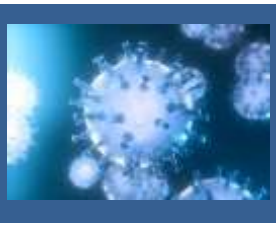
COVID-19

Oct 07 – 13, 2021



RESEARCH PUBLICATIONS

Publication Date: Oct 13, 2021

Clinical validation of automated and rapid mariPOC SARS-CoV-2 antigen test

Abstract

COVID-19 diagnostics was quickly ramped up worldwide early 2020 based on the detection of viral RNA. However, based on the scientific knowledge for pre-existing coronaviruses, it was expected that the SARS-CoV-2 RNA will be detected from symptomatic and at significant rates also from asymptomatic individuals due to persistence of non-infectious RNA. To increase the efficacy of diagnostics, surveillance, screening and pandemic control, rapid methods, such as antigen tests, are needed for decentralized testing and to assess infectiousness. A novel automated mariPOC SARS-CoV-2 test was developed for the detection of conserved structural viral nucleocapsid proteins. The test utilizes sophisticated optical laser technology for two-photon excitation and individual detection of immunoassay solid-phase particles. We validated the new method against qRT-PCR. Sensitivity of the test was 100.0% (13/13) directly from nasopharyngeal swab specimens and 84.4% (38/45) from swab specimens in undefined transport mediums. Specificity of the test was 100.0% (201/201). The test's limit of detection was 2.7 TCID50/test. It showed no cross-reactions. Our study shows that the new test can detect infectious individuals already in 20 min with clinical sensitivity close to qRT-PCR. The mariPOC is a versatile platform for syndromic testing and for high capacity infection control screening of infectious individuals.

Reference

https://www.nature.com/articles/s41598-021-99886-6

Identification of antiviral phytochemicals as a potential SARS-CoV-2 main protease (M^{pro}) inhibitor using docking and molecular dynamics simulations

Abstract

Novel SARS-CoV-2, an etiological factor of Coronavirus disease 2019 (COVID-19), poses a great challenge to the public health care system. Among other druggable targets of SARS-Cov-2, the main protease (Mpro) is regarded as a prominent enzyme target for drug developments owing to its crucial role in virus replication and transcription. We pursued a computational investigation to identify Mpro inhibitors from a compiled library of natural compounds with proven antiviral activities using a hierarchical workflow of molecular docking, ADMET assessment, dynamic simulations and binding free-energy calculations. Five natural compounds, Withanosides V and VI, Racemosides A and B, and Shatavarin IX, obtained better binding affinity and attained stable interactions with Mpro key pocket residues. These intermolecular key interactions were also retained profoundly in the simulation trajectory of 100 ns time scale indicating tight receptor binding. Free energy calculations prioritized Withanosides V and VI as the top candidates that can act as effective SARS-CoV-2 Mpro inhibitors.

Reference

https://www.nature.com/articles/s41598-021-99165-4

Clinical validation of automated and rapid mariPOC SARS-CoV-2 antigen test

Abstract

COVID-19 diagnostics was quickly ramped up worldwide early 2020 based on the detection of viral RNA. However, based on the scientific knowledge for pre-existing coronaviruses, it was expected that the SARS-CoV-2 RNA will be detected from symptomatic and at significant rates also from asymptomatic individuals due to persistence of non-infectious RNA. To increase the efficacy of diagnostics, surveillance, screening and pandemic control, rapid methods, such as antigen tests, are needed for decentralized testing and to assess infectiousness. A novel automated mariPOC SARS-CoV-2 test was developed for the detection of conserved structural viral nucleocapsid proteins. The test utilizes sophisticated optical laser technology for two-photon excitation and individual detection of immunoassay solid-phase particles. We validated

the new method against qRT-PCR. Sensitivity of the test was 100.0% (13/13) directly from nasopharyngeal swab specimens and 84.4% (38/45) from swab specimens in undefined transport mediums. Specificity of the test was 100.0% (201/201). The test's limit of detection was 2.7 TCID50/test. It showed no cross-reactions. The study shows that the new test can detect infectious individuals already in 20 min with clinical sensitivity close to qRT-PCR. The mariPOC is a versatile platform for syndromic testing and for high capacity infection control screening of infectious individuals.

Reference

https://www.nature.com/articles/s41598-021-99886-6

Characterization of SARS-CoV-2-specific humoral immunity and its potential applications and therapeutic prospects

Abstract

Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is an ongoing pandemic that poses a great threat to human health worldwide. As the humoral immune response plays essential roles in disease occurrence and development, understanding the dynamics and characteristics of virus-specific humoral immunity in SARS-CoV-2-infected patients is of great importance for controlling this disease. In this review, we summarize the characteristics of the humoral immune response after SARS-CoV-2 infection and further emphasize the potential applications and therapeutic prospects of SARS-CoV-2-specific humoral immunity and the critical role of this immunity in vaccine development. Notably, serological antibody testing based on the humoral immune response can guide public health measures and control strategies; however, it is not recommended for population surveys in areas with very low prevalence. Existing evidence suggests that asymptomatic individuals have a weaker immune response to SARS-CoV-2 infection, whereas SARS-CoV-2-infected children have a more effective humoral immune response than adults. The correlations between antibody (especially neutralizing antibody) titers and protection against SARS-CoV-2 reinfection should be further examined. In addition, the emergence of cross-reactions among different coronavirus antigens in the development of screening technology and the risk of antibody-

dependent enhancement related to SARS-CoV-2 vaccination should be given further attention.

Reference

https://www.nature.com/articles/s41423-021-00774-w

SARS-CoV-2 immunity and functional recovery of COVID-19 patients 1-year after infection

Abstract

The long-term immunity and functional recovery after SARS-CoV-2 infection have implications in preventive measures and patient quality of life. Here we analyzed a prospective cohort of 121 recovered COVID-19 patients from Xiangyang, China at 1-year after diagnosis. Among them, chemiluminescence immunoassay-based screening showed 99% (95% CI, 98–100%) seroprevalence 10–12 months after infection, comparing to 0.8% (95% CI, 0.7–0.9%) in the general population. Total anti-receptor-binding domain (RBD) antibodies remained stable since discharge, while anti-RBD IgG and neutralization levels decreased over time. A predictive model estimates 17% (95% CI, 11–24%) and 87% (95% CI, 80–92%) participants were still 50% protected against detectable and severe re-infection of WT SARS-CoV-2, respectively, while neutralization levels against B.1.1.7 and B.1.351 variants were significantly reduced. All non-severe patients showed normal chest CT and 21% reported COVID-19-related symptoms. In contrast, 53% severe patients had abnormal chest CT, decreased pulmonary function or cardiac involvement and 79% were still symptomatic. Our findings suggest long-lasting immune protection after SARS-CoV-2 infection, while also highlight the risk of immune evasive variants and long-term consequences for COVID-19 survivors.

Reference

https://www.nature.com/articles/s41392-021-00777-z

A novel benchmark for COVID-19 pandemic testing effectiveness enables the accurate prediction of new Intensive Care Unit admissions

Abstract

The positivity rate of testing is currently used both as a benchmark of testing adequacy and for assessing the evolution of the COVID-19 pandemic. However, since the former is a prerequisite for the latter, its interpretation is often conflicting. We propose as a benchmark for COVID-19 testing effectiveness a new metric, termed 'Severity Detection Rate' (SDR), that represents the daily needs for new Intensive Care Unit (ICU) admissions, per 100 cases detected (t − i) days ago, per 10,000 tests performed (t − i) days ago. Based on the announced COVID-19 monitoring data in Greece from May 2020 until August 2021, we show that beyond a certain threshold of daily tests, SDR reaches a plateau of very low variability that begins to reflect testing adequacy. Due to the stabilization of SDR, it was possible to predict with great accuracy the daily needs for new ICU admissions, 12 days ahead of each testing data point, over a period of 10 months, with Pearson r = 0.98 (p = 10–197), RMSE = 7.16. We strongly believe that this metric will help guide the timely decisions of both scientists and government officials to tackle pandemic spread and prevent ICU overload by setting effective testing requirements for accurate pandemic monitoring. We propose further study of this novel metric with data from more countries to confirm the validity of the current findings.

Reference

https://www.nature.com/articles/s41598-021-99543-y

Sociodemographic, clinical, and immunological factors associated with SARS-CoV-2 diagnosis and severe COVID-19 outcomes in people living with HIV: A retrospective cohort study

Abstract

Background: Factors affecting outcomes of SARS-CoV-2 infection in people living with HIV are unclear. We assessed the factors associated with SARS-CoV-2 diagnosis and severe outcomes among people living with HIV.

Methods: We did a retrospective cohort study using data from the PISCIS cohort of people with HIV in Catalonia (Spain) between March 1 and Dec 15, 2020. We linked

PISCIS data with integrated health-care, clinical, and surveillance registries through the Public Data Analysis for Health Research and Innovation Program of Catalonia (PADRIS) to obtain data on SARS-CoV-2 diagnosis, chronic comorbidities, as well as clinical and mortality outcomes. Participants were aged at least 16 years in care at 16 hospitals in Catalonia. Factors associated with SARS-CoV-2 diagnoses and severe outcomes were assessed using univariable and multivariable Cox regression models. We estimated the effect of immunosuppression on severe outcomes (hospital admission for >24 h with dyspnoea, tachypnoea, hypoxaemia, asphyxia, or hyperventilation; or death) using Kaplan-Meier survival analysis.

Findings: We linked 20 847 (72·8%) of 28 666 participants in the PISCIS cohort with PADRIS data; 13 142 people had HIV. 749 (5·7%) people with HIV were diagnosed with SARS-CoV-2: their median age was 43·5 years (IQR 37·0–52·7), 131 (17·5%) were female, and 618 (82·5%) were male. 103 people with HIV (13·8%) were hospitalised, seven (0·9%) admitted to intensive care, and 13 (1·7%) died. SARS-CoV-2 diagnosis was more common among migrants (adjusted hazard ratio 1·55, 95% CI 1·31–1·83), men who have sex with men (1·42, 1·09–1·86), and those with four or more chronic comorbidities (1·46, 1·09–1·97). Age at least 75 years (5·2, 1·8–15·3), non-Spanish origin (2·1, 1·3–3·4), and neuropsychiatric (1·69, 1·07–2·69), autoimmune disease (1·92, 1·14–3·23), respiratory disease (1·84, 1·09–3·09), and metabolic disease (2·59, 1·59–4·23) chronic comorbidities were associated with increased risk of severe outcomes. A Kaplan-Meier estimator showed differences in the risk of severe outcomes according to CD4 cell count in patients with detectable HIV RNA (p=0·039) but no differences were observed in patients with undetectable HIV RNA (p=0·15).

Interpretation: People living with HIV with detectable HIV viraemia, chronic comorbidities, and some subpopulations could be at increased risk of severe outcomes from COVID-19. These groups should be prioritised in clinical management and SARS-CoV-2 vaccination programmes.

Reference

https://www.thelancet.com/journals/lanhiv/article/PIIS2352-3018(21)00240-X/fulltext

Molecular rationale for SARS-CoV-2 spike circulating mutations able to escape bamlanivimab and etesevimab monoclonal antibodies

Abstract

The purpose of this work is to provide an in silico molecular rationale of the role eventually played by currently circulating mutations in the receptor binding domain of the SARS-CoV-2 spike protein (S-RBDCoV-2) in evading the immune surveillance effects elicited by the two Eli Lilly LY-CoV555/bamlanivimab and LY-CoV016/etesevimab monoclonal antibodies. The main findings from this study show that, compared to the wild-type SARS-CoV-2 spike protein, mutations E484A/G/K/Q/R/V, Q493K/L/R, S494A/P/R, L452R and F490S are predicted to be markedly resistant to neutralization by LY-CoV555, while mutations K417E/N/T, D420A/G/N, N460I/K/S/T, T415P, and Y489C/S are predicted to confer LY-CoV016 escaping advantage to the viral protein. A challenge of our global in silico results against relevant experimental data resulted in an overall 90% agreement. Thus, the results presented provide a molecular-based rationale for all relative experimental findings, constitute a fast and reliable tool for identifying and prioritizing all present and newly reported circulating spike SARS-CoV-2 variants with respect to antibody neutralization, and yield substantial structural information for the development of next-generation vaccines and monoclonal antibodies more resilient to viral evolution.

Reference

https://www.nature.com/articles/s41598-021-99827-3

Dynamic alterations in monocyte numbers, subset frequencies and activation markers in acute and convalescent COVID-19 individuals

Abstract

Monocytes are thought to play an important role in host defence and pathogenesis of COVID-19. However, a comprehensive examination of monocyte numbers and function has not been performed longitudinally in acute and convalescent COVID-19. We examined the absolute counts of monocytes, the frequency of monocyte subsets, the plasma levels of monocyte activation markers using flowcytometry and ELISA in seven

groups of COVID-19 individuals, classified based on days since RT-PCR confirmation of SARS-CoV2 infection. Our data shows that the absolute counts of total monocytes and the frequencies of intermediate and non-classical monocytes increases from Days 15–30 to Days 61–90 and plateau thereafter. In contrast, the frequency of classical monocytes decreases from Days 15–30 till Days 121–150. The plasma levels of sCD14, CRP, sCD163 and sTissue Factor (sTF)—all decrease from Days 15–30 till Days 151–180. COVID-19 patients with severe disease exhibit higher levels of monocyte counts and higher frequencies of classical monocytes and lower frequencies of intermediate and non-classical monocytes and elevated plasma levels of sCD14, CRP, sCD163 and sTF in comparison with mild disease. Thus, our study provides evidence of dynamic alterations in monocyte counts, subset frequencies and activation status in acute and convalescent COVID-19 individuals.

Reference

https://www.nature.com/articles/s41598-021-99705-y

Diagnostic performances of common nucleic acid tests for SARS-CoV-2 in hospitals and clinics: A systematic review and meta-analysis

Abstract

Background: An optimised standard experimental setup across different hospitals is urgently needed to ensure consistency in nucleic acid test results for SARS-CoV-2 detection. A standard comparison across different nucleic acid tests and their optimal experimental setups is not present. We assessed the performance of three common nucleic acid tests, namely digital PCR (dPCR), quantitative PCR (qPCR), and loop-mediated isothermal amplification (LAMP), to detect SARS-CoV-2 in clinical settings.

Methods: In this systematic review and meta-analysis we compared sensitivity and specificity of qPCR, dPCR, and LAMP and their performances when different experimental setups (namely specimen type used, use of RNA extraction, primer–probe sets, and RNA extraction methods) are applied. We searched PubMed, BioRxiv, MedRxiv, SciFinder, and ScienceDirect for studies and preprints published between Feb 29 and Dec 15, 2020. Included dPCR, qPCR, and LAMP studies using any type of human specimens should report the number of true-positive, true-negative, false-positive, and false-negative cases with Emergency Use Authorization (EUA)-approved

PCR assays as the comparator. Studies with a sample size of less than ten, descriptive studies, case studies, reviews, and duplicated studies were excluded. Pooled sensitivity and specificity were computed from the true and false positive and negative cases using Reitsma's bivariate random-effects and bivariate latent class models. Test performance reported in area under the curve (AUC) of the three nucleic acid tests was further compared by pooling studies with similar experimental setups (eg, tests that used RNA extracted pharyngeal swabs but with either the open reading frame 1ab or the N primer). Heterogeneity was assessed and reported in I2 and τ2.

Findings: Our search identified 1277 studies of which we included 66 studies (11 dPCR, 32 qPCR, and 23 LAMP) with 15 017 clinical samples in total in our systematic review and 52 studies in our meta-analysis. dPCR had the highest pooled diagnostic sensitivity (94·1%, 95% CI 88·9–96·6, by Reitsma's model and 95·8%, 54·9–100·0, by latent class model), followed by qPCR (92·7%, 88·3–95·6, and 93·4%, 60·9–99·9) and LAMP (83·3%, 76·9–88·2, and 86·2%, 20·7–99·9), using EUA-approved PCR kits as the reference standard. LAMP was the most specific with a pooled estimate of 96·3% (93·8–97·8) by Reitsma's model and 94·3% (49·1–100·0) by latent class model, followed by qPCR (92·9%, 87·2–96·2, and 93·1%, 47·1–100·0) and dPCR (78·5%, 57·4–90·8, and 73·8%, 0·9–100·0). The overall heterogeneity was I2 0·5% (τ2 2·79) for dPCR studies, 0% (4·60) for qPCR studies, and 0% (3·96) for LAMP studies. AUCs of the three nucleic acid tests were the highest and differed the least between tests (ie, AUC>0·98 for all tests) when performed with RNA extracted pharyngeal swabs using SARS-CoV-2 open reading frame 1ab primer.

Interpretation: All three nucleic acid tests consistently perform better with pharyngeal swabs using SARS-CoV-2 open reading frame 1ab primer with RNA extraction. dPCR was shown to be the most sensitive, followed by qPCR and LAMP. However, their accuracy does not differ significantly. Instead, accuracy depends on specific experimental conditions, implying that more efforts should be directed to optimising the experimental setups for the nucleic acid tests. Hence, our results could be a reference for optimising and establishing a standard nucleic acid test protocol that is applicable in laboratories worldwide.

Reference

https://www.thelancet.com/journals/lanmic/article/PIIS2666-5247(21)00214-7/fulltext

Publication Date: Oct 08, 2021

SARS-CoV-2 inhibition using a mucoadhesive, amphiphilic chitosan that may serve as an anti-viral nasal spray

Abstract

There are currently no cures for coronavirus infections, making the prevention of infections the only course open at the present time. The COVID-19 pandemic has been difficult to prevent, as the infection is spread by respiratory droplets and thus effective, scalable and safe preventive interventions are urgently needed. We hypothesise that preventing viral entry into mammalian nasal epithelial cells may be one way to limit the spread of COVID-19. Here we show that N-palmitoyl-N-monomethyl-N,N-dimethyl-N,N,N-trimethyl-6-O-glycolchitosan (GCPQ), a positively charged polymer that has been through an extensive Good Laboratory Practice toxicology screen, is able to reduce the infectivity of SARS-COV-2 in A549ACE2+ and Vero E6 cells with a log removal value of − 3 to − 4 at a concentration of 10–100 μg/ mL ($p < 0.05$ compared to untreated controls) and to limit infectivity in human airway epithelial cells at a concentration of 500 μg/ mL ($p < 0.05$ compared to untreated controls). In vivo studies using transgenic mice expressing the ACE-2 receptor, dosed nasally with SARS-COV-2 (426,000 TCID50/mL) showed a trend for nasal GCPQ (20 mg/kg) to inhibit viral load in the respiratory tract and brain, although the study was not powered to detect statistical significance. GCPQ's electrostatic binding to the virus, preventing viral entry into the host cells, is the most likely mechanism of viral inhibition. Radiolabelled GCPQ studies in mice show that at a dose of 10 mg/kg, GCPQ has a long residence time in mouse nares, with 13.1% of the injected dose identified from SPECT/CT in the nares, 24 h after nasal dosing. With a no observed adverse effect level of 18 mg/kg in rats, following a 28-day repeat dose study, clinical testing of this polymer, as a COVID-19 prophylactic is warranted.

Reference

https://www.nature.com/articles/s41598-021-99404-8

Anti-SARS-CoV-2 receptor binding domain antibody evolution after mRNA vaccination

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection produces B cell responses that continue to evolve for at least one year. During that time, memory B cells express increasingly broad and potent antibodies that are resistant to mutations found in variants of concern. As a result, vaccination of coronavirus disease 2019 (COVID-19) convalescent individuals with currently available mRNA vaccines produces high levels of plasma neutralizing activity against all variants tested. Here we examine memory B cell evolution 5 months after vaccination with either Moderna (mRNA-1273) or Pfizer-BioNTech (BNT162b2) mRNA vaccines in a cohort of SARS-CoV-2 naive individuals. Between prime and boost, memory B cells produce antibodies that evolve increased neutralizing activity, but there is no further increase in potency or breadth thereafter. Instead, memory B cells that emerge 5 months after vaccination of naive individuals express antibodies that are similar to those that dominate the initial response. While individual memory antibodies selected over time by natural infection have greater potency and breadth than antibodies elicited by vaccination, the overall neutralizing potency of plasma is greater following vaccination. These results suggest that boosting vaccinated individuals with currently available mRNA vaccines will increase plasma neutralizing activity but may not produce antibodies with equivalent breadth to those obtained by vaccinating convalescent individuals.

Reference

https://www.nature.com/articles/s41586-021-04060-7

SARS-CoV-2 binding and neutralizing antibody levels after Ad26.COV2.S vaccination predict durable protection in rhesus macaques

Abstract

Several COVID-19 vaccines have recently gained authorization for emergency use. Limited knowledge on duration of immunity and efficacy of these vaccines is currently available. Data on other coronaviruses after natural infection suggest that immunity to

SARS-CoV-2 might be short-lived, and preliminary evidence indicates waning antibody titers following SARS-CoV-2 infection. In this work, we model the relationship between immunogenicity and protective efficacy of a series of Ad26 vectors encoding stabilized variants of the SARS-CoV-2 Spike protein in rhesus macaques and validate the analyses by challenging macaques 6 months after immunization with the Ad26.COV2.S vaccine candidate that has been selected for clinical development. We show that Ad26.COV2.S confers durable protection against replication of SARS-CoV-2 in the lungs that is predicted by the levels of Spike-binding and neutralizing antibodies, indicating that Ad26.COV2.S could confer durable protection in humans and immunological correlates of protection may enable the prediction of durability of protection.

Reference

https://www.nature.com/articles/s41467-021-26117-x

ChAdOx1 nCoV-19 (AZD1222) protects Syrian hamsters against SARS-CoV-2 B.1.351 and B.1.1.7

Abstract

We investigated ChAdOx1 nCoV-19 (AZD1222) vaccine efficacy against SARS-CoV-2 variants of concern (VOCs) B.1.1.7 and B.1.351 in Syrian hamsters. We previously showed protection against SARS-CoV-2 disease and pneumonia in hamsters vaccinated with a single dose of ChAdOx1 nCoV-19. Here, we observe a 9.5-fold reduction of virus neutralizing antibody titer in vaccinated hamster sera against B.1.351 compared to B.1.1.7. Vaccinated hamsters challenged with B.1.1.7 or B.1.351 do not lose weight compared to control animals. In contrast to control animals, the lungs of vaccinated animals do not show any gross lesions. Minimal to no viral subgenomic RNA (sgRNA) and no infectious virus can be detected in lungs of vaccinated animals. Histopathological evaluation shows extensive pulmonary pathology caused by B.1.1.7 or B.1.351 replication in the control animals, but none in the vaccinated animals. These data demonstrate the effectiveness of the ChAdOx1 nCoV-19 vaccine against clinical disease caused by B.1.1.7 or B.1.351 VOCs.

Reference

https://www.nature.com/articles/s41467-021-26178-y

Scalable, effective, and rapid decontamination of SARS-CoV-2 contaminated N95 respirators using germicidal ultraviolet C (UVC) irradiation device

Abstract

Particulate respirators such as N95s are an essential component of personal protective equipment (PPE) for front-line workers. This study describes a rapid and effective UVC irradiation system that would facilitate the safe re-use of N95 respirators and provides supporting information for deploying UVC for decontamination of SARS-CoV-2 during the COVID-19 pandemic. To assess the inactivation potential of the proposed UVC germicidal device as a function of time by using 3 M 8211-N95 particulate respirators inoculated with SARS-CoV-2. A germicidal UVC device to deliver tailored UVC dose was developed and test coupons (2.5 cm2) of the 3 M-N95 respirator were inoculated with 106 plaque-forming units (PFU) of SARS-CoV-2 and were UV irradiated. Different exposure times were tested (0–164 s) by fixing the distance between the lamp and the test coupon to 15.2 cm while providing an exposure of at least 5.43 mWcm−2. Primary measure of outcome was titration of infectious virus recovered from virus-inoculated respirator test coupons after UVC exposure. Other measures included the method validation of the irradiation protocol, using lentiviruses (biosafety level-2 agent) and establishment of the germicidal UVC exposure protocol. An average of 4.38 × 103 PFU ml−1 (SD 772.68) was recovered from untreated test coupons while 4.44 × 102 PFU ml−1 (SD 203.67), 4.00 × 102 PFU ml−1 (SD 115.47), 1.56 × 102 PFU ml−1 (SD 76.98) and 4.44 × 101 PFU ml−1 (SD 76.98) was recovered in exposures 2, 6, 18 and 54 s per side respectively. The germicidal device output and positioning was monitored and a minimum output of 5.43 mW cm−2 was maintained. Infectious SARS-CoV-2 was not detected by plaque assays (minimal level of detection is 67 PFU ml−1) on N95 respirator test coupons when irradiated for 120 s per side or longer suggesting 3.5 log reduction in 240 s of irradiation, 1.3 J cm−2. A scalable germicidal UVC device to deliver tailored UVC dose for rapid decontamination of SARS-CoV-2 was developed. UVC germicidal irradiation of N95 test coupons inoculated with SARS-CoV-2 for 120 s per side resulted in 3.5 log reduction of virus. These data support the reuse of N95

particle-filtrate apparatus upon irradiation with UVC and supports use of UVC-based decontamination of SARS-CoV-2 during the COVID-19 pandemic.

Reference

https://www.nature.com/articles/s41598-021-99431-5

Reliably quantifying the evolving worldwide dynamic state of the COVID-19 outbreak from death records, clinical parametrization, and demographic data

Abstract

The dynamic characterization of the COVID-19 outbreak is critical to implement effective actions for its control and eradication but the information available at a global scale is not sufficiently reliable to be used directly. Here, we develop a quantitative approach to reliably quantify its temporal evolution and controllability through the integration of multiple data sources, including death records, clinical parametrization of the disease, and demographic data, and we explicitly apply it to countries worldwide, covering 97.4% of the human population, and to states within the United States (US). The validation of the approach shows that it can accurately reproduce the available prevalence data and that it can precisely infer the timing of nonpharmaceutical interventions. The results of the analysis identified general patterns of recession, stabilization, and resurgence. The diversity of dynamic behaviors of the outbreak across countries is paralleled by those of states and territories in the US, converging to remarkably similar global states in both cases. Our results offer precise insights into the dynamics of the outbreak and an efficient avenue for the estimation of the prevalence rates over time.

Reference

https://www.nature.com/articles/s41598-021-99273-1

sFlt-1 and CA 15.3 are indicators of endothelial damage and pulmonary fibrosis in SARS-CoV-2 infection

Abstract

COVID-19 pandemic led to a worldwide increase of hospitalizations for interstitial pneumonia with thrombosis complications, endothelial injury and multiorgan disease.

Common CT findings include lung bilateral infiltrates, bilateral ground-glass opacities and/or consolidation whilst no current laboratory parameter consents rapidly evaluation of COVID-19 risk and disease severity. In the present work we investigated the association of sFLT-1 and CA 15.3 with endothelial damage and pulmonary fibrosis. Serum sFlt-1 has been associated with endothelial injury and sepsis severity, CA 15.3 seems an alternative marker for KL-6 for fibrotic lung diseases and pulmonary interstitial damage. We analysed 262 SARS-CoV-2 patients with differing levels of clinical severity; we found an association of serum sFlt-1 (ROC AUC 0.902, decision threshold > 90.3 pg/mL, $p < 0.001$ Sens. 83.9% and Spec. 86.7%) with presence, extent and severity of the disease. Moreover, CA 15.3 appeared significantly increased in COVID-19 severe lung fibrosis (ICU vs NON-ICU patients 42.6 ± 3.3 vs 25.7 ± 1.5 U/mL, $p < 0.0001$) and was associated with lung damage severity grade (ROC AUC 0.958, decision threshold > 24.8 U/mL, $p < 0.0001$, Sens. 88.4% and Spec. 91.8%). In conclusion, serum levels of sFlt-1 and CA 15.3 appeared useful tools for categorizing COVID-19 clinical stage and may represent a valid aid for clinicians to better personalise treatment.

Reference

https://www.nature.com/articles/s41598-021-99470-y

Physical, cognitive, and mental health impacts of COVID-19 after hospitalisation (PHOSP-COVID): A UK multicentre, prospective cohort study

Abstract

Background: The impact of COVID-19 on physical and mental health and employment after hospitalisation with acute disease is not well understood. The aim of this study was to determine the effects of COVID-19-related hospitalisation on health and employment, to identify factors associated with recovery, and to describe recovery phenotypes.

Methods: The Post-hospitalisation COVID-19 study (PHOSP-COVID) is a multicentre, long-term follow-up study of adults (aged ≥18 years) discharged from hospital in the UK with a clinical diagnosis of COVID-19, involving an assessment between 2 and 7 months after discharge, including detailed recording of symptoms, and physiological and biochemical testing. Multivariable logistic regression was done for the primary outcome of patient-perceived recovery, with age, sex, ethnicity, body-mass index,

comorbidities, and severity of acute illness as covariates. A post-hoc cluster analysis of outcomes for breathlessness, fatigue, mental health, cognitive impairment, and physical performance was done using the clustering large applications k-medoids approach. The study is registered on the ISRCTN Registry (ISRCTN10980107).

Findings: We report findings for 1077 patients discharged from hospital between March 5 and Nov 30, 2020, who underwent assessment at a median of 5·9 months (IQR 4·9–6·5) after discharge. Participants had a mean age of 58 years (SD 13); 384 (36%) were female, 710 (69%) were of white ethnicity, 288 (27%) had received mechanical ventilation, and 540 (50%) had at least two comorbidities. At follow-up, only 239 (29%) of 830 participants felt fully recovered, 158 (20%) of 806 had a new disability (assessed by the Washington Group Short Set on Functioning), and 124 (19%) of 641 experienced a health-related change in occupation. Factors associated with not recovering were female sex, middle age (40–59 years), two or more comorbidities, and more severe acute illness. The magnitude of the persistent health burden was substantial but only weakly associated with the severity of acute illness. Four clusters were identified with different severities of mental and physical health impairment (n=767): very severe (131 patients, 17%), severe (159, 21%), moderate along with cognitive impairment (127, 17%), and mild (350, 46%). Of the outcomes used in the cluster analysis, all were closely related except for cognitive impairment. Three (3%) of 113 patients in the very severe cluster, nine (7%) of 129 in the severe cluster, 36 (36%) of 99 in the moderate cluster, and 114 (43%) of 267 in the mild cluster reported feeling fully recovered. Persistently elevated serum C-reactive protein was positively associated with cluster severity.

Interpretation: We identified factors related to not recovering after hospital admission with COVID-19 at 6 months after discharge (eg, female sex, middle age, two or more comorbidities, and more acute severe illness), and four different recovery phenotypes. The severity of physical and mental health impairments were closely related, whereas cognitive health impairments were independent. In clinical care, a proactive approach is needed across the acute severity spectrum, with interdisciplinary working, wide access to COVID-19 holistic clinical services, and the potential to stratify care.

Reference

https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(21)00383-0/fulltext