for COVID-19 in Haikou, capital of Hainan province, from January 20 to February 19, 2020. Data on demographic, epidemiological, clinical and laboratory characteristics were extracted from medical records.

Findings: Of the 91 patients, 78 (85·7%) patients were diagnosed within the first three weeks after the first case identified (Day 1: Jan 22, 2020), while the number of local cases started to increase from the third week. No new cases occurred after Day 29. Fever (79·1%) and cough (79·1%) were two main clinical manifestations. 15 (16·5%) were severe, 14 (15·4%) had complicated infections, nine (9·9%) were admitted to ICU, and three died. All patients had abnormalities in the chest CT scan, with ground-glass opacity as the main presentation. Median duration of viral shedding in feces was longer than that in nasopharyngeal swabs (19 days vs 16 days, P=0·007). Compared with local cases, imported cases were older, have higher incidence of fever and concurrent infections, higher CRP levels, lower lymphocyte and platelet counts and levels of albumin. There was no difference in outcomes between the two groups.

Interpretation: Imported cases were more severe than local cases, but could have similar prognosis. The short epidemic period in Hainan suggests that the epidemics could be quickly brought under control if proper timely measures were taken.

Funding Statement: This study was funded by the National Science and Technology Major Project (Bing-Liang Lin, 2018ZX10302204, Bing-Liang Lin, 2017ZX10203201003), Emergency special program for 2019-nCoV of Guangdong province science and technology project (GDSTP-ESP) (Zhi-Liang Gao, 2020B111105001).

Declaration of Interests: The authors declare no competing interests.

Ethics Approval Statement: This study was approved by the Ethics Committee of Hainan General Hospital and The Second Affiliated Hospital of Hainan Medical University (HN-2020-31), and oral consents were obtained from all patients. Keywords: coronavirus disease 2019 (COVID-19); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2); Epidemiology; clinical chracteristics; imported case

URL: https://ssrn.com/abstract=3555222

Objective To determine the dynamic changes of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) RNA in respiratory and fecal specimens in children with coronavirus disease 2019 (COVID-19). Methods From January 17, 2020 to February 23, 2020, three paediatric cases of COVID-19 were reported in Qingdao, Shandong Province, China. Epidemiological, clinical, laboratory, and radiological characteristics and treatment data were collected. Patients were followed up to March 10, 2020, and dynamic profiles of nucleic acid testing results in throat swabs and fecal specimens were closely monitored. Results Clearance of SARS-CoV-2 in respiratory tract occurred within two weeks after abatement of fever, whereas viral RNA remained detectable in stools of pediatric patients for longer than 4 weeks. Two children had fecal SARS-CoV-2 undetectable 20 days after throat swabs showing negative, while that of another child lagged behind for 8 days. Conclusions SARS-CoV-2 may exist in children’s gastrointestinal tract for a longer time than respiratory system. Persistent shedding of SARS-CoV-2 in stools of infected children raises the possibility that the virus might be transmitted through contaminated fomites. Massive efforts should be made at all levels to prevent spreading of the infection among children after reopening of kindergartens and schools.

URL: http://www.sciencedirect.com/science/article/pii/S1684118220300815
DOI: https://doi.org/10.1016/j.jmii.2020.03.021


BACKGROUND: An outbreak of coronavirus disease 2019 (COVID-19) is becoming a public health emergency. Data are limited on the duration and host factors related to viral shedding. METHODS: In this retrospective study, risk factors associated with severe acute respiratory coronavirus 2 (SARS-CoV-2) RNA shedding were evaluated in a cohort of 113 symptomatic patients from two hospitals outside Wuhan. RESULTS: The median duration of SARS-CoV-2 RNA detection was 17 days (Interquartile Range [IQR], 13-22 days) as measured from illness onset. When comparing patients with early (<15 days) and late viral RNA clearance (≥15 days after illness onset), prolonged SARS-CoV-2 RNA shedding was associated with male sex (p=0.009), old age (p=0.033), concomitated with hypertension (p=0.009), delayed admission to hospital after illness onset (p=0.001), severe illness at admission (p=0.049), invasive mechanical ventilation (p=0.006), and corticosteroid treatment (p=0.025). Patients with longer SARS-CoV-2 RNA shedding duration had slower recovery of body temperature (p 0.001) and focal absorption on radiograph images (p 0.001) than patients with early SARS-CoV-2 RNA clearance. Male sex (odds ratio [OR], 3.24 [95% CI, 1.31-8.02]), delayed hospital admission (OR, 1.30 [95% CI, 1.10-1.54]), and invasive mechanical ventilation (OR, 9.88 [95% CI, 1.11-88.02]) were independent risk factors for prolonged SARS-CoV-2 RNA shedding. CONCLUSIONS: Male sex, delayed admission to hospital after illness onset, and invasive mechanical ventilation were associated with prolonged SARS-CoV-2 RNA shedding. Hospital admission and general treatments should be started as soon as possible in symptomatic COVID-19 patients, especially male patients.

DOI: https://dx.doi.org/10.1093/cid/ciaa351


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.
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. To report the initial experience in Singapore with the epidemiologic investigation of this outbreak, clinical features, and management. 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.
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. 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.

URL: https://doi.org/10.1001/jama.2020.3204
DOI: 10.1001/jama.2020.3204


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.

URL: https://pubmed.ncbi.nlm.nih.gov/32125362
DOI: 10.1001/jama.2020.3204


Senecavirus A (SVA), an emerging infectious disease, is associated with the porcine idiopathic vesicular disease. Here, the pathogenesis of different strains of SVA was investigated in growing-finishing pigs. We aimed to evaluate the replication characteristics, virus particle morphology, clinical signs, and vesicular lesions in comparison with two different strains of SVA. The animals were infected with SVA HB-CH-2016 or CH/AH-02/2017 by intranasal routes (3 mL, 10(9)TCID50/mL) and monitored daily for 14 days post-inoculation (dpi) for clinical signs and vesicular lesions. Viremia or viral shedding was detected in the
blood, fecal swab, and nasal swab samples. Results showed no distinct differences in plaque size, replication ability, and characteristic virions between SVA HB-CH-2016 and CH/AH-02/2017 strains. Animal experimental results showed that both SVA CH/AH-02/2017 and SVA HB-CH-2016 could infect pigs. However, an obvious difference in the pathogenicity and dynamics of infection was observed between SVA HB-CH-2016 and CH/AH-02/2017 strains. The pathogenesis of SVA CH/AH-02/2017 was similar to that of published results of USA strains, whereas the SVA HB-CH-2016 strain had low pathogenicity to pigs. Clinical signs and vesicular lesions were observed in SVA CH/AH-02/2017-infected pigs. Additionally, the different branches of SVA should be capable of inducing broad cross-reactive neutralizing antibodies, which play an important role in clearing the SVA virus. This study of animal models for SVA infection will be beneficial to develop vaccines and antivirals.

URL: DOI: 10.3390/pathogens9010039


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/L (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/L 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.

URL: https://www.thelancet.com/pb-assets/Lancet/pdfs/S014067362305663.pdf
DOI: https://doi.org/10.1016/S0140-6736(20)30566-3


Dromedary camels have been shown to be the main reservoir for human Middle East respiratory syndrome (MERS) infections. This systematic review aims to compile and analyse all published data on MERS-coronavirus (CoV) in the global camel population to provide an overview of current knowledge on the
distribution, spread and risk factors of infections in dromedary camels. We included original research articles containing laboratory evidence of MERS-CoV infections in dromedary camels in the field from 2013 to April 2018. In general, camels only show minor clinical signs of disease after being infected with MERS-CoV. Serological evidence of MERS-CoV in camels has been found in 20 countries, with molecular evidence for virus circulation in 13 countries. The seroprevalence of MERS-CoV antibodies increases with age in camels, while the prevalence of viral shedding as determined by MERS-CoV RNA detection in nasal swabs decreases. In several studies, camels that were sampled at animal markets or quarantine facilities were seropositive more often than camels at farms as well as imported camels vs. locally bred camels. Some studies show a relatively higher seroprevalence and viral detection during the cooler winter months. Knowledge of the animal reservoir of MERS-CoV is essential to develop intervention and control measures to prevent human infections.

URL: DOI: 10.1017/s095026881800345x


• Highly virulent PEAV strain GDS04 was passaged regularly to a total of 100 passages in Vero cells. • PEAV strain P100 is low pathogenic to newborn piglets. • The amino acid changes in P100 might be associated with PEAV attenuation. Porcine enteric alphacoronavirus (PEAV) is a newly identified swine enteropathogenic coronavirus that causes watery diarrhea in newborn piglets. In this study, an original, highly virulent PEAV strain GDS04 was serially passaged in Vero cells. The virus titers and sizes of syncytia increased gradually with the cell passages. Newborn piglets were orally inoculated with PEAV P15, P67 and P100. Compared with P15 and P67, P100 resulted in only mild clinical signs and intestinal lesions in piglets. The virus shedding in feces and viral antigens in intestinal tract were markedly reduced in P100-inoculated piglets. Importantly, all P100-inoculated newborn piglets survived, indicating that P100 was an attenuated variant. Sequence analysis revealed that the virulent strain GDS04 had four, one, six and eleven amino acid differences in membrane, nucleocapsid, spike and ORF1ab proteins, respectively, from P100. Furthermore, more differences in the predicted three-dimensional structure of S protein between GDS04 and P100 were observed, indicating that these differences might be associated with the pathogenicity of PEAV. Collectively, our research successfully prepared a PEAV attenuated variant which might serve as a live attenuated vaccine candidate against PEAV infection. [ABSTRACT FROM AUTHOR] Copyright of Veterinary Microbiology is the property of Elsevier B.V. and its content may not be copied or emailed to multiple sites or posted to a listserv without the copyright holder’s express written permission. However, users may print, download, or email articles for individual use. This abstract may be abridged. No warranty is given about the accuracy of the copy. Users should refer to the original published version of the material for the full abstract. (Copyright applies to all Abstracts.)

URL: http://search.ebscohost.com/login.aspx?direct=true&db=a9h&AN=141776899&site=ehost-live
DOI: 10.1016/j.vetmic.2019.108489

SEARCH STRATEGIES

Pubmed – May 15, 2020
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Medline – May 15, 2020

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PubMed – April 15, 2020, 4:25pm
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