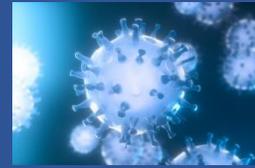


COVID-19

Jul 30 – Aug 05, 2020



RESEARCH PUBLICATIONS

Publication Date: Aug 05, 2020

Elevated calprotectin and abnormal myeloid cell subsets discriminate severe from mild COVID-19

Abstract

Blood myeloid cells are known to be dysregulated in the coronavirus disease 2019 (COVID-19) caused by SARS-CoV-2. It is unknown whether the innate myeloid response differs with disease severity, and whether markers of innate immunity discriminate high risk patients. Thus, we performed high dimensional flow cytometry and single cell RNA sequencing of COVID-19 patient peripheral blood cells and detected the disappearance of non-classical CD14^{Low}CD16^{High} monocytes, the accumulation of HLA-DR^{Low} classical monocytes, and the release of massive amounts of calprotectin (S100A8/S100A9) in severe cases. Immature CD10^{Low}CD101-CXCR4^{+/-} neutrophils with an immuno-suppressive profile accumulated as well in blood and lungs, suggesting emergency myelopoiesis. We finally showed that calprotectin plasma level and a routine flow cytometry assay detecting decreased frequencies of non-classical monocytes could discriminate patients who develop a severe COVID-19 form, suggesting a predictive value that deserves prospective evaluation.

Reference

[https://www.cell.com/cell/fulltext/S0092-8674\(20\)30993-4](https://www.cell.com/cell/fulltext/S0092-8674(20)30993-4)

Modelling the impact of testing, contact tracing and household quarantine on second waves of COVID-19

Abstract

While severe social-distancing measures have proven effective in slowing the coronavirus disease 2019 (COVID-19) pandemic, second-wave scenarios are likely to emerge as restrictions are lifted. Here we integrate anonymized, geolocalized mobility data with census and demographic data to build a detailed agent-based model of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) transmission in the Boston metropolitan area. We find that a period of strict social distancing followed by a robust level of testing, contact-tracing and household quarantine could keep the disease within the capacity of the healthcare system while enabling the reopening of economic activities. Our results show that a response system based on enhanced testing and contact tracing can have a major role in relaxing social-distancing interventions in the absence of herd immunity against SARS-CoV-2.

Reference

<https://www.nature.com/articles/s41562-020-0931-9>

Clinical features and prognosis of COVID-19 in people with spinal cord injury: A case–control study

Abstract

Study design: Observational case–control study.

Objective: Individuals with spinal cord injury (SCI) develop systemic physiological changes that could increase the risk of severe evolution of coronavirus disease 2019 (COVID-19) and result in atypical clinical features of COVID-19 with possible delay in both diagnosis and treatment. We evaluated differences in clinical features and evolution of COVID-19 between people with SCI and able-bodied individuals.

Setting: The study was conducted in an Italian inpatient rehabilitation referral center for individuals with SCI during the lockdown for the COVID-19 pandemic.

Methods: We compared clinical information between patients with SCI and able-bodied healthcare workers of the same center who tested positive for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) in the nasopharyngeal swab polymerase chain reaction.

Results: Overall, 15 out of the 25 SCI patients admitted to the center and 17 out of the 69 healthcare workers tested positive for SARS-CoV-2. Patients with SCI exhibited a significantly more advanced age and a higher prevalence of comorbidities. Nevertheless, no significant differences in clinical expression of COVID-19 and treatment strategies were observed between the two groups. All hospitalized subjects were treated in nonintensive care units and no deaths occurred in either group.

Conclusions: This study does not support the supposed notion that COVID-19 could exhibit atypical clinical features or a worse evolution in the frail population of people with SCI.

Reference

<https://www.nature.com/articles/s41394-020-0319-0>

A novel Monte Carlo simulation procedure for modelling COVID-19 spread over time

Abstract

The coronavirus disease 2019 (COVID-19) has now spread throughout most countries in the world causing heavy life losses and damaging social-economic impacts. Following a stochastic point process modelling approach, a Monte Carlo simulation model was developed to represent the COVID-19 spread dynamics. First, we examined various expected performances (theoretical properties) of the simulation model assuming a number of arbitrarily defined scenarios. Simulation studies were then performed on the real COVID-19 data reported (over the period of 1 March to 1 May) for Australia and United Kingdom (UK). Given the initial number of COVID-19 infection active cases were around 10 for both countries, the model estimated that the number of active cases would peak around 29 March in Australia ($\approx 1,700$ cases) and around 22 April in UK ($\approx 22,860$ cases); ultimately the total confirmed cases could sum to 6,790 for Australia in about 75 days and 206,480 for UK in about 105 days. The results of the estimated COVID-19 reproduction numbers were consistent with what was reported in the literature. This simulation model was considered an effective and adaptable decision making/what-if analysis tool in battling COVID-19 in the immediate need, and for modelling any other infectious diseases in the future.

Reference

<https://www.nature.com/articles/s41598-020-70091-1>

Emergency response strategy for containing COVID-19 within a psychiatric specialty hospital in the epicenter of the COVID-19 epidemic in China

Abstract

Coronavirus disease 2019 (COVID-19) has been recognized as a global pandemic, and psychiatric institutions located in the epicenter of the epidemic in China are facing severe challenges in fighting the epidemic. This article presents the accumulated experience of the authors during the process of combating COVID-19 in a psychiatric hospital. The aim of this article is to provide a reference for psychiatric specialty

hospitals and institutions that treat large populations of chronically ill patients in other parts of the world.

Reference

<https://www.nature.com/articles/s41398-020-00959-3>

Selective and cross-reactive SARS-CoV-2 T cell epitopes in unexposed humans

Abstract

Many unknowns exist about human immune responses to the SARS-CoV-2 virus. SARS-CoV-2 reactive CD4+ T cells have been reported in unexposed individuals, suggesting pre-existing cross-reactive T cell memory in 20-50% of people. However, the source of those T cells has been speculative. Using human blood samples derived before the SARS-CoV-2 virus was discovered in 2019, we mapped 142 T cell epitopes across the SARS-CoV-2 genome to facilitate precise interrogation of the SARS-CoV-2-specific CD4+ T cell repertoire. We demonstrate a range of pre-existing memory CD4+ T cells that are cross-reactive with comparable affinity to SARS-CoV-2 and the common cold coronaviruses HCoV-OC43, HCoV-229E, HCoV-NL63, or HCoV-HKU1. Thus, variegated T cell memory to coronaviruses that cause the common cold may underlie at least some of the extensive heterogeneity observed in COVID-19 disease.

Reference

<https://science.sciencemag.org/content/early/2020/08/04/science.abd3871>

Publication Date: Aug 03, 2020

A Learning-based model to evaluate hospitalization priority in COVID-19 pandemics

Abstract

The emergence of novel coronavirus disease 2019 (COVID-19) is placing an increasing burden on the healthcare systems. Although the majority of infected patients have non-severe symptoms and can be managed at home, some individuals may develop severe

disease and are demanding the hospital admission. Therefore, it becomes paramount to efficiently assess the severity of COVID-19 and identify hospitalization priority with precision. In this respect, a 4-variable assessment model, including lymphocyte, lactate dehydrogenase (LDH), C-reactive protein (CRP) and neutrophil, is established and validated using the XGBoost algorithm. This model is found effective to identify severe COVID-19 cases on admission, with a sensitivity of 84.6%, a specificity of 84.6%, and an accuracy of 100% to predict the disease progression toward rapid deterioration. It also suggests that a computation-derived formula of clinical measures is practically applicable for the healthcare administrators to distribute hospitalization resources to the most needed in epidemics and pandemics.

Reference

[https://www.cell.com/patterns/fulltext/S2666-3899\(20\)30120-3](https://www.cell.com/patterns/fulltext/S2666-3899(20)30120-3)

Dexamethasone nanomedicines for COVID-19

Abstract

Nano-formulating dexamethasone, and administering it via intravenous injection or inhalation, may help to improve anti-COVID-19 treatment efficacy by targeting the potent corticosteroid drug to hyper-activated immune cells, by potentiating its anti-oedema activity and by exploiting its anti-fibrotic effects. For more details, view the link given below.

Reference

<https://www.nature.com/articles/s41565-020-0752-z>

Publication Date: Aug 01, 2020

Modelling lockdown and exit strategies for COVID-19 in Singapore

Abstract

Background: With at least 94 countries undergoing or exiting lockdowns for contact suppression to control the COVID-19 outbreak, sustainable and public health-driven exit

strategies are required. Here we explore the impact of lockdown and exit strategies in Singapore for immediate planning.

Methods: We use an agent-based model to examine the impacts of epidemic control over 480 days. A limited control baseline of case isolation and household member quarantining is used. We measure the impact of lockdown duration and start date on final infection attack sizes. We then apply a 3-month gradual exit strategy, immediately re-opening schools and easing workplace distancing measures, and compare this to long-term social distancing measures.

Findings: At baseline, we estimated 815 400 total infections (21.6% of the population). Early lockdown at 5 weeks with no exit strategy averted 18 500 (2.27% of baseline averted), 21 300 (2.61%) and 22 400 (2.75%) infections for 6, 8 and 9-week lockdown durations. Using the exit strategy averted a corresponding 114 700, 121 700 and 126 000 total cases, representing 12.07–13.06% of the total epidemic size under baseline. This diminishes to 9 900–11 300 for a late 8-week start time. Long-term social distancing at 6 and 8-week durations are viable but less effective.

Interpretation: Gradual release exit strategies are critical to maintain epidemic suppression under a new normal. We present final infection attack sizes assuming the ongoing importation of cases, which require preparation for a potential second epidemic wave due to ongoing epidemics elsewhere.

Reference

[https://www.thelancet.com/journals/lanwpc/article/PIIS2666-6065\(20\)30004-3/fulltext](https://www.thelancet.com/journals/lanwpc/article/PIIS2666-6065(20)30004-3/fulltext)

Publication Date: July 31, 2020

Assessment of monthly economic losses in Wuhan under the lockdown against COVID-19

Abstract

With the outbreak of COVID-19 in Wuhan, aggressive countermeasures have been taken, including the implementation of the unprecedented lockdown of the city, which will necessarily cause huge economic losses for the city of Wuhan. In this paper, we

attempt to uncover the interactions between epidemic prevention and control measures and economic-social development by estimating the health loss and meso-economic loss from a human-oriented perspective. We implemented a compartmental model for the transmission dynamics and health burden assessment to evaluate the health losses, then estimated the direct and indirect economic losses of industries using the Input-Output model. Based on these estimates, the first monthly health losses and meso-economic losses caused by the lockdown was assessed. The overall policy effect of the lockdown policy in Wuhan was also investigated. The health loss and meso-economic losses are used to evaluate the health burden and loss of residents' mental health, the direct economic loss of several worst-hit industries, and the indirect economic loss of all industries, respectively. Our findings reveal that the health burden caused by this pandemic is estimated to be 4.4899 billion yuan (CNY), and the loss of residents' mental health is evaluated to be 114.545 billion yuan, the direct economic losses in transport, logistics, and warehousing, postal service, food, and beverage service industries reach 21.6094 billion yuan, and the monthly indirect economic losses of all industries are 36.39661994 billion yuan caused by the lockdown. The total monthly economic losses during the lockdown reach 177.0413 billion yuan. However, the lockdown policy has been considered to reduce COVID-19 infections by >180 thousand, which saves about 20 thousand lives, as well as nearly 30 billion yuan on medical costs. Therefore, the lockdown policy in Wuhan has obvious long-term benefits on the society and the total economic losses will be at a controllable level if effective measures are taken to combat COVID-19.

Reference

You, Shibing, Hengli Wang, Miao Zhang, Haitao Song, Xiaoting Xu, and Yongzeng Lai. "Assessment of monthly economic losses in Wuhan under the lockdown against COVID-19." *Humanities and Social Sciences Communications* 7, no. 1 (2020): 1-12.

Epidemiology of mental health problems among patients with cancer during COVID-19 pandemic

Abstract

The current study aimed to explore mental health problems in patients diagnosed with cancer during the COVID-19 pandemic. A cluster sampling, cross-sectional survey with 6213 cancer patients was conducted in one of the largest cancer centers in China. The socio-demographic and clinical characteristics, psychosomatic conditions, interpersonal relationships and social support, COVID-19 infection-related psychological stress, and mental health status were measured. Medical conditions were extracted from patients' electronic healthcare records. Among the 6213 cancer patients, 23.4% had depression, 17.7% had anxiety, 9.3% had PTSD, and 13.5% had hostility. Hierarchical linear regression models showed that having a history of mental disorder, excessive alcohol consumption, having a higher frequency of worrying about cancer management due to COVID-19, having a higher frequency feeling of overwhelming psychological pressure from COVID-19, and having a higher level of fatigue and pain were the predominant risk factors for mental health problems in cancer patients. However, there were only 1.6% of them were seeking psychological counseling during COVID-19. We also revealed the protective factors associated with lower risk of mental health problems among cancer patients. The present study revealed a high prevalence of mental health problems and gaps in mental health services for cancer patients, which also indicated high distress from COVID-19-elevated risks. We call for systematic screening of mental health status for all cancer patients, and developing specific psychological interventions for this vulnerable population.

Reference

Wang, Yuanyuan, Zhizhou Duan, Zikun Ma, Yize Mao, Xiyuan Li, Amanda Wilson, Huiying Qin et al. "Epidemiology of mental health problems among patients with cancer during COVID-19 pandemic." *Translational Psychiatry* 10, no. 1 (2020): 1-10.

Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil

Abstract

The first case of COVID-19 was detected in Brazil on 25 February 2020. We report and contextualize epidemiological, demographic and clinical findings for COVID-19 cases during the first 3 months of the epidemic. By 31 May 2020, 514,200 COVID-19 cases, including 29,314 deaths, had been reported in 75.3% (4,196 of 5,570) of municipalities across all five administrative regions of Brazil. The R0 value for Brazil was estimated at 3.1 (95% Bayesian credible interval = 2.4–5.5), with a higher median but overlapping credible intervals compared with some other seriously affected countries. A positive association between higher per-capita income and COVID-19 diagnosis was identified. Furthermore, the severe acute respiratory infection cases with unknown aetiology were associated with lower per-capita income. Co-circulation of six respiratory viruses was detected but at very low levels. These findings provide a comprehensive description of the ongoing COVID-19 epidemic in Brazil and may help to guide subsequent measures to control virus transmission.

Reference

de Souza, William Marciel, Lewis Fletcher Buss, Darlan da Silva Candido, Jean-Paul Carrera, Sabrina Li, Alexander E. Zarebski, Rafael Henrique Moraes Pereira *et al.* "Epidemiological and clinical characteristics of the COVID-19 epidemic in Brazil." *Nature Human Behaviour* (2020): 1-9.

Hypertension and related diseases in the era of COVID-19: A report from the Japanese Society of Hypertension Task Force on COVID-19

Abstract

Coronavirus disease-2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has affected more than seven million people worldwide, contributing to 0.4 million deaths as of June 2020. The fact that the virus uses angiotensin-converting enzyme (ACE)-2 as the cell entry receptor and that hypertension as well as cardiovascular disorders frequently coexist with COVID-19 have generated considerable discussion on the management of patients with hypertension. In addition,

the COVID-19 pandemic necessitates the development of and adaptation to a “New Normal” lifestyle, which will have a profound impact not only on communicable diseases but also on noncommunicable diseases, including hypertension. Summarizing what is known and what requires further investigation in this field may help to address the challenges we face. In the present review, we critically evaluate the existing evidence for the epidemiological association between COVID-19 and hypertension. We also summarize the current knowledge regarding the pathophysiology of SARS-CoV-2 infection with an emphasis on ACE2, the cardiovascular system, and the kidney. Finally, we review evidence on the use of antihypertensive medication, namely, ACE inhibitors and angiotensin receptor blockers, in patients with COVID-19.

Reference

Shibata, Shigeru, Hisatomi Arima, Kei Asayama, Satoshi Hoshide, Atsuhiko Ichihara, Toshihiko Ishimitsu, Kazuomi Kario et al. "Hypertension and related diseases in the era of COVID-19: A report from the Japanese Society of Hypertension Task Force on COVID-19." *Hypertension Research* (2020): 1-19.

Publication Date: July 30, 2020

Replication-competent vesicular stomatitis virus vaccine vector protects against SARS-CoV-2-mediated pathogenesis in mice

Abstract

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused millions of human infections and an effective vaccine is critical to mitigate coronavirus-induced disease 2019 (COVID-19). Previously, we developed a replication-competent vesicular stomatitis virus (VSV) expressing a modified form of the SARS-CoV-2 spike gene in place of the native glycoprotein gene (VSV-eGFP-SARS-CoV-2). Here, we show that vaccination with VSV-eGFP-SARS-CoV-2 generates neutralizing immune responses and protects mice from SARS-CoV-2. Immunization of mice with VSV-eGFP-SARS-CoV-2 elicits high antibody titers that neutralize SARS-CoV-2 and target the receptor binding domain that engages human angiotensin converting enzyme-2 (ACE2). Upon challenge with a human isolate of SARS-CoV-2, mice expressing human ACE2 and

immunized with VSV-eGFP-SARS-CoV-2 show profoundly reduced viral infection and inflammation in the lung, indicating protection against pneumonia. Passive transfer of sera from VSV-eGFP-SARS-CoV-2-immunized animals also protects naïve mice from SARS-CoV-2 challenge. These data support development of VSV-eGFP-SARS-CoV-2 as an attenuated, replication-competent vaccine against SARS-CoV-2.

Reference

Case, James Brett, Paul W. Rothlauf, Rita E. Chen, Natasha M. Kafai, Julie M. Fox, Brittany Smith, Swathi Shrihari et al. "Replication-competent vesicular stomatitis virus vaccine vector protects against SARS-CoV-2-mediated pathogenesis in mice." *Cell Host & Microbe* (2020).

Adaptation of SARS-CoV-2 in BALB/c mice for testing vaccine efficacy

Abstract

The ongoing COVID-19 pandemic has prioritized the development of small animal models for SARS-CoV-2. Herein, we adapted a clinical isolate of SARS-CoV-2 by serial passaging in the respiratory tract of aged BALB/c mice. The resulting mouse-adapted strain at passage 6 (termed MASCP6) showed increased infectivity in mouse lung, and led to interstitial pneumonia and inflammatory responses in both young and aged mice following intranasal inoculation. Deep sequencing revealed a panel of adaptive mutations potentially associated with the increased virulence. In particular, the N501Y mutation is located at the receptor binding domain (RBD) of the spike protein. The protective efficacy of a recombinant RBD vaccine candidate was validated using this model. Thus, this mouse-adapted strain and associated challenge model should be of value in evaluating vaccines and antivirals against SARS-CoV-2.

Reference

Gu, Hongjing, Qi Chen, Guan Yang, Lei He, Hang Fan, Yong-Qiang Deng, Yanxiao Wang *et al.* "Adaptation of SARS-CoV-2 in BALB/c mice for testing vaccine efficacy." *Science* (2020).

REPORT

Publication Date: Aug 04, 2020

Engineering human ACE2 to optimize binding to the spike protein of SARS coronavirus 2

The spike protein S of SARS coronavirus 2 (SARS-CoV-2) binds ACE2 on host cells to initiate entry, and soluble ACE2 is a therapeutic candidate that neutralizes infection by acting as a decoy. Using deep mutagenesis, mutations in ACE2 that increase S binding are found across the interaction surface, in the N90-glycosylation motif and at buried sites. The mutational landscape provides a blueprint for understanding the specificity of the interaction between ACE2 and S and for engineering high affinity decoy receptors. Combining mutations gives ACE2 variants with affinities that rival monoclonal antibodies. A stable dimeric variant shows potent SARS-CoV-2 and -1 neutralization in vitro. The engineered receptor is catalytically active and its close similarity with the native receptor may limit the potential for viral escape.

Reference

<https://science.sciencemag.org/content/early/2020/08/03/science.abc0870>

PERSPECTIVE

Publication Date: July 31, 2020

How does SARS-CoV-2 cause COVID-19?

Abstract

Viruses enter cells and initiate infection by binding to their cognate cell surface receptors. The expression and distribution of viral entry receptors therefore regulates their tropism, determining the tissues that are infected and thus disease pathogenesis. Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is the third human coronavirus, known to co-opt the peptidase angiotensin-converting enzyme 2 (ACE2) for cell entry. The interaction between SARS-CoV-2 and ACE2 is critical to determining both tissue tropism and progression from early SARS-CoV-2 infection to severe coronavirus disease 2019 (COVID-19). Understanding the cellular basis of SARS-CoV-2 infection could reveal treatments that prevent the development of severe disease, and thus reduce mortality. For more details, click the link given below.

Reference

<https://science.sciencemag.org/content/369/6503/510>

Publication Date: July 30, 2020

ACE2, metformin, and COVID-19

Abstract

COVID-19 is becoming a leading cause of mortality throughout the world, and few effective therapies are currently available. Angiotensin converting enzyme 2 (ACE2) is essential to COVID-19 pathogenesis, as the binding of SARS-CoV-2 spike protein (S protein) is required for viral entry and development of COVID-19. ACE2 regulates the protective arm of the renin-angiotensin-aldosterone system (RAAS) that endows anti-hypertensive and anti-inflammatory effects in the cardiovascular and pulmonary systems. Preclinical data suggest ACE2 might be downregulated after SARS-CoV-2

binding, and treatments that increase ACE2 may prevent cardiopulmonary injury. Development, testing, and mass production of novel ACE2 therapies may take years, while more effective treatments for COVID-19 are needed urgently. Metformin is a widely available anti-diabetic agent that has an excellent safety profile, and clinical and preclinical data suggest metformin may offer cardiopulmonary protection in COVID-19 via enhanced ACE2 expression.

Reference

Malhotra, Atul, Mark Hepokoski, Karen C. McCowen, and John YJ Shyy. "ACE2, Metformin, and COVID-19." *iScience* (2020): 101425.

Emerging evidence of a COVID-19 thrombotic syndrome has treatment implications

Abstract

Reports of widespread thromboses and disseminated intravascular coagulation (DIC) in patients with coronavirus disease 19 (COVID-19) have been rapidly increasing in number. Key features of this disorder include a lack of bleeding risk, only mildly low platelet counts, elevated plasma fibrinogen levels, and detection of both severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and complement components in regions of thrombotic microangiopathy (TMA). This disorder is not typical DIC. Rather, it might be more similar to complement-mediated TMA syndromes, which are well known to rheumatologists who care for patients with severe systemic lupus erythematosus or catastrophic antiphospholipid syndrome. This perspective has critical implications for treatment. Anticoagulation and antiviral agents are standard treatments for DIC but are gravely insufficient for any of the TMA disorders that involve disorders of complement. Mediators of TMA syndromes overlap with those released in cytokine storm, suggesting close connections between ineffective immune responses to SARS-CoV-2, severe pneumonia and life-threatening microangiopathy.

Reference

<https://www.nature.com/articles/s41584-020-0474-5>

PREVIEW

Publication Date: Aug 04, 2020

Teaching old drugs new tricks: Statins for COVID-19?

Abstract

The COVID-19 pandemic has driven unprecedented efforts to identify existing treatments that can be quickly and effectively repurposed to reduce morbidity and mortality. In this issue of Cell Metabolism, Zhang *et al.* (2020) report an association between statin use and improved outcomes in a large observational study of hospitalized COVID-19 patients. Given the widespread availability, low cost, and safety of statins, this promising result should be further investigated in randomized controlled trials. For more details, read the link given below.

Reference

[https://www.cell.com/cell-metabolism/fulltext/S1550-4131\(20\)30364-8](https://www.cell.com/cell-metabolism/fulltext/S1550-4131(20)30364-8)

COMMENT

Publication Date: Aug 04, 2020

Corona Virus Disease (COVID-19); Lessons learnt from international response and advice to Georgia government

This commentary presents an analysis of the containment and mitigation efforts by different countries against the recent COVID-19 pandemic. It was developed in response to Georgia government's decision to relieve lock down restrictions. The article also provides recommendations based on interventions that have been observed to be effective which will guide decision making for not only Georgia but other states and countries that are currently struggling to manage this outbreak.

Reference

[https://www.cell.com/the-innovation/fulltext/S2666-6758\(20\)30025-4](https://www.cell.com/the-innovation/fulltext/S2666-6758(20)30025-4)

Publication Date: Aug 03, 2020

Vitamin D for COVID-19: A case to answer?

Interest in a potential role for vitamin D in the prevention or treatment of acute respiratory infections dates back to the 1930s, when cod liver oil was investigated as a means to reduce industrial absenteeism due to the common cold. Meta-analyses of randomised controlled trials conducted from 2007–20 reveal protective effects of vitamin D against acute respiratory infections, albeit these effects were of modest size and with substantial heterogeneity.

The striking overlap between risk factors for severe COVID-19 and vitamin D deficiency, including obesity, older age, and Black or Asian ethnic origin, has led some researchers to hypothesise that vitamin D supplementation could hold promise as a preventive or therapeutic agent for COVID-19.

Reference

[https://www.thelancet.com/journals/landia/article/PIIS2213-8587\(20\)30268-0/fulltext](https://www.thelancet.com/journals/landia/article/PIIS2213-8587(20)30268-0/fulltext)

NEWSLETTER

Publication Date: Aug 05, 2020

Focus shifts to antibody cocktails for COVID-19 cytokine storm

Abstract

Emerging clinical trial data suggested that individual immunomodulatory drugs can dampen the hyperactive immune system in severe COVID-19, but polytherapy is the way forward. These therapies include IL-6 inhibitors, GM-CSF, anti-IL-1, anti-TNF and anti-IL-6 mAbs, cytokine-targeting antibodies, and use of steroids. Several drugs were screened for these trials, such as including IIsira, tocilizumab, mavrilimumab, Actemra, siltuximab, sarilumab, infliximab, etc. For more details, view the link given below.

Reference

<https://www.nature.com/articles/s41587-020-0634-9>

Publication Date: Aug 03, 2020

Coronavirus research updates: Summer-camp outbreak infects more than 200 children

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

Summer-camp outbreak infects more than 200 children (Aug 03, 2020):

Despite measures to prevent the spread of the new coronavirus, at least 250 campers and staff members tested positive for SARS-CoV-2 after attending an overnight camp in the US state of Georgia.

Christine Szablewski at the Georgia Department of Public Health in Atlanta and her colleagues investigated the outbreak, which began two days after the first campers' arrival on 21 June (C. M. Szablewski et al. *Morb. Mortal. Wkly Rep.* <http://doi.org/d5ms>; 2020). All campers and staff were required to test negative for the virus fewer than 13

days before arrival, and campers did not mix with those sleeping in other cabins. Campers were not required to wear masks. The researchers found that nearly 100 staff members — many of them teenagers — tested positive in the two weeks after leaving camp. So did 168 campers, including half of those aged between 6 and 10. Factors contributing to the outbreak included the large number of campers sleeping in each cabin and what the researchers describe as “daily vigorous singing and cheering”.

Vaccine candidate protects monkeys from infection (Jul 30, 2020):

An experimental coronavirus vaccine seems to have completely prevented infection in most monkeys that received the jab.

Hanneke Schuitemaker at Janssen Vaccines and Prevention in Leiden, the Netherlands, Dan Barouch at Beth Israel Deaconess Medical Center in Boston, Massachusetts, and their colleagues gave 32 rhesus macaques (*Macaca mulatta*) a single dose of one of 7 vaccines (N. B. Mercado et al. *Nature* <http://doi.org/d5d4>; 2020). Each vaccine comprised a weakened respiratory virus coding for one of seven forms of SARS-CoV-2’s spike protein. After vaccination, nearly all the monkeys made neutralizing antibodies — powerful immune molecules that can block infection — and T cells that trigger other immune responses. When monkeys were exposed to SARS-CoV-2, the most potent of the vaccines prevented lung infection in six out of six animals that received it, and nasal infection in five out of six. Across all the vaccinated monkeys, levels of neutralizing antibodies were associated with protection from SARS-CoV-2 infection, but levels of T cells were not.

Reference

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

Publication Date: Jul 30, 2020

WHO publishes interactive timeline of its response

To mark six months since WHO declared a public health emergency of international concern, the highest level of alarm under international law, WHO published an interactive timeline showcasing how the organization has taken action on information, science, leadership, advice, response and resourcing.

Reference

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

CORRESPONDANCE

Publication Date: Aug 04, 2020

SeroTracker: A global SARS-CoV-2 seroprevalence dashboard

As the initial phase of the COVID-19 pandemic passes its peak in many countries, serological studies are becoming increasingly important in guiding public health responses. Antibody testing is crucial for monitoring the evolution of the pandemic, providing a more complete picture of the total number of people infected with severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) than molecular diagnostic testing alone. All individuals with SARS-CoV-2-specific antibodies have been exposed to the virus, so antibody testing can highlight differences in past exposure between regions, demographic groups, and occupations. Seroprevalence estimates can also be used to estimate the infection fatality rate. Dashboards that visualise COVID-19 cases confirmed by diagnostic testing have been pivotal in enabling policy makers and researchers to monitor the pandemic. Yet, despite the value of antibody testing, there is no unified resource for seroprevalence estimates.

To address this need, we created SeroTracker, a custom-built dashboard that systematically monitors and synthesises findings from hundreds of global SARS-CoV-2 serological studies. The dashboard allows users to visualise seroprevalence estimates on a world map and compare estimates between regions, population groups, and testing modalities (*e.g.*, assay type or antibody isotype).

SeroTracker integrates evidence from serosurveillance studies through a live systematic review. Each day, published articles (MEDLINE, Embase, Web of Science, and Cochrane), preprints (medRxiv and bioRxiv), government reports, and news articles are reviewed for newly reported SARS-CoV-2 seroprevalence estimates by a team of doctoral and medical students. Over 13 000 records have been screened to date. Seroprevalence estimates are extracted from each article, in addition to the sample size, sampling approach, study population, and antibody test used. Risk of bias for each prevalence estimate is assessed using the Joanna Briggs Institute Critical Appraisal Guidelines for Prevalence studies. As of July 23, 2020, 162 studies are being

monitored, with data available through the SeroTracker website and dashboard code accessible through GitHub. For more details, read the link given below.

Reference

[https://www.thelancet.com/journals/laninf/article/PIIS1473-3099\(20\)30631-9/fulltext](https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30631-9/fulltext)

POLICY FORUM

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COVID-19 risks to global food security

As the COVID-19 pandemic progresses, trade-offs have emerged between the need to contain the virus and to avoid disastrous economic and food security crises that hurt the world's poor and hungry most. Although no major food shortages have emerged as yet, agricultural and food markets are facing disruptions because of labor shortages created by restrictions on movements of people and shifts in food demand resulting from closures of restaurants and schools as well as from income losses. Export restrictions imposed by some countries have disrupted trade flows for staple foods such as wheat and rice. The pandemic is affecting all four pillars of food security (1): availability (is the supply of food adequate?), access (can people obtain the food they need?), utilization (do people have enough intake of nutrients?), and stability (can people access food at all times?). COVID-19 is most directly and severely impacting access to food, even though impacts are also felt through disruptions to availability; shifts in consumer demand toward cheaper, less nutritious foods; and food price instability. We outline the main threats COVID-19 poses to food security and suggest critical responses that policy-makers should consider to prevent this global health crisis from becoming a global food crisis.

Reference

<https://science.sciencemag.org/content/369/6503/500>