COVID-19

Dec 10 - 16, 2020

RESEARCH PUBLICATIONS

Publication Date: Dec 16, 2020

Exploring optimal control of epidemic spread using reinforcement learning

Abstract

Pandemic defines the global outbreak of a disease having a high transmission rate. The impact of a pandemic situation can be lessened by restricting the movement of the mass. However, one of its concomitant circumstances is an economic crisis. In this article, we demonstrate what actions an agent (trained using reinforcement learning) may take in different possible scenarios of a pandemic depending on the spread of disease and economic factors. To train the agent, we design a virtual pandemic scenario closely related to the present COVID-19 crisis. Then, we apply reinforcement learning, a branch of artificial intelligence, that deals with how an individual (human/machine) should interact on an environment (real/virtual) to achieve the cherished goal. Finally, we demonstrate what optimal actions the agent perform to reduce the spread of disease while considering the economic factors. In our experiment, we let the agent find an optimal solution without providing any prior knowledge. After training, we observed that the agent places a long length lockdown to reduce the first surge of a disease. Furthermore, the agent places a combination of cyclic lockdowns and short length lockdowns to halt the resurgence of the disease. Analyzing the agent's performed actions, we discover that the agent decides movement restrictions not only based on the number of the infectious population but also considering the reproduction rate of the disease. The estimation and policy of the agent may improve the human-strategy of placing lockdown so that an economic crisis may be avoided while mitigating an infectious disease.

Reference

https://www.nature.com/articles/s41598-020-79147-8

Prediction of disease progression in patients with COVID-19 by artificial intelligence assisted lesion quantification

Abstract

To investigate the value of artificial intelligence (AI) assisted quantification on initial chest CT for prediction of disease progression and clinical outcome in patients with coronavirus disease 2019 (COVID-19). Patients with confirmed COVID-19 infection and initially of non-severe type were retrospectively included. The initial CT scan on admission was used for imaging analysis. The presence of ground glass opacity (GGO), consolidation and other findings were visually evaluated. CT severity score was calculated according to the extent of lesion involvement. In addition, AI based quantification of GGO and consolidation volume were also performed. 123 patients (mean age: 64.43 ± 14.02; 62 males) were included. GGO + consolidation was more frequently revealed in progress-to-severe group whereas pure GGO was more likely to be found in non-severe group. Compared to non-severe group, patients in progress-to-severe group had larger GGO volume (167.33 ± 167.88 cm3 versus 101.12 ± 127 cm3, $p = 0.013$) as well as consolidation volume (40.85 ± 60.4 cm3 versus 6.63 ± 14.91 cm3, $p < 0.001$). Among imaging parameters, consolidation volume had the largest area under curve (AUC) in discriminating non-severe from progress-to-severe group (AUC = 0.796, $p < 0.001$) and patients with or without critical events (AUC = 0.754, $p < 0.001$). According to multivariate regression, consolidation volume and age were two strongest predictors for disease progression (hazard ratio: 1.053 and 1.071, p: 0.006 and 0.008) whereas age and diabetes were predictors for unfavorable outcome. Consolidation volume quantified on initial chest CT was the strongest predictor for disease severity progression and larger consolidation volume was associated with unfavorable clinical outcome.

Reference

https://www.nature.com/articles/s41598-020-79097-1

Genetic architecture of host proteins involved in SARS-CoV-2 infection

Abstract

Understanding the genetic architecture of host proteins interacting with SARS-CoV-2 or mediating the maladaptive host response to COVID-19 can help to identify new or repurpose existing drugs targeting those proteins. We present a genetic discovery study of 179 such host proteins among 10,708 individuals using an aptamer-based technique. We identify 220 host DNA sequence variants acting in cis (MAF 0.01-49.9%) and explaining 0.3-70.9% of the variance of 97 of these proteins, including 45 with no previously known protein quantitative trait loci (pQTL) and 38 encoding current drug targets. Systematic characterization of pQTLs across the phenome identified protein-drug-disease links and evidence that putative viral interaction partners such as MARK3 affect immune response. Our results accelerate the evaluation and prioritization of new drug development programmes and repurposing of trials to prevent, treat or reduce adverse outcomes. Rapid sharing and detailed interrogation of results is facilitated through an interactive webserver (https://omicscience.org/apps/covidpgwas/).

Reference

https://www.nature.com/articles/s41467-020-19996-z

Dynamic profiles of SARS-Cov-2 infection from five Chinese family clusters in the early stage of the COVID-19 pandemic

Abstract

Although several cases of family clusters with SARS-Cov-2 infection have been reported, there are still limited data preventing conclusions from being drawn regarding the characteristics and laboratory findings in the COVID-19 population within family clusters. In the present study, we retrospectively collected five family clusters with COVID-19 and summarized the dynamic profiles of the clinical characteristics, laboratory findings, immune markers, treatment and prognosis of this population. Furthermore, we also compared clinical and laboratory data between the SARS-Cov-2 infection with family cluster (n = 21) and those without family cluster (n = 16). We demonstrated that the duration of SARS-Cov-2 replication might be varied based on the different family clusters

due to their different genetic backgrounds. The onset improved lung radiology might start at the end of the SARS-Cov-2 positive period. Furthermore, the obtained results demonstrated that similar basic characteristics and clinical findings seem to exist between the cases with SARS-Cov-2 and without family clusters. The serum level of ferritin might have a different biological function and be a new biomarker for the family cluster. Further studies with larger numbers of patients are required.

Reference

https://www.nature.com/articles/s41598-020-79035-1

ORF3a of the COVID-19 virus SARS-CoV-2 blocks HOPS complex-mediated assembly of the SNARE complex required for autolysosome formation

Abstract

Autophagy acts as a cellular surveillance mechanism to combat invading pathogens. Viruses have evolved various strategies to block autophagy and even subvert it for their replication and release. Here we demonstrated that ORF3a of the COVID-19 virus SARS-CoV-2 inhibits autophagy activity by blocking fusion of autophagosomes/amphisomes with lysosomes. The late endosome-localized ORF3a directly interacts with and sequestrates the HOPS component VPS39, thereby preventing HOPS complex from interacting with the autophagosomal SNARE protein STX17. This blocks assembly of the STX17-SNAP29-VAMP8 SNARE complex, which mediates autophagosome/amphisome fusion with lysosomes. Expression of ORF3a also damages lysosomes and impairs their function. SARS-CoV-2 virus infection blocks autophagy, resulting in accumulation of autophagosomes/amphisomes, and causes late endosomal sequestration of VPS39. Surprisingly, ORF3a from the SARS virus SARS-CoV fails to interact with HOPS or block autophagy. Our study reveals a mechanism by which SARS-CoV-2 evades lysosomal destruction and provides insights for developing new strategies to treat COVID-19.

Reference

https://www.cell.com/developmental-cell/fulltext/S1534-5807(20)31016-9

Inclusion of pregnant women in COVID-19 treatment trials: A review and global call to action

Abstract

Inclusion of pregnant women in COVID-19 clinical trials would allow evaluation of effective therapies that might improve maternal health, pregnancy, and birth outcomes, and avoid the delay of developing treatment recommendations for pregnant women. We explored the inclusion of pregnant women in treatment trials of COVID-19 by reviewing ten international clinical trial registries at two timepoints in 2020. We identified 155 COVID-19 treatment studies of non-biological drugs for the April 7–10, 2020 timepoint, of which 124 (80%) specifically excluded pregnant women. The same registry search for the July 10–15, 2020 timepoint, yielded 722 treatment studies, of which 538 (75%) specifically excluded pregnant women. We then focused on studies that included at least one of six drugs (remdesivir, lopinavir–ritonavir, interferon beta, corticosteroids, chloroquine and hydroxychloroquine, and ivermectin) under evaluation for COVID-19. Of 176 such studies, 130 (74%) listed pregnancy as an exclusion criterion. Of 35 studies that evaluated high-dose vitamin treatment for COVID-19, 27 (77%) excluded pregnant women. Despite the surge in treatment studies for COVID-19, the proportion excluding pregnant women remains consistent. Exclusion was not well justified as many of the treatments being evaluated have no or low safety concerns during pregnancy. Inclusion of pregnant women in clinical treatment trials is urgently needed to identify effective COVID-19 treatment for this population.

Reference

https://www.thelancet.com/journals/langlo/article/PIIS2214-109X(20)30484-8/fulltext

Cell-type-specific immune dysregulation in severely ill COVID-19 patients

Abstract

Recent studies have demonstrated immunologic dysfunction in severely ill coronavirus disease 2019 (COVID-19) patients. We use single-cell RNA sequencing (scRNA-seq) to analyze the transcriptome of peripheral blood mononuclear cells (PBMCs) from healthy (n = 3) and COVID-19 patients with moderate disease (n = 5), acute respiratory distress

syndrome (ARDS, n = 6), or recovering from ARDS (n = 6). Our data reveal transcriptomic profiles indicative of defective antigen presentation and interferon (IFN) responsiveness in monocytes from ARDS patients, which contrasts with higher responsiveness to IFN signaling in lymphocytes. Furthermore, genes involved in cytotoxic activity are suppressed in both natural killer (NK) and CD8 T lymphocytes, and B cell activation is deficient, which is consistent with delayed viral clearance in severely ill COVID-19 patients. Our study demonstrates that COVID-19 patients with ARDS have a state of immune imbalance in which dysregulation of both innate and adaptive immune responses may be contributing to a more severe disease course.

Reference

https://www.cell.com/cell-reports/fulltext/S2211-1247(20)31579-5

Force-dependent stimulation of rna unwinding by SARS-CoV-2 nsp13 helicase

Abstract

The superfamily 1 helicase nonstructural protein 13 (nsp13) is required for SARS-CoV-2 replication. The mechanism and regulation of nsp13 has not been explored at the single-molecule level. Specifically, force-dependent unwinding experiments have yet to be performed for any coronavirus helicase. Here, using optical tweezers, we find that nsp13 unwinding frequency, processivity, and velocity increase substantially when a destabilizing force is applied to the RNA substrate. These results, along with bulk assays, depict nsp13 as an intrinsically weak helicase that can be activated >50-fold by piconewton forces. Such force-dependent behavior contrasts the known behavior of other viral monomeric helicases, such as hepatitis C virus NS3, and instead draws stronger parallels to ring-shaped helicases. Our findings suggest that mechanoregulation, which may be provided by a directly bound RNA-dependent RNA polymerase, enables on-demand helicase activity on the relevant polynucleotide substrate during viral replication.

Reference

https://www.cell.com/biophysj/fulltext/S0006-3495(20)33210-0

Hyperactivation of P2X7 receptors as a culprit of COVID-19 neuropathology

Abstract

Scientists and health professionals are exhaustively trying to contain the coronavirus disease 2019 (COVID-19) pandemic by elucidating viral invasion mechanisms, possible drugs to prevent viral infection/replication, and health cares to minimize individual exposure. Although neurological symptoms are being reported worldwide, neural acute and long-term consequences of SARS-CoV-2 are still unknown. COVID-19 complications are associated with exacerbated immunoinflammatory responses to SARS-CoV-2 invasion. In this scenario, pro-inflammatory factors are intensely released into the bloodstream, causing the so-called “cytokine storm”. Both pro-inflammatory factors and viruses may cross the blood–brain barrier and enter the central nervous system, activating neuroinflammatory responses accompanied by hemorrhagic lesions and neuronal impairment, which are largely described processes in psychiatric disorders and neurodegenerative diseases. Therefore, SARS-CoV-2 infection could trigger and/or worse brain diseases. Moreover, patients with central nervous system disorders associated to neuroimmune activation (e.g. depression, Parkinson’s and Alzheimer’s disease) may present increased susceptibility to SARS-CoV-2 infection and/or achieve severe conditions. Elevated levels of extracellular ATP induced by SARS-CoV-2 infection may trigger hyperactivation of P2X7 receptors leading to NLRP3 inflammasome stimulation as a key mediator of neuroinvasion and consequent neuroinflammatory processes, as observed in psychiatric disorders and neurodegenerative diseases. In this context, P2X7 receptor antagonism could be a promising strategy to prevent or treat neurological complications in COVID-19 patients.

Reference

https://www.nature.com/articles/s41380-020-00965-3

Dynamic profiles of SARS-Cov-2 infection from five Chinese family clusters in the early stage of the COVID-19 pandemic

Abstract

Although several cases of family clusters with SARS-Cov-2 infection have been reported, there are still limited data preventing conclusions from being drawn regarding the characteristics and laboratory findings in the COVID-19 population within family clusters. In the present study, we retrospectively collected five family clusters with COVID-19 and summarized the dynamic profiles of the clinical characteristics, laboratory findings, immune markers, treatment and prognosis of this population. Furthermore, we also compared clinical and laboratory data between the SARS-Cov-2 infection with family cluster (n = 21) and those without family cluster (n = 16). We demonstrated that the duration of SARS-Cov-2 replication might be varied based on the different family clusters due to their different genetic backgrounds. The onset improved lung radiology might start at the end of the SARS-Cov-2 positive period. Furthermore, the obtained results demonstrated that similar basic characteristics and clinical findings seem to exist between the cases with SARS-Cov-2 and without family clusters. The serum level of ferritin might have a different biological function and be a new biomarker for the family cluster. Further studies with larger numbers of patients are required.

Reference

https://www.nature.com/articles/s41598-020-79035-1

Genetic architecture of host proteins involved in SARS-CoV-2 infection

Abstract

Understanding the genetic architecture of host proteins interacting with SARS-CoV-2 or mediating the maladaptive host response to COVID-19 can help to identify new or repurpose existing drugs targeting those proteins. We present a genetic discovery study of 179 such host proteins among 10,708 individuals using an aptamer-based technique. We identify 220 host DNA sequence variants acting in cis (MAF 0.01-49.9%) and explaining 0.3-70.9% of the variance of 97 of these proteins, including 45 with no previously known protein quantitative trait loci (pQTL) and 38 encoding current drug

targets. Systematic characterization of pQTLs across the phenome identified protein-drug-disease links and evidence that putative viral interaction partners such as MARK3 affect immune response. Our results accelerate the evaluation and prioritization of new drug development programmes and repurposing of trials to prevent, treat or reduce adverse outcomes. Rapid sharing and detailed interrogation of results is facilitated through an interactive webserver (https://omicscience.org/apps/covidpgwas/).

Reference

https://www.nature.com/articles/s41467-020-19996-z

Prediction of disease progression in patients with COVID-19 by artificial intelligence assisted lesion quantification

Abstract

To investigate the value of artificial intelligence (AI) assisted quantification on initial chest CT for prediction of disease progression and clinical outcome in patients with coronavirus disease 2019 (COVID-19). Patients with confirmed COVID-19 infection and initially of non-severe type were retrospectively included. The initial CT scan on admission was used for imaging analysis. The presence of ground glass opacity (GGO), consolidation and other findings were visually evaluated. CT severity score was calculated according to the extent of lesion involvement. In addition, AI based quantification of GGO and consolidation volume were also performed. 123 patients (mean age: 64.43 ± 14.02; 62 males) were included. GGO + consolidation was more frequently revealed in progress-to-severe group whereas pure GGO was more likely to be found in non-severe group. Compared to non-severe group, patients in progress-to-severe group had larger GGO volume (167.33 ± 167.88 cm3 versus 101.12 ± 127 cm3, $p = 0.013$) as well as consolidation volume (40.85 ± 60.4 cm3 versus 6.63 ± 14.91 cm3, $p < 0.001$). Among imaging parameters, consolidation volume had the largest area under curve (AUC) in discriminating non-severe from progress-to-severe group (AUC = 0.796, $p < 0.001$) and patients with or without critical events (AUC = 0.754, $p < 0.001$). According to multivariate regression, consolidation volume and age were two strongest predictors for disease progression (hazard ratio: 1.053 and 1.071, p: 0.006 and 0.008) whereas age and diabetes were predictors for unfavorable outcome. Consolidation volume quantified on

initial chest CT was the strongest predictor for disease severity progression and larger consolidation volume was associated with unfavorable clinical outcome.

Reference

https://www.nature.com/articles/s41598-020-79097-1

A single dose of recombinant VSV-ΔG-spike vaccine provides protection against SARS-CoV-2 challenge

Abstract

The COVID-19 pandemic caused by SARS-CoV-2 imposes an urgent need for rapid development of an efficient and cost-effective vaccine, suitable for mass immunization. Here, we show the development of a replication competent recombinant VSV-ΔG-spike vaccine, in which the glycoprotein of VSV is replaced by the spike protein of SARS-CoV-2. In-vitro characterization of this vaccine indicates the expression and presentation of the spike protein on the viral membrane with antigenic similarity to SARS-CoV-2. A golden Syrian hamster in-vivo model for COVID-19 is implemented. We show that a single-dose vaccination results in a rapid and potent induction of SARS-CoV-2 neutralizing antibodies. Importantly, vaccination protects hamsters against SARS-CoV-2 challenge, as demonstrated by the abrogation of body weight loss, and alleviation of the extensive tissue damage and viral loads in lungs and nasal turbinates. Taken together, we suggest the recombinant VSV-ΔG-spike as a safe, efficacious and protective vaccine against SARS-CoV-2.

Reference

https://www.nature.com/articles/s41467-020-20228-7

The S1 protein of SARS-CoV-2 crosses the blood–brain barrier in mice

Abstract

It is unclear whether severe acute respiratory syndrome coronavirus 2, which causes coronavirus disease 2019, can enter the brain. Severe acute respiratory syndrome coronavirus 2 binds to cells via the S1 subunit of its spike protein. We show that intravenously injected radioiodinated S1 (I-S1) readily crossed the blood–brain barrier in

male mice, was taken up by brain regions and entered the parenchymal brain space. I-S1 was also taken up by the lung, spleen, kidney and liver. Intranasally administered I-S1 also entered the brain, although at levels roughly ten times lower than after intravenous administration. APOE genotype and sex did not affect whole-brain I-S1 uptake but had variable effects on uptake by the olfactory bulb, liver, spleen and kidney. I-S1 uptake in the hippocampus and olfactory bulb was reduced by lipopolysaccharide-induced inflammation. Mechanistic studies indicated that I-S1 crosses the blood–brain barrier by adsorptive transcytosis and that murine angiotensin-converting enzyme 2 is involved in brain and lung uptake, but not in kidney, liver or spleen uptake.

Reference

https://www.nature.com/articles/s41593-020-00771-8

Publication Date: Dec 15, 2020

Inferring the effectiveness of government interventions against COVID-19

Abstract

Governments are attempting to control the COVID-19 pandemic with nonpharmaceutical interventions (NPIs). However, the effectiveness of different NPIs at reducing transmission is poorly understood. We gathered chronological data on the implementation of NPIs for several European, and other, countries between January and the end of May 2020. We estimate the effectiveness of NPIs, ranging from limiting gathering sizes, business closures, and closure of educational institutions to stay-at-home orders. To do so, we used a Bayesian hierarchical model that links NPI implementation dates to national case and death counts and supported the results with extensive empirical validation. Closing all educational institutions, limiting gatherings to 10 people or less, and closing face-to-face businesses each reduced transmission considerably. The additional effect of stay-at-home orders was comparatively small.

Reference

https://science.sciencemag.org/content/early/2020/12/15/science.abd9338

SARS-CoV-2 antibody seroprevalence in the general population and high-risk occupational groups across 18 cities in Iran: A population-based cross-sectional study

Abstract

Background: Rapid increases in cases of COVID-19 were observed in multiple cities in Iran towards the start of the pandemic. However, the true infection rate remains unknown. We aimed to assess the seroprevalence of antibodies against severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in 18 cities of Iran as an indicator of the infection rate.

Methods: In this population-based cross-sectional study, we randomly selected and invited study participants from the general population (from lists of people registered with the Iranian electronic health record system or health-care centres) and a high-risk population of individuals likely to have close social contact with SARS-CoV-2-infected individuals through their occupation (from employee lists provided by relevant agencies or companies, such as supermarket chains) across 18 cities in 17 Iranian provinces. Participants were asked questions on their demographic characteristics, medical history, recent COVID-19-related symptoms, and COVID-19-related exposures. Iran Food and Drug Administration-approved Pishtaz Teb SARS-CoV-2 ELISA kits were used to detect SARS-CoV-2-specific IgG and IgM antibodies in blood samples from participants. Seroprevalence was estimated on the basis of ELISA test results and adjusted for population weighting (by age, sex, and city population size) and test performance (according to our independent validation of sensitivity and specificity).

Findings: From 9181 individuals who were initially contacted between April 17 and June 2, 2020, 243 individuals refused to provide blood samples and 36 did not provide demographic information and were excluded from the analysis. Among the 8902 individuals included in the analysis, 5372 had occupations with a high risk of exposure to SARS-CoV-2 and 3530 were recruited from the general population. The overall population weight-adjusted and test performance-adjusted prevalence of antibody seropositivity in the general population was 17·1% (95% CI 14·6–19·5), implying that 4 265 542 (95% CI 3 659 043–4 887 078) individuals from the 18 cities included were infected by the end of April, 2020. The adjusted seroprevalence of SARS-CoV-2-specific

antibodies varied greatly by city, with the highest estimates found in Rasht (72·6% [53·9–92·8]) and Qom (58·5% [37·2–83·9]). The overall population weight-adjusted and test performance-adjusted seroprevalence in the high-risk population was 20·0% (18·5–21·7) and showed little variation between the occupations included.

Interpretations: Seroprevalence is likely to be much higher than the reported prevalence of COVID-19 based on confirmed COVID-19 cases in Iran. Despite high seroprevalence in a few cities, a large proportion of the population is still uninfected. The potential shortcomings of current public health policies should therefore be identified to prevent future epidemic waves in Iran.

Reference

https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30858-6/fulltext

Neuroimaging manifestations in children with SARS-CoV-2 infection: A multinational, multicentre collaborative study

Abstract

Background: The CNS manifestations of COVID-19 in children have primarily been described in case reports, which limit the ability to appreciate the full spectrum of the disease in paediatric patients. We aimed to identify enough cases that could be evaluated in aggregate to better understand the neuroimaging manifestations of COVID-19 in the paediatric population.

Methods: An international call for cases of children with encephalopathy related to severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection and abnormal neuroimaging findings was made. Clinical history and associated plasma and cerebrospinal fluid data were requested. These data were reviewed by a central neuroradiology panel, a child neurologist, and a paediatric infectious diseases expert. The children were categorised on the basis of their time of probable exposure to SARS-CoV-2. In addition, cases were excluded when a direct link to SARS-CoV-2 infection could not be established or an established alternate diagnostic cause could be hypothesised. The accepted referral centre imaging data, from ten countries, were remotely reviewed by a

central panel of five paediatric neuroradiologists and a consensus opinion obtained on the imaging findings.

Findings: 38 children with neurological disease related to SARS-CoV-2 infection were identified from France (n=13), the UK (n=8), the USA (n=5), Brazil (n=4), Argentina (n=4), India (n=2), Peru (n=1), and Saudi Arabia (n=1). Recurring patterns of disease were identified, with neuroimaging abnormalities ranging from mild to severe. The most common imaging patterns were postinfectious immune-mediated acute disseminated encephalomyelitis-like changes of the brain (16 patients), myelitis (eight patients), and neural enhancement (13 patients). Cranial nerve enhancement could occur in the absence of corresponding neurological symptoms. Splenial lesions (seven patients) and myositis (four patients) were predominantly observed in children with multisystem inflammatory syndrome. Cerebrovascular complications in children were less common than in adults. Significant pre-existing conditions were absent and most children had favourable outcomes. However, fatal atypical CNS co-infections developed in four previously healthy children infected with SARS-CoV-2.

Interpretation: Acute-phase and delayed-phase SARS-CoV-2-related CNS abnormalities are seen in children. Recurring patterns of disease and atypical neuroimaging manifestations can be found and should be recognised being as potentially due to SARS-CoV-2 infection as an underlying aetiological factor. Studies of paediatric specific cohorts are needed to better understand the effects of SARS-CoV-2 infection on the CNS at presentation and on long-term follow-up in children.

Reference

https://www.thelancet.com/journals/lanchi/article/PIIS2352-4642(20)30362-X/fulltext

Influence of socioeconomic deprivation on interventions and outcomes for patients admitted with COVID-19 to critical care units in Scotland: A national cohort study

Abstract

Background: Coronavirus disease 2019 (COVID-19) can lead to significant respiratory failure with between 14% and 18% of hospitalised patients requiring critical care

admission. This study describes the impact of socioeconomic deprivation on 30-day survival following critical care admission for COVID-19, and the impact of the COVID-19 pandemic on critical care capacity in Scotland.

Methods: This cohort study used linked national hospital records including ICU, virology testing and national death records to identify and describe patients with COVID-19 admitted to critical care units in Scotland. Multivariable logistic regression was used to assess the impact of deprivation on 30-day mortality. Critical care capacity was described by reporting the percentage of baseline ICU bed utilisation required.

Findings: There were 735 patients with COVID-19 admitted to critical care units across Scotland from 1/3/2020 to 20/6/2020. There was a higher proportion of patients from more deprived areas, with 183 admissions (24.9%) from the most deprived quintile and 100 (13.6%) from the least deprived quintile. Overall, 30-day mortality was 34.8%. After adjusting for age, sex and ethnicity, mortality was significantly higher in patients from the most deprived quintile (OR 1.97, 95%CI 1.13, 3.41, p=0.016). ICUs serving populations with higher levels of deprivation spent a greater amount of time over their baseline ICU bed capacity.

Interpretation: Patients with COVID-19 living in areas with greatest socioeconomic deprivation had a higher frequency of critical care admission and a higher adjusted 30-day mortality. ICUs in health boards with higher levels of socioeconomic deprivation had both higher peak occupancy and longer duration of occupancy over normal maximum capacity.

Reference

https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(20)30005-3/fulltext

A booster dose enhances immunogenicity of the COVID-19 vaccine candidate ChAdOx1 nCoV-19 in aged mice

Abstract

Background: The spread of SARS-CoV-2 has caused a global pandemic that has affected almost every aspect of human life. The development of an effective COVID-19 vaccine could limit the morbidity and mortality caused by infection, and may enable the relaxation

of social distancing measures. Age is one of the most significant risk factors for poor health outcomes after SARS-CoV-2 infection, therefore it is desirable that any new vaccine candidates elicit a robust immune response in older adults.

Methods: Here, we use in-depth immunophenotyping to characterize the innate and adaptive immune response induced upon intramuscular administration of the adenoviral vectored ChAdOx1 nCoV-19 (AZD-1222) COVID-19 vaccine candidate in mice.

Findings: A single vaccination generates spike-specific Th1 cells, Th1-like Foxp3+ regulatory T cells, polyfunctional spike-specific CD8+ T cells and granzyme B producing CD8 effectors. Spike-specific IgG and IgM are generated from both the early extrafollicular antibody response and the T follicular helper cell-supported germinal centre reaction, which is associated with the production of virus neutralising antibodies. A single dose of this vaccine generated a similar type of immune response in aged mice, but of a reduced magnitude than in younger mice. We report that a second dose enhances the immune response to this vaccine in aged mice.

Conclusions: This study shows that ChAdOx1 nCoV-19 induces both cellular and humoral immunity in adult and aged mice, and suggests a prime-boost strategy is a rational approach to enhance immunogenicity in older persons.

Reference

https://www.cell.com/med/fulltext/S2666-6340(20)30034-9

COVID-19 neutralizing antibodies predict disease severity and survival

Abstract

COVID-19 exhibits variable symptom severity ranging from asymptomatic to life-threatening, yet the relationship between severity and the humoral immune response is poorly understood. We examined antibody responses in 113 COVID-19 patients and found that severe cases resulting in intubation or death exhibited increased inflammatory markers, lymphopenia, pro-inflammatory cytokines, and high anti-RBD antibody levels. While anti-RBD IgG levels generally correlated with neutralization titer, quantitation of neutralization potency revealed that high potency was a predictor of survival. In addition

to neutralization of wild-type SARS-CoV-2, patient sera were also able to neutralize the recently emerged SARS-CoV-2 mutant D614G, suggesting cross-protection from reinfection by either strain. However, SARS-CoV-2 sera generally lacked cross-neutralization to a highly-homologous pre-emergent bat coronavirus, WIV1-CoV, that has not yet crossed the species barrier. These results highlight the importance of neutralizing humoral immunity on disease progression and the need to develop broadly protective interventions to prevent future coronavirus pandemics.

Reference

https://www.cell.com/cell/fulltext/S0092-8674(20)31685-8

Heterogeneity and effectiveness analysis of COVID-19 prevention and control in major cities in China through time-varying reproduction number estimation

Abstract

Beginning on December 31, 2019, the large-scale novel coronavirus disease 2019 (COVID-19) emerged in China. Tracking and analysing the heterogeneity and effectiveness of cities' prevention and control of the COVID-19 epidemic is essential to design and adjust epidemic prevention and control measures. The number of newly confirmed cases in 25 of China's most-affected cities for the COVID-19 epidemic from January 11 to February 10 was collected. The heterogeneity and effectiveness of these 25 cities' prevention and control measures for COVID-19 were analysed by using an estimated time-varying reproduction number method and a serial correlation method. The results showed that the effective reproduction number (R) in 25 cities showed a downward trend overall, but there was a significant difference in the R change trends among cities, indicating that there was heterogeneity in the spread and control of COVID-19 in cities. Moreover, the COVID-19 control in 21 of 25 cities was effective, and the risk of infection decreased because their R had dropped below 1 by February 10, 2020. In contrast, the cities of Wuhan, Tianmen, Ezhou and Enshi still had difficulty effectively controlling the COVID-19 epidemic in a short period of time because their R was greater than 1.

Reference

https://www.nature.com/articles/s41598-020-79063-x

Development of immunohistochemistry and in situ hybridisation for the detection of SARS-CoV and SARS-CoV-2 in formalin-fixed paraffin-embedded specimens

Abstract

The rapid emergence of SARS-CoV-2, the causative agent of COVID-19, and its dissemination globally has caused an unprecedented strain on public health. Animal models are urgently being developed for SARS-CoV-2 to aid rational design of vaccines and therapeutics. Immunohistochemistry and in situ hybridisation techniques that facilitate reliable and reproducible detection of SARS-CoV and SARS-CoV-2 viral products in formalin-fixed paraffin-embedded (FFPE) specimens would be of great utility. A selection of commercial antibodies generated against SARS-CoV spike protein and nucleoprotein, double stranded RNA, and RNA probe for spike genes were evaluated for the ability to detect FFPE infected cells. We also tested both heat- and enzymatic-mediated virus antigen retrieval methods to determine the optimal virus antigen recovery as well as identifying alternative retrieval methods to enable flexibility of IHC methods. In addition to using native virus infected cells as positive control material, the evaluation of non-infected cells expressing coronavirus (SARS, MERS) spike as a biosecure alternative to assays involving live virus was undertaken. Optimized protocols were successfully applied to experimental animal-derived tissues. The diverse techniques for virus detection and control material generation demonstrated in this study can be applied to investigations of coronavirus pathogenesis and therapeutic research in animal models.

Reference

https://www.nature.com/articles/s41598-020-78949-0

Minimal system for assembly of SARS-CoV-2 virus like particles

Abstract

SARS-CoV-2 virus is the causative agent of COVID-19. Here we demonstrate that non-infectious SARS-CoV-2 virus like particles (VLPs) can be assembled by co-expressing the viral proteins S, M and E in mammalian cells. The assembled SARS-CoV-2 VLPs possess S protein spikes on particle exterior, making them ideal for vaccine development. The particles range in shape from spherical to elongated with a characteristic size of

129 ± 32 nm. We further show that SARS-CoV-2 VLPs dried in ambient conditions can retain their structural integrity upon repeated scans with Atomic Force Microscopy up to a peak force of 1 nN.

Reference

https://www.nature.com/articles/s41598-020-78656-w

Social media and smartphone app use predicts maintenance of physical activity during Covid-19 enforced isolation in psychiatric outpatients

Abstract

There is growing concern that the social and physical distancing measures implemented in response to the Covid-19 pandemic may negatively impact health in other areas, via both decreased physical activity and increased social isolation. Here, we investigated whether increased engagement with digital social tools may help mitigate effects of enforced isolation on physical activity and mood, in a naturalistic study of at-risk individuals. Passively sensed smartphone app use and actigraphy data were collected from a group of psychiatric outpatients before and during imposition of strict Covid-19 lockdown measures. Data were analysed using Gaussian graphical models: a form of network analysis which gives insight into the predictive relationships between measures across timepoints. Within-individuals, we found evidence of a positive predictive path between digital social engagement, general smartphone use, and physical activity—selectively under lockdown conditions (N = 127 individual users, M = 6201 daily observations). Further, we observed a positive relationship between social media use and total daily steps across individuals during (but not prior to) lockdown. Although there are important limitations on the validity of drawing causal conclusions from observational data, a plausible explanation for our findings is that, during lockdown, individuals use their smartphones to access social support, which may help guard against negative effects of in-person social deprivation and other pandemic-related stress. Importantly, passive monitoring of smartphone app usage is low burden and non-intrusive. Given appropriate consent, this could help identify people who are failing to engage in usual patterns of digital social interaction, providing a route to early intervention.

Reference

https://www.nature.com/articles/s41380-020-00963-5

Gene editing and RNAi approaches for COVID-19 diagnostics and therapeutics

Abstract

The novel coronavirus pneumonia (COVID-19) is a highly infectious acute respiratory disease caused by Severe Acute Respiratory Syndrome-Related Coronavirus (SARS-CoV-2) (Prec Clin Med 2020;3:9–13, Lancet 2020;395:497–506, N. Engl J Med 2020a;382:1199–207, Nature 2020;579:270–3). SARS-CoV-2 surveillance is essential to controlling widespread transmission. However, there are several challenges associated with the diagnostic of the COVID-19 during the current outbreak (Liu and Li (2019), Nature 2020;579:265–9, N. Engl J Med 2020;382:727–33). Firstly, the high number of cases overwhelms diagnostic test capacity and proposes the need for a rapid solution for sample processing (Science 2018;360:444–8). Secondly, SARS-CoV-2 is closely related to other important coronavirus species and subspecies, so detection assays can give false-positive results if they are not efficiently specific to SARS-CoV-2. Thirdly, patients with suspected SARS-CoV-2 infection sometimes have a different respiratory viral infection or co-infections with SARS-CoV-2 and other respiratory viruses (MedRxiv 2020a;1–18). Confirmation of the COVID-19 is performed mainly by virus isolation followed by RT-PCR and sequencing (N. Engl J Med 2020;382:727–33, MedRxiv 2020a, Turkish J Biol 2020;44:192–202). The emergence and outbreak of the novel coronavirus highlighted the urgent need for new therapeutic technologies that are fast, precise, stable, easy to manufacture, and target-specific for surveillance and treatment. Molecular biology tools that include gene-editing approaches such as CRISPR-Cas12/13-based SHERLOCK, DETECTR, CARVER and PAC-MAN, antisense oligonucleotides, antisense peptide nucleic acids, ribozymes, aptamers, and RNAi silencing approaches produced with cutting-edge scientific advances compared to conventional diagnostic or treatment methods could be vital in COVID-19 and other future outbreaks. Thus, in this review, we will discuss potent the molecular biology approaches that can revolutionize diagnostic of viral infections and therapies to fight COVID-19 in a highly specific, stable, and efficient way.

Reference

https://www.nature.com/articles/s41434-020-00209-7

Gene expression network analysis provides potential targets against SARS-CoV-2

Abstract

Cell entry of SARS-CoV-2, the novel coronavirus causing COVID-19, is facilitated by host cell angiotensin-converting enzyme 2 (ACE2) and transmembrane serine protease 2 (TMPRSS2). We aimed to identify and characterize genes that are co-expressed with ACE2 and TMPRSS2, and to further explore their biological functions and potential as druggable targets. Using the gene expression profiles of 1,038 lung tissue samples, we performed a weighted gene correlation network analysis (WGCNA) to identify modules of co-expressed genes. We explored the biology of co-expressed genes using bioinformatics databases, and identified known drug-gene interactions. ACE2 was in a module of 681 co-expressed genes; 10 genes with moderate-high correlation with ACE2 ($r > 0.3$, FDR < 0.05) had known interactions with existing drug compounds. TMPRSS2 was in a module of 1,086 co-expressed genes; 31 of these genes were enriched in the gene ontology biologic process 'receptor-mediated endocytosis', and 52 TMPRSS2-correlated genes had known interactions with drug compounds. Dozens of genes are co-expressed with ACE2 and TMPRSS2, many of which have plausible links to COVID-19 pathophysiology. Many of the co-expressed genes are potentially targetable with existing drugs, which may accelerate the development of COVID-19 therapeutics.

Reference

https://www.nature.com/articles/s41598-020-78818-w

Treatment of COVID-19 with remdesivir in the absence of humoral immunity: A case report

Abstract

The response to the coronavirus disease 2019 (COVID-19) pandemic has been hampered by lack of an effective severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) antiviral therapy. Here we report the use of remdesivir in a patient with COVID-19 and the prototypic genetic antibody deficiency X-linked agammaglobulinaemia (XLA). Despite evidence of complement activation and a robust T cell response, the patient developed persistent SARS-CoV-2 pneumonitis, without progressing to multi-

organ involvement. This unusual clinical course is consistent with a contribution of antibodies to both viral clearance and progression to severe disease. In the absence of these confounders, we take an experimental medicine approach to examine the in vivo utility of remdesivir. Over two independent courses of treatment, we observe a temporally correlated clinical and virological response, leading to clinical resolution and viral clearance, with no evidence of acquired drug resistance. We therefore provide evidence for the antiviral efficacy of remdesivir in vivo, and its potential benefit in selected patients.

Reference

https://www.nature.com/articles/s41467-020-19761-2

Defining and managing COVID-19-associated pulmonary aspergillosis: The 2020 ECMM/ISHAM consensus criteria for research and clinical guidance

Abstract

Severe acute respiratory syndrome coronavirus 2 causes direct damage to the airway epithelium, enabling aspergillus invasion. Reports of COVID-19-associated pulmonary aspergillosis have raised concerns about it worsening the disease course of COVID-19 and increasing mortality. Additionally, the first cases of COVID-19-associated pulmonary aspergillosis caused by azole-resistant aspergillus have been reported. This article constitutes a consensus statement on defining and managing COVID-19-associated pulmonary aspergillosis, prepared by experts and endorsed by medical mycology societies. COVID-19-associated pulmonary aspergillosis is proposed to be defined as possible, probable, or proven on the basis of sample validity and thus diagnostic certainty. Recommended first-line therapy is either voriconazole or isavuconazole. If azole resistance is a concern, then liposomal amphotericin B is the drug of choice. Our aim is to provide definitions for clinical research and up-to-date recommendations for clinical management of the diagnosis and treatment of COVID-19-associated pulmonary aspergillosis.

Reference

https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30847-1/fulltext

Synergistic and Antagonistic Drug Combinations against SARS-CoV-2

Abstract

Antiviral drug development for coronavirus disease 2019 (COVID-19) is occurring at an unprecedented pace, yet there are still limited therapeutic options for treating this disease. We hypothesized that combining drugs with independent mechanisms of action could result in synergy against SARS-CoV-2, thus generating better antiviral efficacy. Using in silico approaches, we prioritized 73 combinations of 32 drugs with potential activity against SARS-CoV-2 and then tested them in vitro. Sixteen synergistic and eight antagonistic combinations were identified; among 16 synergistic cases, combinations of the US Food and Drug Administration (FDA)-approved drug nitazoxanide with remdesivir, amodiaquine, or umifenovir were most notable, all exhibiting significant synergy against SARS-CoV-2 in a cell model. However, the combination of remdesivir and lysosomotropic drugs, such as hydroxychloroquine, demonstrated strong antagonism. Overall, these results highlight the utility of drug repurposing and preclinical testing of drug combinations for discovering potential therapies to treat COVID-19.

Reference

https://www.cell.com/molecular-therapy-family/molecular-therapy/fulltext/S1525-0016(20)30673-0

Transcriptomic similarities and differences in host response between SARS-CoV-2 and other viral infections

Abstract

The pandemic COVID-19 disease shares certain clinical characteristics with other acute viral infections. We studied the whole-blood transcriptomic host response to SARS-CoV-2 using RNAseq from 24 healthy controls and 62 prospectively enrolled patients with COVID-19. We then compared these data to non-COVID-19 viral infections, curated from 23 independent studies profiling 1,855 blood samples covering six viruses (influenza, RSV, HRV, Ebola, Dengue, SARS-CoV-1). We show gene expression changes in COVID-19 versus non-COVID-19 viral infections are highly correlated ($r=0.74$, $p<0.001$). However, we also found 416 genes specific to COVID-19. Inspection of top genes

revealed dynamic immune evasion and counter host responses specific to COVID-19. Statistical deconvolution of cell proportions maps many cell type proportions concordantly shifting. Discordantly increased in COVID-19 were CD56bright NK cells and M2 macrophages. The concordant and discordant responses mapped out here provide a window to explore the pathophysiology of the host response to SARS-CoV-2.

Reference

https://www.cell.com/iscience/fulltext/S2589-0042(20)31144-5

Intranasal vaccination with a lentiviral vector protects against SARS-CoV-2 in preclinical animal models

Abstract

To develop a vaccine candidate against coronavirus disease 2019 (COVID-19), we generated a lentiviral vector (LV) eliciting neutralizing antibodies against the Spike glycoprotein of SARS-CoV-2. Systemic vaccination by this vector in mice, in which the expression of the SARS-CoV-2 receptor hACE2 has been induced by transduction of respiratory tract cells by an adenoviral vector, confers only partial protection despite high levels of serum neutralizing activity. However, eliciting an immune response in the respiratory tract through an intranasal boost results in a >3 log10 decrease in the lung viral loads and reduces local inflammation. Moreover, both integrative and non-integrative LV platforms display strong vaccine efficacy and inhibit lung deleterious injury in golden hamsters, which are naturally permissive to SARS-CoV-2 replication and closely mirror human COVID-19 physiopathology. Our results provide evidence of marked prophylactic effects of LV-based vaccination against SARS-CoV-2 and designate intranasal immunization as a powerful approach against COVID-19.

Reference

https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(20)30672-7

Functional interrogation of a SARS-CoV-2 host protein interactome identifies unique and shared coronavirus host factors

Abstract

The ongoing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic has devastated the global economy and claimed more than 1.7 million lives, presenting an urgent global health crisis. To identify host factors required for infection by SARS-CoV-2 and seasonal coronaviruses, we designed a focused high-coverage CRISPR-Cas9 library targeting 332 members of a recently published SARS-CoV-2 protein interactome. We leveraged the compact nature of this library to systematically screen SARS-CoV-2 at two physiologically relevant temperatures along with three related coronaviruses (human coronavirus 229E [HCoV-229E], HCoV-NL63, and HCoV-OC43), allowing us to probe this interactome at a much higher resolution than genome-scale studies. This approach yielded several insights, including potential virus-specific differences in Rab GTPase requirements and glycosylphosphatidylinositol (GPI) anchor biosynthesis, as well as identification of multiple pan-coronavirus factors involved in cholesterol homeostasis. This coronavirus essentiality catalog could inform ongoing drug development efforts aimed at intercepting and treating coronavirus disease 2019 (COVID-19) and help prepare for future coronavirus outbreaks.

Reference

https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(20)30671-5

Publication Date: Dec 12, 2020

Characterizing COVID-19 and influenza illnesses in the real world via person-generated health data

Abstract

The fight against COVID-19 is hindered by similarly presenting viral infections that may confound detection and monitoring. We examined person-generated health data (PGHD), consisting of survey and commercial wearable data from individuals' everyday lives, for 230 people who reported a COVID-19 diagnosis between March 30, 2020, and April 27, 2020 (N = 41 with wearable data). Compared with self-reported diagnosed flu cases from

the same time frame (N = 426, 85 with wearable data) or pre-pandemic (N = 6,270, 1,265 with wearable data), COVID-19 patients reported a distinct symptom constellation that lasted longer (median of 12 versus 9 and 7 days, respectively) and peaked later after illness onset. Wearable data showed significant changes in daily steps and prevalence of anomalous resting heart rate measurements, of similar magnitudes for both the flu and COVID-19 cohorts. Our findings highlight the need to include flu comparator arms when evaluating PGHD applications aimed to be highly specific for COVID-19.

Reference

https://www.cell.com/patterns/fulltext/S2666-3899(20)30258-0

Publication Date: Dec 11, 2020

Structural and functional comparison of SARS-CoV-2-spike receptor binding domain produced in Pichia pastoris and mammalian cells

Abstract

The yeast Pichia pastoris is a cost-effective and easily scalable system for recombinant protein production. In this work we compared the conformation of the receptor binding domain (RBD) from severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) Spike protein expressed in P. pastoris and in the well established HEK-293T mammalian cell system. RBD obtained from both yeast and mammalian cells was properly folded, as indicated by UV-absorption, circular dichroism and tryptophan fluorescence. They also had similar stability, as indicated by temperature-induced unfolding (observed Tm were 50 °C and 52 °C for RBD produced in P. pastoris and HEK-293T cells, respectively). Moreover, the stability of both variants was similarly reduced when the ionic strength was increased, in agreement with a computational analysis predicting that a set of ionic interactions may stabilize RBD structure. Further characterization by high-performance liquid chromatography, size-exclusion chromatography and mass spectrometry revealed a higher heterogeneity of RBD expressed in P. pastoris relative to that produced in HEK-293T cells, which disappeared after enzymatic removal of glycans. The production of RBD in P. pastoris was scaled-up in a bioreactor, with yields above 45 mg/L of 90% pure protein, thus potentially allowing large scale immunizations to produce neutralizing antibodies, as well as the large scale production of serological tests for SARS-CoV-2.

Reference

https://www.nature.com/articles/s41598-020-78711-6

Blockage of interleukin-1β with canakinumab in patients with COVID-19

Abstract

There is the urgent need to study the effects of immunomodulating agents as therapy for Covid-19. An observational, cohort, prospective study with 30 days of observation was carried out to assess clinical outcomes in 88 patients hospitalized for Covid-19 pneumonia and treated with canakinumab (300 mg sc). Median time from diagnosis of Covid-19 by viral swab to administration of canakinumab was 7.5 days (range 0–30, IQR 4–11). Median PaO2/FiO2 increased from 160 (range 53–409, IQR 122–210) at baseline to 237 (range 72–533, IQR 158–331) at day 7 after treatment with canakinumab ($p < 0.0001$). Improvement of oxygen support category was observed in 61.4% of cases. Median duration of hospitalization following administration of canakinumab was 6 days (range 0–30, IQR 4–11). At 7 days, 58% of patients had been discharged and 12 (13.6%) had died. Significant differences between baseline and 7 days were observed for absolute lymphocyte counts (mean 0.60 vs 1.11 × 109/L, respectively, $p < 0.0001$) and C-reactive protein (mean 31.5 vs 5.8 mg/L, respectively, $p < 0.0001$).Overall survival at 1 month was 79.5% (95% CI 68.7–90.3). Oxygen-support requirements improved and overall mortality was 13.6%. Confirmation of the efficacy of canakinumab for Covid-19 warrants further study in randomized controlled trials.

Reference

https://www.nature.com/articles/s41598-020-78492-y

The kinetics of humoral response and its relationship with the disease severity in COVID-19

Abstract

Coronavirus Disease 2019 (COVID-19) has caused a global pandemic. Here we profiled the humoral response against Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) by measuring immunoglobulin (Ig) A, IgM, and IgG against nucleocapsid and spike proteins, along with IgM and IgG antibodies against receptor-binding domain

(RBD) of the spike protein and total neutralizing antibodies (NAbs). We tested 279 plasma samples collected from 176 COVID-19 patients who presented and enrolled at different stages of their disease. Plasma dilutions were optimized and based on the data, a single dilution of plasma was used. The mean absorbance at 450 nm was measured for Ig levels and NAbs were measured using geometric mean titers. We demonstrate that more severe cases have a late-onset in the humoral response compared to mild/moderate infections. All the antibody titers continue to rise in patients with COVID-19 over the disease course. However, these levels are mostly unrelated to disease severity. The appearance time and titers of NAbs showed a significant positive correlation to the antibodies against spike protein. Our results suggest the late onset of antibody response as a risk factor for disease severity, however, there is a limited role of antibody titers in predicting disease severity of COVID-19.

Reference

https://www.nature.com/articles/s42003-020-01526-8

Impact of comorbid asthma on severity of coronavirus disease (COVID-19)

Abstract

The severity of the coronavirus disease (COVID-19) is associated with various comorbidities. However, no studies have yet demonstrated the potential risk of respiratory failure and mortality in COVID-19 patients with pre-existing asthma. We selected 7272 adult COVID-19 patients from the Korean Health Insurance Review and Assessment COVID-19 database for this nationwide retrospective cohort study. Among these, 686 patients with asthma were assessed by their severities and evaluated by the clinical outcome of COVID-19 compared to patients without asthma. Of 7272 adult COVID-19 patients, 686 with asthma and 6586 without asthma were compared. Asthma was not a significant risk factor for respiratory failure or mortality among all COVID-19 patients (odds ratio [OR] = 0.99, P = 0.997 and OR = 1.06, P = 0.759) after adjusting for age, sex, and the Charlson comorbidity score. However, a history of acute exacerbation (OR = 2.63, P = 0.043) was significant risk factors for death among COVID-19 patients with asthma. Asthma is not a risk factor for poor prognosis of COVID-19. However, asthma patients who had any experience of acute exacerbation in the previous year before COVID-19 showed higher COVID-19-related mortality, especially in case of old age and male sex.

Reference

https://www.nature.com/articles/s41598-020-77791-8

HIV infection and COVID-19 death: A population-based cohort analysis of UK primary care data and linked national death registrations within the OpenSAFELY platform

Abstract

Background: Whether HIV infection is associated with risk of death due to COVID-19 is unclear. We aimed to investigate this association in a large-scale population-based study in England.

Methods: We did a retrospective cohort study. Working on behalf of NHS England, we used the OpenSAFELY platform to analyse routinely collected electronic primary care data linked to national death registrations. We included all adults (aged ≥18 years) alive and in follow-up on Feb 1, 2020, and with at least 1 year of continuous registration with a general practitioner before this date. People with a primary care record for HIV infection were compared with people without HIV. The outcome was COVID-19 death, defined as the presence of International Classification of Diseases 10 codes U07.1 or U07.2 anywhere on the death certificate. Cox regression models were used to estimate the association between HIV infection and COVID-19 death; they were initially adjusted for age and sex, then we added adjustment for index of multiple deprivation and ethnicity, and then for a broad range of comorbidities. Interaction terms were added to assess effect modification by age, sex, ethnicity, comorbidities, and calendar time.

Results: 17 282 905 adults were included, of whom 27 480 (0·16%) had HIV recorded. People living with HIV were more likely to be male, of Black ethnicity, and from a more deprived geographical area than the general population. 14 882 COVID-19 deaths occurred during the study period, with 25 among people with HIV. People living with HIV had higher risk of COVID-19 death than those without HIV after adjusting for age and sex: hazard ratio (HR) 2·90 (95% CI 1·96–4·30; p<0·0001). The association was attenuated, but risk remained high, after adjustment for deprivation, ethnicity, smoking and obesity: adjusted HR 2·59 (95% CI 1·74–3·84; p<0·0001). There was some evidence that the association was larger among people of Black ethnicity: HR 4·31 (95% CI 2·42–7·65) versus 1·84 (1·03–3·26) in non-Black individuals (p-interaction=0·044).

Interpretation: People with HIV in the UK seem to be at increased risk of COVID-19 mortality. Targeted policies should be considered to address this raised risk as the pandemic response evolves.

Reference

https://www.thelancet.com/journals/lanhiv/article/PIIS2352-3018(20)30305-2/fulltext

Rapid triage for COVID-19 using routine clinical data for patients attending hospital: Development and prospective validation of an artificial intelligence screening test

Abstract

Background: The early clinical course of COVID-19 can be difficult to distinguish from other illnesses driving presentation to hospital. However, viral-specific PCR testing has limited sensitivity and results can take up to 72 h for operational reasons. We aimed to develop and validate two early-detection models for COVID-19, screening for the disease among patients attending the emergency department and the subset being admitted to hospital, using routinely collected health-care data (laboratory tests, blood gas measurements, and vital signs). These data are typically available within the first hour of presentation to hospitals in high-income and middle-income countries, within the existing laboratory infrastructure.

Methods: We trained linear and non-linear machine learning classifiers to distinguish patients with COVID-19 from pre-pandemic controls, using electronic health record data for patients presenting to the emergency department and admitted across a group of four teaching hospitals in Oxfordshire, UK (Oxford University Hospitals). Data extracted included presentation blood tests, blood gas testing, vital signs, and results of PCR testing for respiratory viruses. Adult patients (>18 years) presenting to hospital before Dec 1, 2019 (before the first COVID-19 outbreak), were included in the COVID-19-negative cohort; those presenting to hospital between Dec 1, 2019, and April 19, 2020, with PCR-confirmed severe acute respiratory syndrome coronavirus 2 infection were included in the COVID-19-positive cohort. Patients who were subsequently admitted to hospital were included in their respective COVID-19-negative or COVID-19-positive admissions cohorts. Models were calibrated to sensitivities of 70%, 80%, and 90% during training, and performance was initially assessed on a held-out test set generated by an 80:20 split

stratified by patients with COVID-19 and balanced equally with pre-pandemic controls. To simulate real-world performance at different stages of an epidemic, we generated test sets with varying prevalences of COVID-19 and assessed predictive values for our models. We prospectively validated our 80% sensitivity models for all patients presenting or admitted to the Oxford University Hospitals between April 20 and May 6, 2020, comparing model predictions with PCR test results.

Findings: We assessed 155 689 adult patients presenting to hospital between Dec 1, 2017, and April 19, 2020. 114 957 patients were included in the COVID-negative cohort and 437 in the COVID-positive cohort, for a full study population of 115 394 patients, with 72 310 admitted to hospital. With a sensitive configuration of 80%, our emergency department (ED) model achieved 77·4% sensitivity and 95·7% specificity (area under the receiver operating characteristic curve [AUROC] 0·939) for COVID-19 among all patients attending hospital, and the admissions model achieved 77·4% sensitivity and 94·8% specificity (AUROC 0·940) for the subset of patients admitted to hospital. Both models achieved high negative predictive values (NPV; >98·5%) across a range of prevalences (≤5%). We prospectively validated our models for all patients presenting and admitted to Oxford University Hospitals in a 2-week test period. The ED model (3326 patients) achieved 92·3% accuracy (NPV 97·6%, AUROC 0·881), and the admissions model (1715 patients) achieved 92·5% accuracy (97·7%, 0·871) in comparison with PCR results. Sensitivity analyses to account for uncertainty in negative PCR results improved apparent accuracy (ED model 95·1%, admissions model 94·1%) and NPV (ED model 99·0%, admissions model 98·5%).

Interpretation: Our models performed effectively as a screening test for COVID-19, excluding the illness with high-confidence by use of clinical data routinely available within 1 h of presentation to hospital. Our approach is rapidly scalable, fitting within the existing laboratory testing infrastructure and standard of care of hospitals in high-income and middle-income countries.

Reference

https://www.thelancet.com/journals/landig/article/PIIS2589-7500(20)30274-0/fulltext

Can limonene be a possible candidate for evaluation as an agent or adjuvant against infection, immunity, and inflammation in COVID-19?

Abstract

Coronavirus disease (COVID-19) caused by novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is an ongoing pandemic and presents a public health emergency. It has affected millions of people and continues to affect more, despite the tremendous social preventive measures. The therapeutic strategy relies on suppressing infectivity and inflammation, along with immune modulation. The identification of candidate drugs effective for COVID-19 is crucial, thus many natural products including phytochemicals are also being proposed for repurposing and evaluated for their potential in COVID-19. Among numerous phytochemicals, limonene (LMN), a dietary terpene of natural origin has been recently showed to target viral proteins in the in-silico studies. LMN is one of the main compounds identified in many citrus plants, available and accessible in diets and well-studied for its therapeutic benefits. Due to dietary nature, relative safety and efficacy along with favorable physicochemical properties, LMN has been suggested to be a fascinating candidate for further investigation in COVID-19. LMN showed to modulate numerous signaling pathways and inhibits inflammatory mediators, including cytokines, chemokines, adhesion molecules, prostanoids, and eicosanoids. We hypothesized that given the pathogenesis of COVID-19 involving infection, inflammation, and immunity, LMN may have potential to limit the severity and progression of the disease owing to its immunomodulatory, anti-inflammatory, and antiviral properties. The present article discusses the possibilities of LMN in SARS-CoV-2 infections based on its immunomodulatory, anti-inflammatory, and antiviral properties. Though, the suggestion on the possible use of LMN in COVID-19 remains inconclusive until the in-silico effects confirmed in the experimental studies and further proof of the concept studies. The candidature of LMN in COVID-19 treatment somewhat appear speculative but cannot be overlooked provided favorable physiochemical and druggable properties. The safety and efficacy of LMN are necessary to be established in preclinical and clinical studies before making suggestions for use in humans.

Reference

https://www.cell.com/heliyon/fulltext/S2405-8440(20)32546-9

Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events

Abstract

Analysis of 772 complete SARS-CoV-2 genomes from early in the Boston area epidemic revealed numerous introductions of the virus, a small number of which led to most cases. The data revealed two superspreading events. One, in a skilled nursing facility, led to rapid transmission and significant mortality in this vulnerable population but little broader spread, while other introductions into the facility had little effect. The second, at an international business conference, produced sustained community transmission and was exported, resulting in extensive regional, national, and international spread. The two events also differed significantly in the genetic variation they generated, suggesting varying transmission dynamics in superspreading events. Our results show how genomic epidemiology can help understand the link between individual clusters and wider community spread.

Reference

https://science.sciencemag.org/content/early/2020/12/09/science.abe3261

Publication Date: Dec 10, 2020

Genomic recombination events may reveal the evolution of coronavirus and the origin of SARS-CoV-2

Abstract

To trace the evolution of coronaviruses and reveal the possible origin of the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), which causes the coronavirus disease 2019 (COVID-19), we collected and thoroughly analyzed 29,452 publicly available coronavirus genomes, including 26,312 genomes of SARS-CoV-2 strains. We observed coronavirus recombination events among different hosts including 3 independent recombination events with statistical significance between some isolates from humans, bats and pangolins. Consistent with previous records, we also detected putative recombination between strains similar or related to Bat-CoV-RaTG13 and Pangolin-CoV-2019. The putative recombination region is located inside the receptor-

binding domain (RBD) of the spike glycoprotein (S protein), which may represent the origin of SARS-CoV-2. Population genetic analyses provide estimates suggesting that the putative introduced DNA within the RBD is undergoing directional evolution. This may result in the adaptation of the virus to hosts. Unsurprisingly, we found that the putative recombination region in S protein was highly diverse among strains from bats. Bats harbor numerous coronavirus subclades that frequently participate in recombination events with human coronavirus. Therefore, bats may provide a pool of genetic diversity for the origin of SARS-CoV-2.

Reference

https://www.nature.com/articles/s41598-020-78703-6

Rapid and sensitive detection of SARS-CoV-2 antibodies by biolayer interferometry

Abstract

Serological testing to evaluate antigen-specific antibodies in plasma is generally performed by rapid lateral flow test strips that lack quantitative results or by high complexity immunoassays that are time- and labor-intensive but provide semi-quantitative results. Here, we describe a novel application of biolayer interferometry for the rapid detection of antigen-specific antibody levels in plasma samples, and demonstrate its utility for quantification of SARS-CoV-2 antibodies. Our biolayer interferometry immunosorbent assay (BLI-ISA) utilizes single-use biosensors in an automated “dip-and-read” format, providing real-time optical measurements of antigen loading, plasma antibody binding, and antibody isotype detection. Complete semi-quantitative results are obtained in less than 20 min. BLI-ISA meets or exceeds the performance of high complexity methods such as Enzyme-Linked Immunosorbent Assay (ELISA) and Chemiluminescent Immunoassay. Importantly, our method can be immediately implemented on existing BLI platforms for urgent COVID-19 studies, such as serosurveillance and the evaluation of vaccine candidates. In a broader sense, BLI-ISA can be developed as a novel diagnostic platform to evaluate antibodies and other biomolecules in clinical specimens.

Reference

https://www.nature.com/articles/s41598-020-78895-x

***In vitro* virucidal activity of povidone iodine gargle and mouthwash against SARS-CoV-2: Implications for dental practice**

Abstract

Introduction: Virus particles in respiratory droplets and aerosols generated during medical/dental procedures are a potential source of SARS-CoV-2 cross infection. In the dental setting, oral decontamination could be an important adjunct to personal protective equipment and is recommended by a number of national COVID-19 guidance documents for dental settings.

Aim: To assess the *in vitro* virucidal activity of an oral povidone iodine (PVP-I) product against SARS-CoV-2.

Material and methods: BETADINE gargle and mouthwash (1% PVP-I) was tested against SARS-CoV-2 virus under both clean and dirty conditions using a suspension assay based on EN14476 methodology. Virucidal activity of the product, undiluted and at 1:2 dilution, was tested at contact times of 15, 30 and 60 seconds. Viral titres were calculated using the Spearman-Kärber method and reported as median tissue culture infectious dose (TCID50/ml).

Results: The undiluted product achieved >5 log10 reduction in viral titres compared to the control at 15, 30 and 60 seconds under both clean and dirty conditions. At a twofold dilution (0.5% PVP-I), the test product demonstrated >4 log10 kill at 15 seconds and >5 log10 kill at 30 and 60 seconds in both clean and dirty conditions.

Conclusion: PVP-I gargle and mouthwash product, undiluted and at 1:2 dilution, demonstrated potent and rapid virucidal activity (≥4 log10 reduction of viral titre) in 15 seconds against SARS-CoV-2 in vitro. The PVP-I gargle and mouthwash product is widely available and could be readily integrated into infection control measures during dental treatment including pre-procedural oral decontamination.

Reference

https://www.nature.com/articles/s41415-020-2402-0

Increased interleukin-6 and macrophage chemoattractant protein-1 are associated with respiratory failure in COVID-19

Abstract

In SARS-CoV-2 infection there is an urgent need to identify patients that will progress to severe COVID-19 and may benefit from targeted treatment. In this study we analyzed plasma cytokines in COVID-19 patients and investigated their association with respiratory failure (RF) and treatment in Intensive Care Unit (ICU). Hospitalized patients (n = 34) with confirmed COVID-19 were recruited into a prospective cohort study. Clinical data and blood samples were collected at inclusion and after 2–5 and 7–10 days. RF was defined as PaO2/FiO2 ratio (P/F) < 40 kPa. Plasma cytokines were analyzed by a Human Cytokine 27-plex assay. COVID-19 patients with RF and/or treated in ICU showed overall increased systemic cytokine levels. Plasma IL-6, IL-8, G-CSF, MCP-1, MIP-1α levels were negatively correlated with P/F, whereas combinations of IL-6, IP-10, IL-1ra and MCP-1 showed the best association with RF in ROC analysis (AUC 0.79–0.80, $p < 0.05$). During hospitalization the decline was most significant for IP-10 ($p < 0.001$). Elevated levels of pro-inflammatory cytokines were present in patients with severe COVID-19. IL-6 and MCP-1 were inversely correlated with P/F with the largest AUC in ROC analyses and should be further explored as biomarkers to identify patients at risk for severe RF and as targets for improved treatment strategies.

Reference

https://www.nature.com/articles/s41598-020-78710-7

Studying the effect of lockdown using epidemiological modelling of COVID-19 and a quantum computational approach using the Ising spin interaction

Abstract

COVID-19 is a respiratory tract infection that can range from being mild to fatal. In India, the countrywide lockdown has been imposed since 24th march 2020, and has got multiple extensions with different guidelines for each phase. Among various models of epidemiology, we use the SIR(D) model to analyze the extent to which this multi-phased lockdown has been active in ‘flattening the curve’ and lower the threat. Analyzing the effect of lockdown on the infection may provide a better insight into the evolution of

epidemic while implementing the quarantine procedures as well as improving the healthcare facilities. For accurate modelling, incorporating various parameters along with sophisticated computational facilities are required. Parallel to SIRD modelling, we tend to compare it with the Ising model and derive a quantum circuit that incorporates the rate of infection and rate of recovery, etc as its parameters. The probabilistic plots obtained from the circuit qualitatively resemble the shape of the curve for the spread of Coronavirus. We also demonstrate how the curve flattens when the lockdown is imposed. This kind of quantum computational approach can be useful in reducing space and time complexities of a huge amount of information related to the epidemic.

Reference

https://www.nature.com/articles/s41598-020-78652-0

Multidisciplinary approach to COVID-19 risk communication: a framework and tool for individual and regional risk assessment

Abstract

The COVID-19 pandemic has exceeded over sixty-five million cases globally. Different approaches are followed to mitigate its impact and reduce its spreading in different countries, but limiting mobility and exposure have been de-facto precautions to reduce transmission. However, a full lockdown cannot be sustained for a prolonged period. An evidence-based, multidisciplinary approach on risk zoning, personal and transmission risk assessment in near real-time, and risk communication would support the optimized decisions to minimize the impact of coronavirus on our lives. This paper presents a framework to assess the individual and regional risk of COVID-19 along with risk communication tools and mechanisms. Relative risk scores on a scale of 100 represent the integrated risk of influential factors. The personal risk model incorporates age, exposure history, symptoms, local risk and existing health condition, whereas regional risk is computed through the actual cases of COVID-19, public health risk factors, socioeconomic condition of the region, and immigration statistics. A web application tool (http://www.covira.info) has been developed, where anyone can assess their risk and find the guided information links primarily for Nepal. This study provides regional risk for Nepal, but the framework is scalable across the world. However, personal risk can be assessed immediately from anywhere.

Reference

https://www.nature.com/articles/s41598-020-78779-0

CORRESPONDANCE

Publication Date: Dec 15, 2020

Genetic IL-6R variants and therapeutic inhibition of IL-6 receptor signalling in COVID-19

The COVID-19 pandemic, caused by infections with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is a major challenge for treating physicians as long as neither a vaccine nor an available therapy is generally effective. Patients with SARS-CoV-2 often display hyperinflammation, and several small studies reported a benefit when patients were treated with tocilizumab, a monoclonal antibody targeting the interleukin (IL)-6 receptor (IL-6R). However, the phase 3 COVACTA trial did not show an improvement in clinical status in patients with COVID-19-associated pneumonia nor a reduction in patient mortality with tocilizumab, suggesting that IL-6 blockade might not be beneficial in all COVID-19 patients.

In their Correspondence in The Lancet Rheumatology, Jonas Bovijn and colleagues analysed seven genetic IL-6R variants in the context of COVID-19. Of these, only one single nucleotide polymorphism, rs2228145, which encodes the non-synonymous IL-6R variant Asp358Ala, has been functionally analysed, whereas data for the other, mostly intronic, variants are lacking. These variants have previously been shown to be associated with reduced serum concentrations of C-reactive protein and fibrinogen and increased serum concentrations of IL-6 and soluble IL-6R (sIL-6R).

Reference

https://www.thelancet.com/journals/lanrhe/article/PIIS2665-9913(20)30416-1/fulltext

PERSPECTIVE

Publication Date: Dec 14, 2020

A historical perspective on ACE2 in the COVID-19 era

Coronavirus disease 2019 (COVID-19) is caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Lessons learned from severe acute respiratory syndrome coronavirus (SARS-CoV) have facilitated a better understanding of the COVID-19 pandemic and efforts to develop targeted therapies. In particular, COVID-19 reminds us of the importance of the renin-angiotensin-aldosterone system (RAAS) in cardiovascular, pulmonary, and kidney physiology. After decades of RAAS research, we can apply this knowledge to better understand COVID-19 pathophysiology and to inform rigorous studies. For more details, read the link given below.

Reference

https://www.nature.com/articles/s41371-020-00459-3

Publication Date: Dec 11, 2020

Remembering seasonal coronaviruses

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has differential effects according to age, with symptomatic and severe infections mostly occurring in older adults. One possible explanation for this variation is that children and younger adults have more preexisting immunity against seasonal human coronaviruses (HCoVs) that cross-react with SARS-CoV-2, providing protection from severe and even symptomatic SARS-CoV-2 infection. Consistently, SARS-CoV-2 cross-reactive memory CD4+ and CD8+ T cells against the spike protein, the major surface protein of coronaviruses, have been reported in unexposed individuals (1, 2). Whether humoral immunity (antibodies and memory B cells) against SARS-CoV-2 cross-reacts with seasonal HCoVs is now emerging. On page 1339 of this issue, Ng et al. (3) and Shrock et al. (4) reveal that individuals exposed and unexposed to SARS-CoV-2 have cross-reactive serum antibodies against the spike protein of SARS-CoV-2 and seasonal HCoVs.

Reference

https://science.sciencemag.org/content/370/6522/1272

COMMENT

Publication Date: Dec 16, 2020

Reducing transmission of SARS-CoV-2 with intranasal prophylaxis

In a global effort to combat the COVID-19 pandemic, a diverse number of strategies may reduce viral transmission. Non-pharmaceutical interventions (NPIs) slow down epidemic spread without necessarily stopping it. In the absence of a distributed vaccine or highly effective antiviral, NPIs form one of the few readily available tactics we can employ to delay and/or reduce the spread. NPIs, however, have no influence on one's immunity to SARS-CoV-2, which is attained in one of two ways – infection, or immunisation. As SARS-CoV-2 infection probably does not result in lifelong immunity, the necessity for a therapy that might prevent transmission is of importance.

Both Regeneron's and Lilly's antibodies have recently received emergency use authorisation from the FDA as a treatment of mild-to-moderate COVID-19. Despite their promising results, the approach taken to derive such treatment comes with various impediments. Notably, the complexity and time associated with the production of monoclonal antibodies are likely to incur substantial costs. The necessity for infusion also poses greater limitations than would the opportunity to self-administer. It is therefore worthwhile to explore alternative methods for developing prophylaxis for COVID-19.

Such an alternative could include regulating transmission of SARS-CoV-2 by preventing attachment in the upper respiratory tract (URT). Previously, a group achieved this in animal models by administering the toll-like receptor-2 (TLR-2) agonist Pam2Cys in mice, in which reduced influenza virus levels in the URT and lungs were observed. Pam2Cys seemed a suitable candidate for the treatment of other respiratory pathogens. However, the presence of oligo-lysine sequences in the compound's solubilising agent has been found to interfere with infection processes independent of TLR activation. Specifically, they are known to enhance respiratory syncytial virus infection in primary epithelial, myeloid, and lymphoid cells. This effect was mitigated by incorporating polyethylene glycol as a solubilising agent, forming the INNA-X series of compounds. For more details, read the link given below.

Reference

https://www.thelancet.com/journals/ebiom/article/PIIS2352-3964(20)30546-6/fulltext

FORUM

Publication Date: Dec 16, 2020

Slaying SARS-CoV-2 one (single-domain) antibody at a time

Camelid-derived and synthetic single-domain antibodies (sdAbs) are emerging as potent weapons against the novel coronavirus, SARS-CoV-2. SdAbs are small, compact, thermostable immunoglobulin elements capable of binding targets with sub-nanomolar affinities. By leveraging the power of phage- and yeast surface-display technologies, rare sdAbs can be isolated from highly diverse and complex antibody libraries. Once in hand, sdAbs can be engineered to improve binding affinity, avidity, target specificities, and bio-distribution. In this Opinion piece, we highlight a series of sophisticated studies describing the identification of ultrapotent sdAbs directed against the receptor binding domain (RBD) of the SARS-CoV-2 Spike protein. We discuss the possible applications of these antibodies in the global fight against COVID-19.

Reference

https://www.cell.com/trends/microbiology/fulltext/S0966-842X(20)30323-1

Publication Date: Dec 14, 2020

Unraveling the zoonotic origin and transmission of SARS-CoV-2

The origin and zoonotic transmission route of SARS-CoV-2 remain speculative. We discuss scenarios for the zoonotic emergence of SARS-CoV-2, and also explore the missing evidence and ecological considerations that are necessary to confidently identify the origin and transmission route of SARS-CoV-2 and to prevent future pandemics of zoonotic viruses.

Reference

https://www.cell.com/trends/ecology-evolution/fulltext/S0169-5347(20)30348-7

REPORT

Publication Date: Dec 15, 2020

Contribution of temperature increase to restrain the transmission of COVID-19

COVID-19 outbreak has already become a global pandemic and containing this rapid worldwide transmission is of great challenge. The impacts of temperature and humidity on the COVID-19 transmission rate are still under discussion. Here, we elucidated these relationships by utilizing two unique scenarios, repeated measurement and natural experiment, using the COVID-19 cases reported from Jan. 23–Feb. 21, 2020, in China. The modeling results revealed that higher temperature was most strongly associated with decreased COVID-19 transmission at lag time of 8 days. Relative humidity (RH) appeared to have only a slight effect. These findings were verified by assessing SARS-CoV-2 infectivity under the relevant conditions of temperature (4–37°C) and RH (> 40%). We concluded that temperature increase made an important, but not determined, contribution to restraining the COVID-19 outbreak in China. It suggested that the emphasis of other effective controlling polices should be strictly implemented to restrain COVID-19 transmission for the cold seasons. For more details, read the link given below.

Reference

https://www.cell.com/the-innovation/fulltext/S2666-6758(20)30074-6

NEWSLETTER

Publication Date: Dec 15, 2020

Coronavirus (COVID-19) update: FDA authorizes antigen test as first over-the-counter fully at-home diagnostic test for COVID-19

U.S. Food and Drug Administration has authorized more than 225 diagnostic tests for COVID-19 since the start of the pandemic, including more than 25 tests that allow for home collection of samples, which are then sent to a lab for testing. The Ellume COVID-19 Home Test is the first COVID-19 test that can be used completely at home without a prescription.

The FDA issued an emergency use authorization (EUA) for the first over-the-counter (OTC) fully at-home diagnostic test for COVID-19. The Ellume COVID-19 Home Test is a rapid, lateral flow antigen test, a type of test that runs a liquid sample along a surface with reactive molecules. The test detects fragments of proteins of the SARS-CoV-2 virus from a nasal swab sample from any individual 2 years of age or older. For more details, read the link given below.

Reference

https://www.fda.gov/news-events/press-announcements/coronavirus-covid-19-update-fda-authorizes-antigen-test-first-over-counter-fully-home-diagnostic