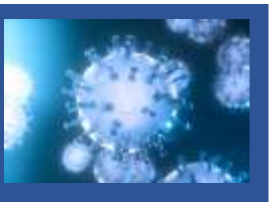
# COVID-19

***Jul 23-29, 2020***



# RESEARCH PUBLICATIONS

**Publication Date: July 29, 2020**

## Observations of the global epidemiology of COVID-19 from the prepandemic period using web-based surveillance: A cross-sectional analysis

### Abstract

*Background*: Scant data are available about global patterns of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) spread and global epidemiology of early confirmed cases of COVID-19 outside mainland China. We describe the global spread of SARS-CoV-2 and characteristics of COVID-19 cases and clusters before the characterisation of COVID-19 as a pandemic.

*Methods*: Cases of COVID-19 reported between Dec 31, 2019, and March 10, 2020 (ie, the prepandemic period), were identified daily from official websites, press releases, press conference transcripts, and social media feeds of national ministries of health or other government agencies. Case characteristics, travel history, and exposures to other cases were abstracted. Countries with at least one case were classified as affected. Early cases were defined as those among the first 100 cases reported from each country. Later cases were defined as those after the first 100 cases. We analysed reported travel to affected countries among the first case reported from each country outside mainland China, demographic and exposure characteristics among cases with age or sex information, and cluster frequencies and sizes by transmission settings.

*Findings*: Among the first case reported from each of 99 affected countries outside of mainland China, 75 (76%) had recent travel to affected countries; 60 (61%) had travelled to China, Italy, or Iran. Among 1200 cases with age or sex information, 874 (73%) were early cases. Among 762 early cases with age information, the median age was 51 years (IQR 35–63); 25 (3%) of 762 early cases occurred in children younger

than 18 years. Overall, 21 (2%) of 1200 cases were in health-care workers and none were in pregnant women. 101 clusters were identified, of which the most commonly identified transmission setting was households (76 [75%]; mean 2·6 cases per cluster [range 2–7]), followed by non-health-care occupational settings (14 [14%]; mean 4·3 cases per cluster [2–14]), and community gatherings (11 [11%]; mean 14·2 cases per cluster [4–36]).

*Interpretation*: Cases with travel links to China, Italy, or Iran accounted for almost two-thirds of the first reported COVID-19 cases from affected countries. Among cases with age information available, most were among adults aged 18 years and older. Although there were many clusters of household transmission among early cases, clusters in occupational or community settings tended to be larger, supporting a possible role for physical distancing to slow the progression of SARS-CoV-2 spread.

**Reference**

https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30581-8/fulltext

**Publication Date: July 27, 2020**

## Computationally optimized SARS-CoV-2 MHC class I and II vaccine formulations predicted to target human haplotype distributions

**Abstract**

A combinatorial machine learning method was presented to evaluate and optimize peptide vaccine formulations for SARS-CoV-2. This approach optimized the presentation likelihood of a diverse set of vaccine peptides conditioned on a target human-population HLA haplotype distribution and expected epitope drift. The proposed SARS-CoV-2 MHC class I vaccine formulations provided 93.21% predicted population coverage with at least five vaccine peptide-HLA average hits per person (≥ 1 peptide: 99.91%) with all vaccine peptides perfectly conserved across 4,690 geographically sampled SARS-CoV-2 genomes. The proposed MHC class II vaccine formulations provided 97.21% predicted coverage with at least five vaccine peptide-HLA average hits per person with all peptides having an observed mutation probability of ≤ 0.001. An open-source implementation of our design methods (OptiVax), vaccine evaluation tool

(EvalVax), as well as the data used in our design efforts were provided here: https://github.com/gifford-lab/optivax.

### Reference

https://www.cell.com/cell-systems/fulltext/S2405-4712(20)30238-6

## Covid-19 and the cardiovascular system: A comprehensive review

### Abstract

Cardiac injury in patients infected with the novel Coronavirus (COVID-19) seems to be associated with higher morbimortality. A broad review of the clinical evolution of COVID-19 was provided, emphasizing its impact and implications on the cardiovascular system. The pathophysiology of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was characterized by overproduction of inflammatory cytokines (IL-6 and TNF-α) leading to systemic inflammation and multiple organ dysfunction syndrome, acutely affecting the cardiovascular system. Hypertension (56.6%) and diabetes (33.8%) were the most prevalent comorbidities among individuals with COVID-19, who required hospitalization. Furthermore, cardiac injury, defined as elevated us-troponin I, significantly related to inflammation biomarkers (IL-6 and C-reactive protein (CRP), hyperferritinemia, and leukocytosis), portraying an important correlation between myocardial injury and inflammatory hyperactivity triggered by viral infection. Increased risk for myocardial infarction, fulminant myocarditis rapidly evolving with depressed systolic left ventricle function, arrhythmias, venous thromboembolism, and cardiomyopathies mimicking STEMI presentations were the most prevalent cardiovascular complications described in patients with COVID-19. Moreover, SARS-CoV-2 tropism and interaction with the RAAS system, through ACE2 receptor, possibly enhanced inflammation response and cardiac aggression, leading to imperative concerns about the use of ACEi and ARBs in infected patients. Cardiovascular implications resulted in a worse prognosis in patients with COVID-19, emphasizing the importance of precocious detection and implementation of optimal therapeutic strategies.

### Reference

https://www.nature.com/articles/s41371-020-0387-4

## T cell responses in patients with COVID-19

The role of T cells in the resolution or exacerbation of COVID-19, as well as their potential to provide long-term protection from reinfection with SARS-CoV-2, remaind debated. Nevertheless, recent studies have highlighted various aspects of T cell responses to SARS-CoV-2 infection that were starting to enable some general concepts to emerge.

**Reference**

https://www.nature.com/articles/s41577-020-0402-6

## A negative covariation between toxoplasmosis and CoVID-19 with alternative interpretations

Coronaviruses may exert severely negative effects on the mortality and morbidity of birds and mammals including humans and domestic animals. Most recently CoVID-19 has killed about half million people (27th of June, 2020). Susceptibility to this disease appears to differ markedly across different societies but the factors underlying this variability are not known. Given that prevalence of toxoplasmosis in human societies may serve as a proxy for hygiene, and it also exerts both direct and immune-mediated antiviral effects, we hypothesize a negative covariation between toxoplasmosis and measures of the CoVID-19 pandemic across countries. We obtained aged-adjusted toxoplasmosis prevalence of pregnant women from the literature. Since the differences in the CoVID-19 morbidity and mortality may depend on the different timing of the epidemics in each country, we applied the date of first documented CoVID-19 in each country as a proxy of susceptibility, with a statistical control for population size effects. Using these two indices, we show a highly significant negative co-variation between the two pandemics across 86 countries. Then, considering that the wealth of nations often co-varies with the prevalence of diseases, we introduced GDP per capita into our model. The prevalence of toxoplasmosis co-varies negatively, while the date of first CoVID-19 co-varies positively with GDP per capita across countries. Further, to control for the strong spatial autocorrelation among countries, we carried out a Spatial Structure Analyses of the relationships between the date of first CoVID-19, prevalence of toxoplasmosis, and GDP per capita. Results of this analysis did not confirm a direct causal relationship between toxoplasmosis and susceptibility to the CoVID-19 pandemics. As far as an analysis of observational data let us to suggest, it appears that the interaction between CoVID-19 and toxoplasmosis is mediated by GDP per capita and spatial effects. This prompts the question whether the formerly known covariations of CoVID-19 and BCG vaccination or air pollution might have also emerged as spurious indirect effects.

### Reference

https://www.nature.com/articles/s41598-020-69351-x

**Publication Date: July 25, 2020**

## The COVID-19 Drug and Gene Set Library

### Abstract

In a short period, many research publications that report sets of experimentally validated drugs as potential COVID-19 therapies have emerged. To organize this accumulating knowledge, we developed the COVID-19 Drug and Gene Set Library (https://amp.pharm.mssm.edu/covid19/), a collection of drug and gene sets related to COVID-19 research from multiple sources. The platform enables users to view, download, analyze, visualize, and contribute drug and gene sets related to COVID-19 research. To evaluate the content of the library, we compared the results from the six in-vitro drug screens for COVID-19 repurposing candidates. Surprisingly, we observe low overlap across screens while highlighting overlapping candidates that should receive more attention as potential therapeutics for COVID-19. Overall, the COVID-19 Drug and Gene Set Library can be used to identify community consensus, make researchers and clinicians aware of new potential therapies, enable machine learning applications, and facilitating the research community to work together towards a cure.

### Reference

Kuleshov, Maxim V., Daniel J. Stein, Daniel JB Clarke, Eryk Kropiwnicki, Kathleen M. Jagodnik, Alon Bartal, John E. Evangelista *et al*. "The COVID-19 Drug and Gene Set Library." *Patterns* (2020): 100090.

## Molecular and immunological diagnostic tests of COVID-19 – current status and challenges

### Abstract

Rapid spread of coronavirus disease 2019 (COVID-19) is ravaging the globe. Since its first report in December 2019, COVID-19 cases have exploded to over 14 million as of July 2020, claiming more than 600,000 lives. Implementing fast and widespread diagnostic tests is paramount to contain COVID-19, given the current lack of an effective therapeutic or vaccine. This review focuses on a broad description of currently available diagnostic tests to detect either the virus (SARS-CoV-2) or virus-induced immune responses. We specifically explain the working mechanisms of these tests and compare their analytical performance. These analyses will assist in selecting most effective tests for a given application, for example, epidemiology or global pandemic research, population screening, hospital-based testing, home-based and point-of-care testing, and therapeutic trials. Finally, we lay out the shortcomings of certain tests and future needs.

### Reference

Kilic, Tugba, Ralph Weissleder, and Hakho Lee. "Molecular and immunological diagnostic tests of COVID-19–current status and challenges." *iScience* (2020): 101406.

## The impact of obesity on COVID-19 complications: A retrospective cohort study

### Abstract

*Background:* Obesity is an epidemic in New York City, the global epicenter of the coronavirus pandemic. Previous studies suggest that obesity is a possible risk factor for adverse outcomes in COVID-19.

*Objective:* To elucidate the association between obesity and COVID-19 outcomes.

*Design:* Retrospective cohort study of COVID-19 hospitalized patients tested between March 10 and April 13, 2020.

*Setting:* SUNY Downstate Health Sciences University, a COVID-only hospital in New York.

*Participants:* In total, 684 patients were tested for COVID-19 and 504 were analyzed. Patients were categorized into three groups by BMI: normal (BMI 18.50–24.99), overweight (BMI 25.00–29.99), and obese (BMI ≥ 30.00).

*Measurements:* Primary outcome was 30-day in-hospital mortality, and secondary outcomes were intubation, acute kidney injury (AKI), acute respiratory distress syndrome (ARDS), and acute cardiac injury (ACI).

*Results:* There were 139 patients (27%) with normal BMI, 150 patients who were overweight (30%), and 215 patients with obesity (43%). After controlling for age, gender, diabetes, hypertension, and qSOFA score, there was a significantly increased risk of mortality in the overweight (RR 1.4, 95% CI 1.1–1.9) and obese groups (RR 1.3, 95% CI 1.0–1.7) compared with those with normal BMI. Similarly, there was a significantly increased relative risk for intubation in the overweight (RR 2.0, 95% CI 1.2–3.3) and obese groups (RR 2.4, 95% CI 1.5–4.0) compared with those with normal BMI. Obesity did not affect rates of AKI, ACI, or ARDS. Furthermore, obesity appears to significantly increase the risk of mortality in males (RR 1.4, 95% CI 1.0-2.0, P = 0.03), but not in females (RR 1.2, 95% CI 0.77–1.9, P = 0.40).

*Conclusion:* This study reveals that patients with overweight and obesity who have COVID-19 are at increased risk for mortality and intubation compared to those with normal BMI. These findings support the hypothesis that obesity is a risk factor for COVID-19 complications and should be a consideration in management of COVID-19.

### Reference

Nakeshbandi, Mohamed, Rohan Maini, Pia Daniel, Sabrina Rosengarten, Priyanka Parmar, Clara Wilson, Julie Minjae Kim *et al*. "The impact of obesity on COVID-19 complications: A retrospective cohort study." *International Journal of Obesity* (2020): 1-6.

## COVID-19: Immunopathogenesis and Immunotherapeutics

### Abstract

The recent novel coronavirus disease (COVID-19) outbreak, caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is seeing a rapid increase in infected patients worldwide. The host immune response to SARS-CoV-2 appears to play a critical role in disease pathogenesis and clinical manifestations. SARS-CoV-2 not only activates antiviral immune responses, but can also cause uncontrolled inflammatory responses characterized by marked pro-inflammatory cytokine release in patients with severe COVID-19, leading to lymphopenia, lymphocyte dysfunction, and granulocyte and monocyte abnormalities. These SARS-CoV-2-induced immune abnormalities may lead to infections by microorganisms, septic shock, and severe multiple organ dysfunction. Therefore, mechanisms underlying immune abnormalities in patients with COVID-19 must be elucidated to guide clinical management of the disease. Moreover, rational management of the immune responses to SARS-CoV-2, which includes enhancing anti-viral immunity while inhibiting systemic inflammation, may be key to successful treatment. In this review, we discuss the immunopathology of COVID-19, its potential mechanisms, and clinical implications to aid the development of new therapeutic strategies against COVID-19.

### Reference

Yang, Li, Shasha Liu, Jinyan Liu, Zhixin Zhang, Xiaochun Wan, Bo Huang, Youhai Chen, and Yi Zhang. "COVID-19: immunopathogenesis and Immunotherapeutics." *Signal Transduction and Targeted Therapy* 5, no. 1 (2020): 1-8.

**Publication Date: July 24, 2020**

## A carbohydrate-binding protein from the edible Lablab beans effectively blocks the infections of influenza viruses and SARS-CoV-2

### Abstract

The influenza virus hemagglutinin (HA) and coronavirus spike (S) protein mediate virus entry. HA and S proteins are heavily glycosylated, making them potential targets for carbohydrate binding agents such as lectins. Here we show that the lectin FRIL, isolated from hyacinth beans (Lablab purpureus), has anti-influenza and anti-SARS-CoV-2 activity. FRIL can neutralize 11 representative human and avian influenza strains at low nanomolar concentrations, and intranasal administration of FRIL is protective against lethal H1N1 infection in mice. FRIL binds preferentially to complex type N-glycans, and neutralizes viruses that possess complex type N-glycans on their

envelopes. As a homotetramer, FRIL is capable of aggregating influenza particles through multivalent binding and trapping influenza virions in cytoplasmic late endosomes, preventing their nuclear entry. Remarkably, FRIL also effectively neutralizes SARS-CoV-2, preventing viral protein production and cytopathic effect in host cells. These findings suggest potential application of FRIL for prevention and/or treatment of influenza and COVID-19.

### Reference

Liu, Yo-Min, Md Shahed-Al-Mahmud, Xiaorui Chen, Ting-Hua Chen, Kuo-Shiang Liao, Jennifer M. Lo, Yi-Min Wu *et al*. "A carbohydrate-binding protein from the edible Lablab beans effectively blocks the infections of influenza viruses and SARS-CoV-2." *Cell Reports* (2020): 108016.

## Point-of-care serological assays for delayed SARS-CoV-2 case identification among health-care workers in the UK: A prospective multicentre cohort study

### Abstract

*Background*: Health-care workers constitute a high-risk population for acquisition of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. Capacity for acute diagnosis via PCR testing was limited for individuals with mild to moderate SARS-CoV-2 infection in the early phase of the COVID-19 pandemic and a substantial proportion of health-care workers with suspected infection were not tested. We aimed to investigate the performance of point-of-care and laboratory serology assays and their utility in late case identification, and to estimate SARS-CoV-2 seroprevalence.

*Methods*: We did a prospective multicentre cohort study between April 8 and June 12, 2020, in two phases. Symptomatic health-care workers with mild to moderate symptoms were eligible to participate 14 days after onset of COVID-19 symptoms, as per the Public Health England (PHE) case definition. Health-care workers were recruited to the asymptomatic cohort if they had not developed PHE-defined COVID-19 symptoms since Dec 1, 2019. In phase 1, two point-of-care lateral flow serological assays, the Onsite CTK Biotech COVID-19 split IgG/IgM Rapid Test (CTK Bitotech, Poway, CA, USA) and the Encode SARS-CoV-2 split IgM/IgG One Step Rapid Test Device (Zhuhai Encode Medical Engineering, Zhuhai, China), were evaluated for performance against a laboratory immunoassay (EDI Novel Coronavirus COVID-19 IgG ELISA kit [Epitope Diagnostics, San Diego, CA, USA]) in 300 samples from health-care workers and 100 pre-COVID-19 negative control samples. In phase 2 (n=6440), serosurveillance was done among 1299 (93·4%) of 1391 health-care workers reporting symptoms, and in a subset of asymptomatic health-care workers (405 [8·0%] of 5049).

*Findings*: There was variation in test performance between the lateral flow serological assays; however, the Encode assay displayed reasonable IgG sensitivity (127 of 136; 93·4% [95% CI 87·8–96·9]) and specificity (99 of 100; 99·0% [94·6–100·0]) among PCR-proven cases and good agreement (282 of 300; 94·0% [91·3–96·7]) with the laboratory immunoassay. By contrast, the Onsite assay had reduced sensitivity (120 of 136; 88·2% [95% CI 81·6–93·1]) and specificity (94 of 100; 94·0% [87·4–97·8]) and agreement (254 of 300; 84·7% [80·6–88·7]). Five (7%) of 70 PCR-positive cases were negative across all assays. Late changes in lateral flow serological assay bands were recorded in 74 (9·3%) of 800 cassettes (35 [8·8%] of 400 Encode assays; 39 [9·8%] of 400 Onsite assays), but only seven (all Onsite assays) of these changes were concordant with the laboratory immunoassay. In phase 2, seroprevalence among the workforce was estimated to be 10·6% (95% CI 7·6–13·6) in asymptomatic health-care workers and 44·7% (42·0–47·4) in symptomatic health-care workers. Seroprevalence across the entire workforce was estimated at 18·0% (95% CI 17·0–18·9).

*Interpretation*: Although a good positive predictive value was observed with both lateral flow serological assays and ELISA, this agreement only occurred if the pre-test probability was modified by a strict clinical case definition. Late development of lateral flow serological assay bands would preclude postal strategies and potentially home testing. Identification of false-negative results among health-care workers across all assays suggest caution in interpretation of IgG results at this stage; for now, testing is perhaps best delivered in a clinical setting, supported by government advice about physical distancing.

## Reference

Pallett, Scott JC, Michael Rayment, Aatish Patel, Sophia AM Fitzgerald-Smith, Sarah J. Denny, Esmita Charani, Annabelle L. Mai et al. "Point-of-care serological assays for delayed SARS-CoV-2 case identification among health-care workers in the UK: a prospective multicentre cohort study." *The Lancet Respiratory Medicine* (2020).

## Covid-19 mortality is negatively associated with test number and government effectiveness

### Abstract

A question central to the Covid-19 pandemic is why the Covid-19 mortality rate varies so greatly across countries. This study aims to investigate factors associated with cross-country variation in Covid-19 mortality. Covid-19 mortality rate was calculated as number of deaths per 100 Covid-19 cases. To identify factors associated with Covid-19 mortality rate, linear regressions were applied to a cross-sectional dataset comprising 169 countries. We retrieved data from the Worldometer website, the Worldwide Governance Indicators, World Development Indicators, and Logistics Performance Indicators databases. Covid-19 mortality rate was negatively associated with Covid-19 test number per 100 people (RR = 0.92, $P = 0.001$), government effectiveness score (RR = 0.96, $P = 0.017$), and number of hospital beds (RR = 0.85, $P < 0.001$). Covid-19 mortality rate was positively associated with proportion of population aged 65 or older (RR = 1.12, $P < 0.001$) and transport infrastructure quality score (RR = 1.08, $P = 0.002$). Furthermore, the negative association between Covid-19 mortality and test number was stronger among low-income countries and countries with lower government effectiveness scores, younger populations and fewer hospital beds. Predicted mortality rates were highly associated with observed mortality rates (r = 0.77; $P < 0.001$). Increasing Covid-19 testing, improving government effectiveness and increasing hospital beds may have the potential to attenuate Covid-19 mortality.

### Reference

Liang, Li-Lin, Ching-Hung Tseng, Hsiu J. Ho, and Chun-Ying Wu. "Covid-19 mortality is negatively associated with test number and government effectiveness." *Scientific Reports* 10, no. 1 (2020): 1-7.

## Psychosocial effects of the COVID-19 pandemic on staff in a dental teaching hospital

### Abstract

*Introduction:* As COVID-19 rapidly developed across the UK, health services were forced to make radical changes. Within the dental department, all elective procedures

were cancelled and staff members were redeployed to support other services within the trust. Studies have demonstrated increased prevalence of psychiatric disorders among healthcare workers during virus pandemics.

*Aims:* To assess the psychosocial implications of COVID-19 on members of the dental team working within a large dental teaching hospital.

*Methodology:* A survey comprising a series of questions (closed and open) and a Generalised Anxiety Disorder assessment (GAD-7) was distributed to members of the dental team between 1-3 April 2020.

*Results:* A total of 120 surveys were completed; 53.3% of respondents displayed symptoms of generalised anxiety. The highest average GAD-7 score was noted among dental nurses. The most common concern was the impact of COVID-19 on friends and family followed by personal health and nature of the disease.

*Conclusion(s):* High anxiety levels and significant psychosocial implications were noted among dental staff during this virus pandemic. Our findings add to a growing body of data on the psychosocial impact of virus outbreaks on healthcare workers and highlight the importance of wellbeing initiatives for healthcare workers to be placed at the forefront of future pandemic crisis planning.

**Reference**

https://www.nature.com/articles/s41415-020-1792-3

**Publication Date: July 23, 2020**

## SARS-CoV-2 RNA Dependent RNA polymerase (RdRp) – A drug repurposing study

**Abstract**

The outbreak of SARS-CoV-2 in December 2019 in China subsequently lead to a pandemic. Lack of vaccine and specific anti-viral drugs started a global health disaster. For a sustained control and protection, development of potential anti-viral drugs is one of the targeted approach. Although, designing and developing a panel of new drugs molecules are always encouraged. However, in the current emergency, drug

repurposing study is one of the most effective and fast track option. The crystal structure of a SARS-CoV-2 (Severe acute respiratory syndrome coronavirus 2) RNA Dependent RNA Polymerase (RdRp) has recently been deciphered through X-ray crystallography. The single-chain of core RNA Dependent RNA Polymerase relies on virus-encoded cofactors nsp7 and two units of nsp8 for its optimum function. This study explored the FDA approved database of 7922 molecules and screened against the core polymerase along with cofactors. Here we report a panel of FDA approved drugs that show substantial interactions with key amino acid residues of the active site. Interestingly, some of the identified drugs (Ornipressin, Lypressin, Examorelin, Polymyxin B1) bind strongly within the binding pockets of both forms of RdRp. Besides, we found strong candidates for the complex form as well which include Nacortocin, Cistinexine, Cisatracurium (among others). These drugs have the potential to be considered while contriving therapeutic options.

### Reference

Ahmad, Jamshaid, Saima Ikram, Fawad Ahmad, Irshad Ur Rehman, and Maryam Mushtaq. "SARS-CoV-2 RNA Dependent RNA Polymerase (RdRp)–A drug repurposing study." *Heliyon* (2020): e04502.

## A SARS-CoV-2 surrogate virus neutralization test based on antibody-mediated blockage of ACE2–spike protein–protein interaction

### Abstract

A robust serological test to detect neutralizing antibodies to SARS-CoV-2 is urgently needed to determine not only the infection rate, herd immunity and predicted humoral protection, but also vaccine efficacy during clinical trials and after large-scale vaccination. The current gold standard is the conventional virus neutralization test requiring live pathogen and a biosafety level 3 laboratory. Here, we report a SARS-CoV-2 surrogate virus neutralization test that detects total immunodominant neutralizing antibodies targeting the viral spike (S) protein receptor-binding domain in an isotype- and species-independent manner. Our simple and rapid test is based on antibody-mediated blockage of the interaction between the angiotensin-converting enzyme 2 (ACE2) receptor protein and the receptor-binding domain. The test, which has been validated with two cohorts of patients with COVID-19 in two different countries, achieves

99.93% specificity and 95–100% sensitivity, and differentiates antibody responses to several human coronaviruses. The surrogate virus neutralization test does not require biosafety level 3 containment, making it broadly accessible to the wider community for both research and clinical applications.

## Reference

Tan, Chee Wah, Wan Ni Chia, Mark IC Chen, Zhiliang Hu, Barnaby E. Young, Yee-Joo Tan, Yongxiang Yi, David C. Lye, Danielle E. Anderson, and Lin-Fa Wang. "A SARS-CoV-2 surrogate virus neutralization test (sVNT) based on antibody-mediated blockage of ACE2-spike (RBD) protein-protein interaction." *Nature Biotechnology* (2020).

**Publication Date: July 23, 2020**

## Structure-based design of prefusion-stabilized SARS-CoV-2 spikes

The COVID-19 pandemic has led to accelerated efforts to develop therapeutics and vaccines. A key target of these efforts is the spike (S) protein, which is metastable and difficult to produce recombinantly. Here, we characterized 100 structure-guided spike designs and identified 26 individual substitutions that increased protein yields and stability. Testing combinations of beneficial substitutions resulted in the identification of HexaPro, a variant with six beneficial proline substitutions exhibiting ~10-fold higher expression than its parental construct and the ability to withstand heat stress, storage at room temperature, and three freeze-thaw cycles. A 3.2 Å-resolution cryo-EM structure of HexaPro confirmed that it retains the prefusion spike conformation. High-yield production of a stabilized prefusion spike protein will accelerate the development of vaccines and serological diagnostics for SARS-CoV-2.

### Reference

https://science.sciencemag.org/content/early/2020/07/22/science.abd0826?rss=1

## Global quieting of high-frequency seismic noise due to COVID-19 pandemic lockdown measures

Human activity causes vibrations that propagate into the ground as high-frequency seismic waves. Measures to mitigate the COVID-19 pandemic caused widespread changes in human activity, leading to a months-long reduction in seismic noise of up to 50%. The 2020 seismic noise quiet period is the longest and most prominent global anthropogenic seismic noise reduction on record. While the reduction is strongest at surface seismometers in populated areas, this seismic quiescence extends for many kilometers radially and hundreds of meters in depth. This provides an opportunity to detect subtle signals from subsurface seismic sources that would have been concealed in noisier times and to benchmark sources of anthropogenic noise. A strong correlation between seismic noise and independent measurements of human mobility suggests that seismology provides an absolute, real-time estimate of population dynamics.

**Reference**

https://science.sciencemag.org/content/early/2020/07/22/science.abd2438?rss=1

## Structural basis for neutralization of SARS-CoV-2 and SARS-CoV by a potent therapeutic antibody

The COVID-19 pandemic caused by the SARS-CoV-2 virus has resulted in an unprecedented public health crisis. There are no approved vaccines or therapeutics for treating COVID-19. Here we reported a humanized monoclonal antibody, H014, efficiently neutralizes SARS-CoV-2 and SARS-CoV pseudoviruses as well as authentic SARS-CoV-2 at nM level by engaging the S receptor binding domain (RBD). Importantly, H014 administration reduced SARS-CoV-2 titers in the infected lungs and prevented pulmonary pathology in hACE2 mouse model. Cryo-EM characterization of the SARS-CoV-2 S trimer in complex with the H014 Fab fragment unveiled a novel conformational epitope, which is only accessible when the RBD is in open conformation. Biochemical, cellular, virological and structural studies demonstrated that H014 prevents attachment of SARS-CoV-2 to its host cell receptors. Epitope analysis of available neutralizing antibodies against SARS-CoV and SARS-CoV-2 uncover broad cross-protective epitopes. Our results highlight a key role for antibody-based therapeutic interventions in the treatment of COVID-19.

**Reference**

https://science.sciencemag.org/content/early/2020/07/22/science.abc5881?rss=1

## Evolution and epidemic spread of SARS-CoV-2 in Brazil

Brazil currently has one of the fastest growing SARS-CoV-2 epidemics in the world. Owing to limited available data, assessments of the impact of non-pharmaceutical interventions (NPIs) on virus spread remain challenging. Using a mobility-driven transmission model, we show that NPIs reduced the reproduction number from >3 to 1–1.6 in São Paulo and Rio de Janeiro. Sequencing of 427 new genomes and analysis of a geographically representative genomic dataset identified >100 international virus introductions in Brazil. We estimate that most (76%) of the Brazilian strains fell in three clades that were introduced from Europe between 22 February11 March 2020. During the early epidemic phase, we found that SARS-CoV-2 spread mostly locally and withinstate borders. After this period, despite sharp decreases in air travel, we estimated multiple exportations from large urban centers that coincided with a 25% increase in average travelled distances in national flights. This study sheds new light on the epidemic transmission and evolutionary trajectories of SARS-CoV-2 lineages in Brazil, and provide evidence that current interventions remain insufficient to keep virus transmission under control in the country.

**Reference**

https://science.sciencemag.org/content/early/2020/07/22/science.abc5881?rss=1

# PERSPECTIVE

**Publication Date: July 29, 2020**

## The COVID-19 lockdowns: A window into the Earth System

### Abstract

Restrictions to reduce human interaction have helped to avoid greater suffering and death from the COVID-19 pandemic, but have also created socioeconomic hardship. This disruption is unprecedented in the modern era of global observing networks, pervasive sensing and large-scale tracking of human mobility and behaviour, creating a unique test bed for understanding the Earth System. In this Perspective, we hypothesize the immediate and long-term Earth System responses to COVID-19 along two multidisciplinary cascades: energy, emissions, climate and air quality; and poverty, globalization, food and biodiversity. While short-term impacts are dominated by direct effects arising from reduced human activity, longer-lasting impacts are likely to result from cascading effects of the economic recession on global poverty, green investment and human behaviour. These impacts offer the opportunity for novel insight, particularly with the careful deployment of targeted data collection, coordinated model experiments and solution-oriented randomized controlled trials, during and after the pandemic.

### Reference

https://www.nature.com/articles/s41559-020-1275-6

## Conserving Africa’s wildlife and wildlands through the COVID-19 crisis and beyond

The SARS-CoV-2 virus and COVID-19 illness are driving a global crisis. Governments have responded by restricting human movement, which has reduced economic activity. These changes may benefit biodiversity conservation in some ways, but in Africa, we contend that the net conservation impacts of COVID-19 will be strongly negative. Here, we describe how the crisis creates a perfect storm of reduced funding, restrictions on the operations of conservation agencies, and elevated human threats to nature. We identify the immediate steps necessary to address these challenges and support ongoing conservation efforts. We then highlight systemic flaws in contemporary conservation and identify opportunities to restructure for greater resilience. Finally, we emphasize the critical importance of conserving habitat and regulating unsafe wildlife trade practices to reduce the risk of future pandemics.

**Reference**

https://www.nature.com/articles/s41559-020-1275-6

## Publication Date: July 24, 2020

### Mathematical models to guide pandemic response

Models are one tool among many for tackling the pandemic, but they are perhaps the best framework for grappling with these possible futures. The ongoing coronavirus disease 2019 (COVID-19) pandemic has put mathematical models in the spotlight. As the theoretical biologist Robert May wrote: "*the virtue of a mathematical model...is that it forces clarity and precision upon conjecture, thus enabling meaningful comparison between the consequences of basic assumptions and the empirical facts*". On page 413 of this issue, Walker *et al.* use a mathematical model to study the impact and burden of COVID-19 across a wide range of socioeconomic and demographic settings, with a focus on low- and middle-income countries (LMICs). Their analyses showed that limited health care capacity in LMICs could counterbalance the benefits of a generally younger population. Unless these countries control the spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus causing COVID-19, high disease burdens are likely. This work adds to a growing corpus of disease modeling designed to inform and guide the pandemic response. For more details, see the link given below.

**Reference**

https://science.sciencemag.org/content/369/6502/368

### The COVID-19 pandemic and human fertility

The coronavirus disease 2019 (COVID-19) pandemic will have consequences for human populations. Worldwide, mortality levels are certainly affected. The worst-hit northern Italian provinces recorded losses of period life expectancy of 2 to 3.5 years for men and 1.1. to 2.5 years for women, the largest decline in life expectancy since the

1918–1919 influenza pandemic and World War II. Similar patterns follow in other countries. With the focus firmly on deaths, the scientific debate risks overlooking that population dynamics are also shaped by fertility trajectories. Throughout history, spikes in mortality owing to events, such as wars, famines, and pandemics were followed by changes in fertility, resulting in fewer births in the short term and by recuperation in subsequent years. Economic and social change triggered by a pandemic is also likely to influence childbearing intentions and completed fertility. How the COVID-19 pandemic will affect fertility has implications for the rate of population aging, shaping future health challenges and economic growth potential across the globe. For more details, see the link given below.

**Reference**

https://science.sciencemag.org/content/369/6502/370

## Crosstalk between COVID-19 and prostate cancer

A new coronavirus, named SARS-CoV-2, emerged in Wuhan city, China, in December 2019 causing atypical pneumonia and affecting multiple body organs. The rapidly increasing numbers of infected patients and deaths due to COVID-19 disease necessitated declaring it as a global pandemic. Efforts were combined since then to rapidly develop a treatment and/or a vaccine to combat the deadly virus. Drug repurposing approach has been pursued as a temporary management tactic to treat COVID-19 patients. However, reports about the efficacy of many of the used drugs had been controversial with a dire need to keep the ongoing efforts for rapid development of new treatments. Promising data came out pointing to a possible hidden liaison between prostate cancer (PCa) and COVID-19, where androgen-deprivation therapies (ADT) used in PCa had been shown to instigate a protective role against COVID-19. Delving into the possible mechanisms underlying the crosstalk between COVID-19 and PCa alludes a potential association between SARS-CoV-2 targets on host epithelial cells and PCa genetic aberrations and molecular signatures, including AR and TMPRSS2. The question remains: Can PCa treatments serve as potential therapeutic options for COVID-19 patients?

**Reference**

https://www.nature.com/articles/s41391-020-0262-y

# COMMENT

**Publication Date: July 28, 2020**

## The challenges of informative wastewater sampling for SARS-CoV-2 must be met: lessons from polio eradication

Since the emergence and spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which has caused the COVID-19 pandemic, many countries have rapidly expanded their viral surveillance systems. Wastewater sampling has been increasingly implemented, as substantial quantities of SARS-CoV-2 are shed in the stool of infected individuals. So far, wastewater sampling has retrospectively shown that virus is present in cities several months before large COVID-19 outbreaks, that there is a correlation between quantitative RT-PCR data and the reported incidence of cases, and that the presence of SARS-CoV-2 in wastewater is ubiquitous. There are numerous benefits of wastewater sampling, but the collection and interpretation of data is an emerging field. Within the Global Polio Eradication Initiative, wastewater sampling has successfully been used to detect polioviruses and inform eradication for several decades. This virological analysis and investigation of wastewater has been done by the Global Polio Laboratory Network and independent laboratories. In this comment, several challenges of wastewater sampling for SARS-CoV-2 are highlighted and lessons are outlined that can be learnt from polio eradication. For more details, read the link given below.

**Reference**

https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(20)30100-2/fulltext

**Publication Date: July 23, 2020**

## Management of mother–newborn dyads in the COVID-19 era

Severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) has resulted in more than 11·6 million cases of COVID-19 and 538 000 deaths as of July 7, 2020. The USA is the worst affected country, with more than 2·9 million cases. Evidence regarding transmission risk, clinical presentation, and consequences of SARS-CoV-2 among neonates of infected mothers is scarce. Risk of vertical transmission appears to be low, which is consistent with other coronaviruses. SARS-CoV-2 has been detected within 48 h of birth among neonates of positive mothers; however, this might represent horizontal transmission. Early reports indicate that SARS-CoV-2-positive neonates usually have mild disease. Analyses to date suggest that breastmilk is unlikely to be a source of infection. For more details, read the link given below.

**Reference**

https://www.thelancet.com/journals/lanchi/article/PIIS2352-4642(20)30241-8/fulltext

**Publication Date: July 28, 2020**

## Coronavirus research updates: Mutations allow virus to elude antibodies

Nature wades through the literature on the new coronavirus — and summarizes key papers as they appear.

*Mutations in SARS-CoV-2 might help the virus to thwart potent immune molecules (July 28, 2020):*

The blood of many people who recover from COVID-19 contains immune-system molecules called neutralizing antibodies that disable particles of the new coronavirus. Most such antibodies recognize the new coronavirus's spike protein, which the virus uses to infect cells. Researchers hope that these molecules can be used as therapies, and can be elicited by vaccines. Theodora Hatziioannou and Paul Bieniasz at the Rockefeller University in New York City and their colleagues engineered a version of the vesicular stomatitis virus, which infects livestock, to make the spike protein. They then grew the virus in the presence of neutralizing. The spike protein in the engineered viruses acquired mutations that allowed the viruses to escape recognition by a range of neutralizing antibodies.

*The power of China's virus-control campaign is seen in pattern of symptoms (July 27, 2020):*

In China, a key metric of epidemics called the serial interval shrank drastically soon after the new coronavirus's arrival — a finding that underscores the success of China's testing and isolation efforts.

The serial interval is the average time between the onset of symptoms in a chain of people infected by a pathogen. Benjamin Cowling at the University of Hong Kong and his colleagues modelled the spread of SARS-CoV-2 in China and found that the serial interval plummeted from 7.8 days to 2.6 days over a 5-week period starting on 9 January. The researchers said that early isolation of cases prevented transmission that would otherwise have occurred later in an infectious period, leading to fewer cases and slowing the spread of the virus. As a result, most of the remaining transmissions occurred either before infected people showed symptoms or early in the symptomatic phase, and the serial interval shrank. The authors suggest the serial interval distribution be used in real time to track the changing transmissibility of the virus.

*Dogs' and cats' infection rates mirror those of people (July 24, 2020):*

Cats and dogs are just as likely to be infected with SARS-CoV-2 as people are, according to a survey in northern Italy that is the largest study of pets so far.

Nicola Decaro at the University of Bari and his colleagues took nose, throat or rectal swabs of 540 dogs and 277 cats in northern Italy between March and May. The animals lived in homes with infected people, or in regions severely affected by COVID-19. None of the pets tested positive for SARS-CoV-2 viral RNA, but in further tests of antibodies against the virus circulating in the blood of some animals, the researchers found that around 3% of dogs and 4% of cats showed evidence of previous infection. Infection rates among cats and dogs were comparable with those among people in Europe at the time of testing, suggesting that it is not unusual for pets to be infected. The findings have not yet been peer reviewed.

## Reference

https://www.nature.com/articles/d41586-020-00502-w

# CORRESPONDANCE

**Publication Date: July 28, 2020**

## Lung fibrosis: an undervalued finding in COVID-19 pathological series

With the COVID-19 pandemic having reached tremendous proportions, post-mortem series are under the limelight to explain many of the peculiar clinical findings. Pathological descriptions of disease are fundamental for understanding pathogenetic features and might inform new treatments. Indeed, the widely discussed identification of thrombosis in patients with COVID-19 has garnered much interest, and has resulted in new treatment strategies, with anticoagulants now part of patient management.

In their Article, Luca Carsana and colleagues describe the lung findings of 38 patients who died with COVID-19 and show that early-phase or intermediate-phase diffuse alveolar damage is the main pathological finding, as well as fibrin thrombi in small arterial vessels. Other autoptic series, composed of fewer cases, also show thrombotic events to be findings specifically related to COVID-19. The fibrotic changes seen in patients who died with COVID-19 who had severe disease of long duration have been, however, only briefly touched upon in published studies, and no complete pathological description of these cases is available. As more pathological information is being collected from COVID-19 post-mortem series, a clearer picture of the disease, and its possible short-term and long-term complications, will emerge and hopefully aid treatment. For more details, read the link given below.

### Reference

https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30582-X/fulltext

# VIEWPOINT

**Publication Date: July 24, 2020**

## Particle sizes of infectious aerosols: implications for infection control

The global pandemic of COVID-19 has been associated with infections and deaths among health-care workers. This Viewpoint of infectious aerosols is intended to inform appropriate infection control measures to protect health-care workers. Studies of cough aerosols and of exhaled breath from patients with various respiratory infections have shown striking similarities in aerosol size distributions, with a predominance of pathogens in small particles (<5 μm). These are immediately respirable, suggesting the need for personal respiratory protection (respirators) for individuals in close proximity to patients with potentially virulent pathogens. There is no evidence that some pathogens are carried only in large droplets. Surgical masks might offer some respiratory protection from inhalation of infectious aerosols, but not as much as respirators. However, surgical masks worn by patients reduce exposures to infectious aerosols to health-care workers and other individuals. The variability of infectious aerosol production, with some so-called super-emitters producing much higher amounts of infectious aerosol than most, might help to explain the epidemiology of super-spreading. Airborne infection control measures are indicated for potentially lethal respiratory pathogens such as severe acute respiratory syndrome coronavirus 2.

### Reference

https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(20)30323-4/fulltext