

COVID-19

Jun 11-17, 2020



RESEARCH PUBLICATIONS

Publication Date: June 16, 2020

Age-dependent effects in the transmission and control of COVID-19 epidemics

Abstract

The COVID-19 pandemic has shown a markedly low proportion of cases among children. Age disparities in observed cases could be explained by children having lower susceptibility to infection, lower propensity to show clinical symptoms or both. We evaluate these possibilities by fitting an age-structured mathematical model to epidemic data from China, Italy, Japan, Singapore, Canada and South Korea. We estimate that susceptibility to infection in individuals under 20 years of age is approximately half that of adults aged over 20 years, and that clinical symptoms manifest in 21% (95% credible interval: 12–31%) of infections in 10- to 19-year-olds, rising to 69% (57–82%) of infections in people aged over 70 years. Accordingly, we find that interventions aimed at children might have a relatively small impact on reducing SARS-CoV-2 transmission, particularly if the transmissibility of subclinical infections is low. Our age-specific clinical fraction and susceptibility estimates have implications for the expected global burden of COVID-19, as a result of demographic differences across settings. In countries with younger population structures—such as many low-income countries—the expected per capita incidence of clinical cases would be lower than in countries with older population structures, although it is likely that comorbidities in low-income countries will also influence disease severity. Without effective control measures, regions with relatively older populations could see disproportionately more cases of COVID-19, particularly in the later stages of an unmitigated epidemic.

Reference

Davies, Nicholas G., Petra Klepac, Yang Liu, Kiesha Prem, Mark Jit, Rosalind M. Eggo, and CMMID COVID-19 working group. "Age-dependent effects in the transmission and control of COVID-19 epidemics." MedRxiv (2020).

Disease and healthcare burden of COVID-19 in the United States

Abstract

As of 24 April 2020, the SARS-CoV-2 epidemic has resulted in over 830,000 confirmed infections in the United States. The incidence of COVID-19, the disease associated with this new coronavirus, continues to rise. The epidemic threatens to overwhelm healthcare systems, and identifying those regions where the disease burden is likely to be high relative to the rest of the country is critical for enabling prudent and effective distribution of emergency medical care and public health resources. Globally, the risk of severe outcomes associated with COVID-19 has consistently been observed to increase with age. We used age-specific mortality patterns in tandem with demographic data to map projections of the cumulative case burden of COVID-19 and the subsequent burden on healthcare resources. The analysis was performed at the county level across the United States, assuming a scenario in which 20% of the population of each county acquires infection. We identified counties that will probably be consistently, heavily affected relative to the rest of the country across a range of assumptions about transmission patterns, such as the basic reproductive rate, contact patterns and the efficacy of quarantine. We observed a general pattern that per capita disease burden and relative healthcare system demand may be highest away from major population centers. These findings highlight the importance of ensuring equitable and adequate allocation of medical care and public health resources to communities outside of major urban areas.

Reference

<https://www.nature.com/articles/s41591-020-0952-y>

Living in a Covid-19 world

Abstract

To say that we live in uncertain times would be a gross understatement. As the June 2020 issue of the Quarterly goes to press, the United States is reeling from the one-two punch of the lethal COVID-19 pandemic and its shock to the economy, the likes of which we have not seen, respectively, since the 1918-1919 influenza pandemic and the Great Depression of the 1930s. Either calamity alone would be devastating, but together they appear almost apocalyptic.

Just five months ago, few could have imagined the magnitude of the tragic loss of life and the crippling economic effects wrought by the pandemic. Since then, nation after nation has struggled to control the rapid spread of the virus and its consequences. Some (e.g., China, South Korea, Germany) have fared better than others (e.g., Italy, Spain, France), owing in large part to the speed with which civic leaders responded to the crisis. The United States unfortunately failed to take prompt action despite adequate warning of the imminent danger, and the price for this delay is 100,000 COVID-related deaths and 36 million unemployment figures.

There is no denying that we now live in a COVID-19 world—one fraught with constant uncertainty about personal safety as well as our collective health and economic well-being. In addition, those affected the most by the pandemic are low-income individuals and communities of color, and also are the most disadvantaged by poverty and other social determinants of health. As we begin to chart a path toward recovery, we need to recognize the interconnection between health equity and economic security.

It is unclear how long the COVID-19 pandemic will persist and how far-reaching its effects will be. One thing is certain, though: the epidemic has exposed glaring weaknesses in our nation's health care system, not only its inadequacy to respond to emerging public health threats but also its inability to deliver health care effectively and equitably to all citizens. For more detail, read the following given article.

Reference

<https://onlinelibrary.wiley.com/doi/10.1111/1468-0009.12466>

[Diagnosing COVID-19 in the emergency department: A Scoping review of clinical exam, labs, imaging accuracy and biases](#)

Abstract

In December 2019 a novel viral respiratory pathogen emerged in China, ultimately named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with the clinical illness dubbed coronavirus disease (COVID-19). COVID-19 became a global pandemic in early 2020 forcing governments worldwide to enact social isolation policies with dire economic ramifications. Emergency departments (ED) encountered decreased patient volumes before some in Seattle, New York City, New Orleans, and Detroit experienced waves of COVID-19 patients mixed with asymptomatic patients or those concerned about potential exposures. Diagnosing COVID-19 was hampered by inadequate supplies of reagents and kits, which was compounded by clinical and radiographic features that overlap with numerous seasonal viral respiratory infections.

Reference

<https://onlinelibrary.wiley.com/doi/10.1111/acem.14048>

Evolutionary relationships and sequence-structure determinants in human SARS coronavirus-2 spike proteins for host receptor recognition

Abstract

Coronavirus disease 2019 (COVID-19) is a pandemic infectious disease caused by novel Severe Acute Respiratory Syndrome coronavirus-2 (SARS CoV-2). The SARS CoV-2 is transmitted more rapidly and readily than SARS CoV. Both, SARS CoV and SARS CoV-2 via their glycosylated spike proteins recognize the human angiotensin converting enzyme-2 (ACE-2) receptor. We generated multiple sequence alignments and phylogenetic trees for representative spike proteins of SARS CoV and SARS CoV-2 from various host sources in order to analyze the specificity in SARS CoV-2 spike proteins required for causing infection in humans. Our results show that among the genomes analysed, two sequence regions in the N-terminal domain (NTD); "MESEFR" and "SYLTPG" are specific to human SARS CoV-2. In the receptor binding domain (RBD), two sequence regions; "VGGNY" and "EIYQAGSTPCNGV" and a disulfide bridge connecting 480C and 488C in the extended loop are structural determinants for the recognition of human ACE-2 receptor. The complete genome analysis of representative SARS CoVs from bat, civet, human host sources and human SARS CoV-2 identified the bat genome (GenBank code: MN996532.1) as closest to the recent novel human SARS CoV-2 genomes. The bat SARS CoV genomes (GenBank codes: MG772933 and

MG772934) are evolutionary intermediates in the mutagenesis progression towards becoming human SARS CoV-2.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/prot.25967>

Impact of comorbidities on patients with COVID-19: A large retrospective study in Zhejiang, China

Abstract

Background: Since the outbreak of 2019 novel coronavirus (SARS-CoV-2) pneumonia, thousands of patients with fever or cough were flocked into fever clinic of designated hospitals in Wuhan, China. To date, no data have ever been reported to reflect the prevalence of Corona Virus Disease 2019 (COVID-19) among these outpatients. Moreover, it is almost unknown to discriminate COVID-19 and nucleic acid negative patients based on clinical features in the fever clinics.

Methods: The infectious status of SARS-CoV-2 was estimated among the outpatients. The epidemiological and clinical characteristics were compared between COVID-19 and nucleic acid negative patients.

Results: The nucleic acid positive rate for SARS-CoV-2 in the outpatients from our fever clinic was 67.1%, while the majority of COVID-19 patients were mild cases. The predominant initial symptom in those COVID-19 patients was fever (78.2%), followed by cough (15.6%). Very significantly lower number of eosinophils was characterized in COVID-19 patients as compared to that of nucleic acid negative patients. More importantly, the proportion of subjects with eosinophil counts lower than normal levels in COVID-19 patients was much higher than that of nucleic acid negative patients. Fever combined with bilateral ground-glass opacities in CT imaging and eosinophil count below the normal level are probably a valuable indicator of COVID-19 infection in those outpatients.

Conclusions: Those findings may provide critical information for the regions such as Europe and United States that are facing the same situation as Wuhan experienced, and

could be valuable to prevent those nucleic acid negative patients from misdiagnosis before antibody testing.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/jmv.26175>

Dysregulation of the immune response affects the outcome of critical COVID-19 patients

Abstract

Objectives: Critical cases of coronavirus disease 2019 (COVID-19) are associated with a high risk of mortality. It remains unclear why patients with the same critical condition have different outcomes. We aimed to explore relevant factors that may affect the prognosis of critical COVID-19 patients.

Methods: Six critical COVID-19 inpatients were included in our study. The 6 patients were divided into two groups based on whether they had a good or poor prognosis. We collected peripheral blood samples at admission and the time point of exacerbation to compare differences in the phenotypes and functions of major populations of immune cells between the groups.

Results: On admission, compared to patients with poor prognoses, those with good prognoses had significantly higher counts of monocytes ($p < 0.05$), macrophages ($p < 0.05$), higher frequency of CD3+CD4+CD45RO+CXCR3+ subsets ($p < 0.05$), higher frequency of CD14+CD11C+HLA-DR+ subset of dendritic cells (DCs) ($p < 0.05$), and a lower count of neutrophils ($p < 0.05$). At the time point of exacerbation, the proportions of naïve CD4+ T cells ($p < 0.05$), Tregs, and Th2 cells in the poor prognosis group were relatively higher than those in the good prognosis group, and CD4+ memory T cells were relatively lower ($p < 0.05$).

Conclusion: According to our results, the poor prognosis group showed a worse immune response than the good prognosis group at the time of admission and at exacerbation. Dysregulation of the immune response affects the outcome of critical COVID-19 patients.

Reference

Syncope, Brugada syndrome, and COVID-19 lung disease

Abstract

A 52-year-old male with no history of familiar sudden death arrived at our Emergency Department after syncope with loss of consciousness occurred during high fever. The thoracic high-resolution computed tomography demonstrated bilateral multiple ground-glass opacities. The nose-pharyngeal swab resulted positive for SARS-CoV-2. The 12-lead ECG presented a “coved-type” aspect in leads V1 and V2 at the fourth intercostal space and a first degree atrio-ventricular block. As soon as the temperature went down, the 12-lead ECG resumed a normal aspect, maintaining a long PR interval.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/joa3.12375>

Comparison and application of different immunoassay methods for the detection of SARS-CoV-2

Abstract

The detection data of IgM and IgG antibodies in 169 patients with coronavirus disease (COVID-19) were analyzed to evaluate differences in clinical performance between the colloidal gold method and chemiluminescence method. In this study, chemiluminescence detection of IgM antibody showed a positive conversion earlier (about 1~2 days earlier), positive conversion rates higher in different stages of disease, and a trend of declining positive rate later than colloidal gold method. For IgG antibody, the chemiluminescence method showed a positive conversion earlier and the positive rate climbing more quickly than the colloidal gold method. No obvious negative-converting tendency of IgG detection was observed within 35 days after the onset of disease. Although colloidal gold method is generally less sensitive than chemiluminescence method, it shows advantages of shorter turn-around time, more simple procedure and no special equipment required. The two methodologies can be chosen according to different laboratory conditions.

A reasonable understanding of the performance of reagents with different methodologies can help in clinical disease diagnosis effectively and assist in the diagnosis of the

progression of COVID-19, for which the dynamic changes of antibody will provide reliable evidence.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/jmv.26187>

Immune-related factors associated with pneumonia in 127 children with Coronavirus disease 2019 in Wuhan

Abstract

Objective: Information regarding the association of immune-related factors with pneumonia in children with coronavirus disease 2019 (COVID-19) is scarce. This study aims to summarize the immune-related factors and their association with pneumonia in children with COVID-19.

Methods: Children with COVID-19 at Wuhan Children's Hospital from January 28 to March 12, 2020 were enrolled. Pneumonia due to causes other than COVID-19 were excluded. The clinical and laboratory information including routine blood tests, blood biochemistry, lymphocyte subsets, immunoglobulins, cytokines and inflammatory factors were analyzed retrospectively in 127 patients. Normal ranges and mean values of laboratory markers were applied as parameters for logistic regression analyses of their association with pneumonia.

Results: In non-intensive care unit patients, 48.8% and 22.4% of patients had increased levels of procalcitonin and hypersensitive C-reactive protein (hs-CRP) respectively. 12.6% and 18.1% of patients had decreased levels of immunoglobulin (Ig) A and interleukin (IL)-10 respectively. Approximately 65.8% of patients had pneumonia. These patients had decreased levels of globulin (odds ratio [OR] 3.13, 95% confidence interval [CI] 1.41-6.93, P =0.005), IgA (OR 4.00, 95% CI 1.13-14.18, P =0.032), and increased levels of hs-CRP (OR 3.14, 95% CI 1.34-7.36, P =0.008), procalcitonin (OR 3.83, 95% CI 2.03-7.24, P <0.001), IL-10 (OR 7.0, 95% CI 1.59-30.80, P =0.010), and CD4+CD25+ T lymphocyte < 5.0 % (OR 1.93, 95% CI 1.04-3.61, P =0.038).

Conclusion: Decreased IgA and CD4+CD25+ T lymphocyte percentage, and increased hs-CRP, procalcitonin and IL-10 were associated with pneumonia, suggesting that the

immune-related factors may participate in the pathogenesis of pneumonia in children with COVID-19.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/ppul.24907>

A cross-sectional community-based observational study of asymptomatic SARS-CoV-2 prevalence in the greater Indianapolis area

Abstract

The Asymptomatic novel Coronavirus Infection (ACORN) study was designed to investigate the prevalence of SARS-CoV-2 infection in the asymptomatic adult population of the Indianapolis metropolitan area, to follow individuals testing positive for the development of symptoms, and to understand duration of positive test results. ACORN is a cross-sectional community-based observational study of adult residents presenting asymptomatic for COVID-like illness, defined as the self-reported absence of the following 3-symptoms in the last 7-days: fever ($\geq 100^{\circ}\text{F}$), new onset or worsening cough, and new onset or worsening shortness of breath. SARS-CoV-2 infection was determined by RT-PCR in nasopharyngeal swab samples. SARS-CoV-2 infection prevalence was expressed as a point estimate with 95%-CI. Test results are reported for 2953 participants who enrolled and underwent nasopharyngeal swab testing between April 7, 2020 and May 16, 2020. Among tested participants, 91 (3.1%; 95%-CI; 2.5%-3.7%) were positive for SARS-CoV-2. Overall, baseline characteristics, medical history, and infection risk factors were comparable between SARS-CoV-2 positive and negative participants. Within the ongoing 14-day follow-up period for positive participants, 58 (71.6%) of 81-assessed participants remained asymptomatic while others ($n=23$, 28.4%) reported one or more symptoms. Indiana had “Stay-at-Home” orders in place during nearly the entire test period reported here, yet 3.1% of asymptomatic participants tested positive for SARS-CoV-2. These results indicate screening questions had limited predictive utility for testing in an asymptomatic population and suggest broader testing strategies are needed. Importantly, these findings underscore that more research is needed to understand the viral transmission and the role asymptomatic and pre-symptomatic individuals play in this global pandemic.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/jmv.26182>

Publication Date: June 15, 2020

Global, regional, and national estimates of the population at increased risk of severe COVID-19 due to underlying health conditions in 2020: A modelling study

Abstract

Background: The risk of severe COVID-19 if an individual becomes infected is known to be higher in older individuals and those with underlying health conditions. Understanding the number of individuals at increased risk of severe COVID-19 and how this varies between countries should inform the design of possible strategies to shield or vaccinate those at highest risk.

Methods: We estimated the number of individuals at increased risk of severe disease (defined as those with at least one condition listed as “at increased risk of severe COVID-19” in current guidelines) by age (5-year age groups), sex, and country for 188 countries using prevalence data from the Global Burden of Diseases, Injuries, and Risk Factors Study (GBD) 2017 and UN population estimates for 2020. The list of underlying conditions relevant to COVID-19 was determined by mapping the conditions listed in GBD 2017 to those listed in guidelines published by WHO and public health agencies in the UK and the USA. We analysed data from two large multimorbidity studies to determine appropriate adjustment factors for clustering and multimorbidity. To help interpretation of the degree of risk among those at increased risk, we also estimated the number of individuals at high risk (defined as those that would require hospital admission if infected) using age-specific infection–hospitalisation ratios for COVID-19 estimated for mainland China and making adjustments to reflect country-specific differences in the prevalence of underlying conditions and frailty. We assumed males were twice as likely as females to be at high risk. We also calculated the number of individuals without an underlying condition that could be considered at increased risk because of their age, using minimum ages from 50 to 70 years. We generated uncertainty intervals (UIs) for our estimates by running low and high scenarios using the lower and upper 95% confidence limits for country population size, disease prevalences, multimorbidity fractions, and infection–

hospitalisation ratios, and plausible low and high estimates for the degree of clustering, informed by multimorbidity studies.

Findings: We estimated that 1.7 billion (UI 1.0–2.4) people, comprising 22% (UI 15–28) of the global population, have at least one underlying condition that puts them at increased risk of severe COVID-19 if infected (ranging from <5% of those younger than 20 years to >66% of those aged 70 years or older). We estimated that 349 million (186–787) people (4% [3–9] of the global population) are at high risk of severe COVID-19 and would require hospital admission if infected (ranging from <1% of those younger than 20 years to approximately 20% of those aged 70 years or older). We estimated 6% (3–12) of males to be at high risk compared with 3% (2–7) of females. The share of the population at increased risk was highest in countries with older populations, African countries with high HIV/AIDS prevalence, and small island nations with high diabetes prevalence. Estimates of the number of individuals at increased risk were most sensitive to the prevalence of chronic kidney disease, diabetes, cardiovascular disease, and chronic respiratory disease.

Interpretation: About one in five individuals worldwide could be at increased risk of severe COVID-19, should they become infected, due to underlying health conditions, but this risk varies considerably by age. Our estimates are uncertain, and focus on underlying conditions rather than other risk factors such as ethnicity, socioeconomic deprivation, and obesity, but provide a starting point for considering the number of individuals that might need to be shielded or vaccinated as the global pandemic unfolds.

Reference

<https://www.sciencedirect.com/science/article/pii/S2214109X20302643?via%3Dihub>

Publication Date: June 12, 2020

Advice from a systems-biology model of the corona epidemics

Abstract

Using standard systems biology methodologies, a 14-compartment dynamic model was developed for the Corona virus epidemic. The model predicts that: (i) it will be impossible to limit lockdown intensity such that sufficient herd immunity develops for this epidemic to

die down, (ii) the death toll from the SARS-CoV-2 virus decreases very strongly with increasing intensity of the lockdown, but (iii) the duration of the epidemic increases at first with that intensity and then decreases again, such that (iv) it may be best to begin with selecting a lockdown intensity beyond the intensity that leads to the maximum duration, (v) an intermittent lockdown strategy should also work and might be more acceptable socially and economically, (vi) an initially intensive but adaptive lockdown strategy should be most efficient, both in terms of its low number of casualties and shorter duration, (vii) such an adaptive lockdown strategy offers the advantage of being robust to unexpected imports of the virus, e.g. due to international travel, (viii) the eradication strategy may still be superior as it leads to even fewer deaths and a shorter period of economic downturn, but should have the adaptive strategy as backup in case of unexpected infection imports, (ix) earlier detection of infections is the most effective way in which the epidemic can be controlled, whilst waiting for vaccines.

Reference

Westerhoff, Hans V., and Alexey N. Kolodkin. "Advice from a systems-biology model of the Corona epidemics." *npj Systems Biology and Applications* 6, no. 1 (2020): 1-5.

Publication Date: June 11, 2020

Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Geneva, Switzerland (SEROCov-POP): A population-based study

Abstract

Background: Assessing the burden of COVID-19 on the basis of medically attended case numbers is suboptimal given its reliance on testing strategy, changing case definitions, and disease presentation. Population-based serosurveys measuring anti-severe acute respiratory syndrome coronavirus 2 (anti-SARS-CoV-2) antibodies provide one method for estimating infection rates and monitoring the progression of the epidemic. Here, we estimate weekly seroprevalence of anti-SARS-CoV-2 antibodies in the population of Geneva, Switzerland, during the epidemic.

Methods: The SEROCov-POP study is a population-based study of former participants of the Bus Santé study and their household members. We planned a series of 12 consecutive weekly serosurveys among randomly selected participants from a previous

population-representative survey, and their household members aged 5 years and older. We tested each participant for anti-SARS-CoV-2-IgG antibodies using a commercially available ELISA. We estimated seroprevalence using a Bayesian logistic regression model taking into account test performance and adjusting for the age and sex of Geneva's population. Here we present results from the first 5 weeks of the study.

Findings: Between April 6 and May 9, 2020, we enrolled 2766 participants from 1339 households, with a demographic distribution similar to that of the canton of Geneva. In the first week, we estimated a seroprevalence of 4.8% (95% CI 2.4–8.0, n=341). The estimate increased to 8.5% (5.9–11.4, n=469) in the second week, to 10.9% (7.9–14.4, n=577) in the third week, 6.6% (4.3–9.4, n=604) in the fourth week, and 10.8% (8.2–13.9, n=775) in the fifth week. Individuals aged 5–9 years (relative risk [RR] 0.32 [95% CI 0.11–0.63]) and those older than 65 years (RR 0.50 [0.28–0.78]) had a significantly lower risk of being seropositive than those aged 20–49 years. After accounting for the time to seroconversion, we estimated that for every reported confirmed case, there were 11.6 infections in the community.

Interpretation: These results suggest that most of the population of Geneva remained uninfected during this wave of the pandemic, despite the high prevalence of COVID-19 in the region (5000 reported clinical cases over <2.5 months in the population of half a million people). Assuming that the presence of IgG antibodies is associated with immunity, these results highlight that the epidemic is far from coming to an end by means of fewer susceptible people in the population. Further, a significantly lower seroprevalence was observed for children aged 5–9 years and adults older than 65 years, compared with those aged 10–64 years. These results will inform countries considering the easing of restrictions aimed at curbing transmission.

Reference

Stringhini, Silvia, Ania Wisniak, Giovanni Piumatti, Andrew S. Azman, Stephen A. Lauer, H el ene Baysson, David De Ridder et al. "Seroprevalence of anti-SARS-CoV-2 IgG antibodies in Geneva, Switzerland (SEROCoV-POP): A population-based study." *The Lancet* (2020).

[The COVID-19 catastrophe: What's gone wrong and how to stop it happening again](#)

Abstract

The current coronavirus disease 2019 (COVID-19) pandemic caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection has required a complete change in the management of patients with inflammatory bowel disease (IBD) who need to undergo endoscopic procedures. Several preventive measures must be taken to avoid the spread of infection among health-care professionals and patients with IBD, including the use of personal protective equipment, greater attention to endoscopic room hygiene and rescheduling of non-urgent procedures. This Perspective aims to provide a guide based on the Italian and French experience to better face the difficulties encountered by endoscopists during this global health emergency. In particular, recommendations regarding the use of personal protective equipment to prevent COVID-19 transmission, both for patients and health-care professionals, are proposed and different scenarios in endoscopic IBD management are evaluated to suggest when endoscopy could be rescheduled and replaced by alternative biomarkers.

Reference

Furfaro, Federica, Lucine Vuitton, Gionata Fiorino, Stephane Koch, Mariangela Allocca, Daniela Gilardi, Alessandra Zilli et al. "SFED recommendations for IBD endoscopy during COVID-19 pandemic: Italian and French experience." *Nature Reviews Gastroenterology & Hepatology* (2020): 1-10.

COVID-19 and the liver-related deaths to come

Abstract

Coronavirus disease 2019 (COVID-19) itself and/or the use of hepatotoxic drugs might negatively affect the course and management of patients with pre-existing chronic liver diseases. However, the greatest effect of COVID-19 on liver diseases will be indirect and delayed, resulting from the impending global economic crisis.

Reference

Pawlotsky, Jean-Michel. "COVID-19 and the liver-related deaths to come." *Nature Reviews Gastroenterology & Hepatology* (2020): 1-3.

COVID-19 in Africa: The spread and response

Abstract

Given the current trends in incidence and underlying healthcare systems vulnerabilities, Africa could become the next epicenter of the COVID-19 pandemic. As the pandemic transitions to more widespread community transmission, how can the lessons learned thus far be consolidated to effectively curb the spread of COVID-19 while minimizing social disruption and negative humanitarian and economic consequences?

Reference

<https://www.nature.com/articles/s41591-020-0961-x>

NEWSLETTER

Publication Date: June 16, 2020

Coronavirus breakthrough: Dexamethasone is first drug shown to save lives

An inexpensive and commonly used steroid can save the lives of people seriously ill with COVID-19, a randomized, controlled clinical trial in the United Kingdom has found. The drug, called dexamethasone, is the first shown to reduce deaths from the coronavirus that has killed more than 430,000 people globally. In the trial, it cut deaths by about one-third in patients who were on ventilators because of coronavirus infection. For more details, view the link given below.

Reference

<https://www.nature.com/articles/d41586-020-01824-5>

Immune status could determine efficacy of COVID-19 therapies

Emerging evidence suggests that SARS-CoV-2 can drive a diverse array of immune processes, raising the risk that immunosuppressant agents that are in clinical trials might be effective for some patients but detrimental for others. For more details, view the link given below.

Reference

<https://www.nature.com/articles/d41573-020-00110-3>

Coronavirus research updates: More than one billion people face increased risk of severe COVID-19

A host of common health problems boost a person's risk of becoming seriously ill if infected by the new coronavirus. Now an analysis reveals the extent of this vulnerable group: more than 20% of the world's population has at least one underlying condition that raises the risk of severe disease. Some of the findings in this report are given below:

According to Swiss survey finds (*published on June 16*) The researchers found that only one out of the 123 children aged 5–9 tested positive. Children are less susceptible to infection. Oshitani group from Japan (*published on June 16*) revealed that clusters of coronavirus infections are often linked to events many people breathe heavily while packed together, such as karaoke parties and gym sessions. According to a survey in United Kingdom (UK) (*published on June 11*) showed outbreak due to a massive number of viral imports. The new coronavirus has jumped into the UK more than 1,300 times — mostly due to infected travellers from France and Spain. Researchers from UK (*published on June 11*) have found a second protein that SARS-CoV-2 uses to enter human cells, known as human protein neuropilin-1 (NRP1), which potentially offers a new target for vaccines and drugs. For more details, read the link given below.

Reference

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

REPORT

Publication Date: June 16, 2020

Planning and managing a COVID-19 mobile testing site

The State University of New York at Albany is contributing to the battle against COVID-19 in numerous ways, from donations of personal protective equipment to the 3D printing of protective face shields.

One of the most impactful contributions, especially in terms of enabling a return to normalcy in the community in the midst of COVID-19, is the coordination of a state-run mobile testing site on a large campus parking lot. Stephen Conard, Emergency

Management Coordinator at UAlbany, shared some considerations and lessons learned as part of that effort on his campus. Because UAlbany is part of the state university system, and owing to its location in the capital region, it was selected as an early candidate for various programs in support of the state's pandemic response. Mobile COVID-19 testing was one of those programs, and in early April the university became host to the first state-run testing site in upstate New York. Conard stressed that safety is the number one priority for everyone, from the teams working at the testing site to all those who come to get tested. That's why controlling traffic, both vehicular and pedestrian, is such a vital concern. There were numerous other ways that were used to control factors COVID-19 in State University of New York at Albany numerous ways. For more details, read the link given below.

Reference

<https://onlinelibrary.wiley.com/doi/10.1002/casr.30671>

Publication Date: June 15, 2020

Antibody cocktail to SARS-CoV-2 spike protein prevents rapid mutational escape seen with individual antibodies

Abstract

Antibodies targeting the spike protein of SARS-CoV-2 present a promising approach to combat the COVID19 pandemic; however, concerns remain that mutations can yield antibody resistance. We investigate the development of resistance against four antibodies to the spike protein that potently neutralize SARS-CoV-2, individually as well as when combined into cocktails. These antibodies remain effective against spike variants that have arisen in the human population. However, novel spike mutants rapidly appeared following in vitro passaging in the presence of individual antibodies, resulting in loss of neutralization; such escape also occurred with combinations of antibodies binding diverse but overlapping regions of the spike protein. Importantly, escape mutants were not generated following treatment with a non-competing antibody cocktail.

Reference

<https://science.sciencemag.org/content/early/2020/06/15/science.abd0831>

PERSPECTIVE

Publication Date: June 16, 2020

Can existing live vaccines prevent COVID-19?

Abstract

Prophylactic vaccination is the most effective intervention to protect against infectious diseases. The commonly accepted paradigm is that immunization with both attenuated virus (live but with substantially reduced virulence) and inactivated (killed virus particles) vaccines induces adaptive and generally long-term and specific immunity in the form of neutralizing antibodies and/or activating pathogen-specific cellular immune responses. However, an increasing body of evidence suggests that live attenuated vaccines can also induce broader protection against unrelated pathogens likely by inducing interferon and other innate immunity mechanisms that are yet to be identified. The stimulation of innate immunity by live attenuated vaccines in general, and oral poliovirus vaccine (OPV) in particular, could provide temporary protection against coronavirus disease 2019 (COVID-19). For more details, read the link given below.

Reference

<https://science.sciencemag.org/content/368/6496/1187>

CORRESPONDANCE

Publication Date: June 16, 2020

COVID-19 pandemic: A large boulder on the head of stoma patients

Abstract

During the COVID-19 pandemic, numbers of patients with colorectal cancer needing a stoma are likely to increase. The recommendations of scientific societies encourage interventions with a lower risk of complications, short recovery time and less likelihood of ICU admission (particularly Hartmann's procedure) in these patients, especially those who test positive for COVID-19.

At present, patients may have great difficulty handling the paperwork required to obtain stoma bags and aids that prevent peristomal skin complications from the National Health System. The Italian government has requested that regional administrations to protect patients with disabilities. Many regions have introduced self-renewal of medical prescriptions to avoid hospital attendance and provided for direct home delivery of prosthetic devices.

Viral RNA has been detected in gastrointestinal secretions and faeces, so faecal excretion could represent a further potential route of viral transmission. For this reason, adherence to proper handwashing, use of antiseptic foam, as well as use of appropriate personal protective equipment should be strictly enforced for patients, stoma nurses and caregivers. Moreover, the use of stool-containment bags with a safe locking system is recommended to prevent accidental spillage of intestinal material. In conclusion, the COVID-19 pandemic is worsening disability in stoma patients. Only good synergy between adequate government provisions and correct stoma care practices can help overcome this challenging situation.

Reference

<https://bjssjournals.onlinelibrary.wiley.com/doi/10.1002/bjs.11754>

Tracheotomy in COVID-19 patients: Preliminary experience and technical refinements

The COVID-19 pandemic is deeply affecting the surgical landscape. In this context, tracheotomy is considered one of the riskiest procedures, but our experience suggests that rational measures and teamwork can significantly reduce the risk of transmission to staff. Few real-life data about tracheotomy in intubated patients with COVID-19 exist. To avoid aerosolization and airflow from lower airways, we open the trachea above the endotracheal tube (ETT) cuff *via* an open surgical technique, following guidelines, with some technical refinements outlined in this report. For more details, read the link given below.

Reference

Healy, David W., Benjamin H. Cloyd, Michael J. Brenner, Robbi A. Kupfer, Karina S. Anam, and Samuel A. Schechtman. "The COVID-19 pandemic: implications for the head and neck anesthesiologist." *Journal of Head & Neck Anesthesia* 4 (2020).

Reference

<https://bjssjournals.onlinelibrary.wiley.com/doi/10.1002/bjs.11757>

Publication Date: June 15, 2020

Systemically comparing host immunity between survived and deceased COVID-19 patients

Abstract

Novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has caused the disastrous pandemic of Coronavirus Disease-2019 (COVID-19). Although the epidemiological, clinical, and immunological characteristics of COVID-19 have been reported, the kinetics of immune responses and their association with clinical outcomes remain poorly understood. In this report, the characteristics of cellular immune responses in a total of 157 COVID-19 patients enrolled in Tongji Hospital between February and March 2020 were studied, and the properties between 95 survived and 62 deceased patients with different onset time were compared. The demographic and clinical characteristics of these patients showed no significant difference in age, gender, clinical symptoms, and imaging features was recorded between survived and deceased patients. For more detail, see the link given below.

Reference

<https://www.nature.com/articles/s41423-020-0483-y>

Publication Date: June 11, 2020

Considering how biological sex impacts immune responses and COVID-19 outcomes

Abstract

A male bias in mortality has emerged in the COVID-19 pandemic, which is consistent with the pathogenesis of other viral infections. Biological sex differences may manifest themselves in susceptibility to infection, early pathogenesis, innate viral control, adaptive immune responses or the balance of inflammation and tissue repair in the resolution of infection. We discuss available sex-disaggregated epidemiological data from the COVID-19 pandemic, introduce sex-differential features of immunity and highlight potential sex differences underlying COVID-19 severity. We propose that sex differences in immunopathogenesis will inform mechanisms of COVID-19, identify points for therapeutic intervention and improve vaccine design and increase vaccine efficacy.

Reference

<https://www.nature.com/articles/s41577-020-0348-8>