COVID-19

Dec 31, 2020 – Jan 06, 2021

RESEARCH PUBLICATIONS

Publication Date: Jan 06, 2021

Pathogenic virus detection by optical nanobiosensors

Abstract

The novel coronavirus pandemic is sweeping the world and causing global crises. The lack of effective methods of early diagnosis and accurate detection may result in severe infection as well as mortality. Therefore, it is urgently required that rapid, selective, and accurate techniques for detecting pathogenic viruses are developed. Nanotechnology-based biosensors are finding many applications in biological detection, which may address these issues and realize direct detection of molecular targets in real time. Among various nanoplatforms, optical nanobiosensors have aroused much interest due to their inherent advantages of high sensitivity and direct readout. In this review, a summary of recent progress on the optical biosensors based on nanotechnology for pathogenic virus detection is provided, with focus on quantum dots (QDs), upconversion nanoparticles (UCNPs), noble metal nanoparticles, and organic fluorescent molecules-based nanoprobes and chemiluminescence assays. These representative studies demonstrate appealing performance as biosensors and hold great promise for clinical diagnosis.

Reference

https://www.cell.com/cell-reports-physical-science/fulltext/S2666-3864(20)30314-3

A longitudinal study of SARS-CoV-2-infected patients reveals a high correlation between neutralizing antibodies and COVID-19 severity

Abstract

Understanding the immune responses elicited by SARS-CoV-2 infection is critical in terms of protection against reinfection and, thus, for public health policy and vaccine

development for COVID-19. In this study, using either live SARS-CoV-2 particles or retroviruses pseudotyped with the SARS-CoV-2 S viral surface protein (Spike), we studied the neutralizing antibody (nAb) response in serum samples from a cohort of 140 SARS-CoV-2 qPCR-confirmed infections, including patients with mild symptoms and also more severe forms, including those that required intensive care. We show that nAb titers correlated strongly with disease severity and with anti-spike IgG levels. Indeed, patients from intensive care units exhibited high nAb titers; conversely, patients with milder disease symptoms had heterogeneous nAb titers, and asymptomatic or exclusive outpatient-care patients had no or low nAbs. We found that nAb activity in SARS-CoV-2-infected patients displayed a relatively rapid decline after recovery compared to individuals infected with other coronaviruses. Moreover, we found an absence of cross-neutralization between endemic coronaviruses and SARS-CoV-2, indicating that previous infection by human coronaviruses may not generate protective nAbs against SARS-CoV-2. Finally, we found that the D614G mutation in the spike protein, which has recently been identified as the current major variant in Europe, does not allow neutralization escape. Altogether, our results contribute to our understanding of the immune correlates of SARS-CoV-2-induced disease, and rapid evaluation of the role of the humoral response in the pathogenesis of SARS-CoV-2 is warranted.

Reference

https://www.nature.com/articles/s41423-020-00588-2

Responding to the pandemic as a family unit: Social impacts of COVID-19 on rural migrants in China and their coping strategies

Abstract

In 2020, the COVID-19 pandemic has created tremendous chaos in people's daily lives around the world. However, the related social impacts vary across social groups. Compared to people with abundant resources, the more disadvantaged tend to suffer greater negative social impacts from disasters. Although it is a crucial topic, there has been limited research on the social impacts of disastrous epidemics on uninfected people in developing countries. To bridge the gap, this study investigates the social impacts of the spread of COVID-19 on rural migrants and their coping strategies through face-to-face interviews with rural migrants in Nanjing, China. The household perspective is

highlighted to explore how rural migrants deal with various threats induced by COVID-19 spread. The study finds that rural migrants suffered from serious social impacts due to COVID-19, especially during the associated lockdown period. Despite some similar impacts, influences of COVID-19 varied among rural migrants at different life-cycle stages, due to variations in human capital, family burdens, role in a household, and ability to find part-time work. Receiving little support from governments and employers, rural migrants tended to adopt household strategies to deal with difficulties related to COVID-19. Within a household, they assisted each other and worked as a unit to maximize resources and reduce risks. Traditional family values were highly praised by rural migrant households during the period. Findings also suggest that both central and local governments need to provide practical aid to this group and to improve the social security system for rural migrants.

Reference

https://www.nature.com/articles/s41599-020-00686-6

Local measures enable COVID-19 containment with fewer restrictions due to cooperative effects

Abstract

Background: Many countries worldwide are faced with the choice between the (re)surgence of COVID-19 and endangering the economic and mental well-being of their citizens. While infection numbers are monitored and measures adjusted, a systematic strategy for balancing contact restrictions and socioeconomic life in the absence of a vaccine is currently lacking.

Methods: In a mathematical model, we determine the efficacy of regional containment strategies, where contact restrictions are triggered locally in individual regions upon crossing critical infection number thresholds. Our stochastic meta-population model distinguishes between contacts within a region and cross-regional contacts. We use current data on the spread of COVID-19 in Germany, Italy, England, New York State and Florida, including the effects of their individual national lockdowns, and county population sizes obtained from census data to define individual regions. As a performance measure, we determine the number of days citizens will experience contact restrictions over the

next 5 years ('restriction time') and compare it to an equivalent national lockdown strategy. To extract crucial parameters, we vary the proportion of cross-regional contacts (between 0% and 100%), the thresholds for initiating local measures (between 5 and 20 active infections per 100,000 inhabitants) as well as their duration after infection numbers have returned below the threshold (between 7 and 28 days). We compare performance across the five different countries and test how further subdivision of large counties into independently controlled regions of up to 100,000 or 200,000 inhabitants affects the results.

Findings: Our numerical simulations show a substantially reduced restriction time for regional containment, if the effective reproduction number of SARS-CoV-2 without restrictions, R0, is only slightly larger than 1 and the proportion of cross-regional contacts (the so-called leakiness) is low. In Germany, specifically, for R0=1.14, a leakiness of 1% is sufficiently low to reduce the mean restriction time from 468 days (s.d. 3 days) for the national containment strategy to 43 days (s.d. 3 days across simulations) for the regional strategy, when local measures are initiated at 10 infections per 100,000 inhabitants in the past 7 days. For R0=1.28, the allowed leakiness for minimal restriction time reduces to approximately 0.3%. The dependence of the restriction time on the leakiness is threshold-like only for regional containment, due to cooperative effects. It rises to levels similar to the national containment strategy for a leakiness > 10% (517 days national vs. 486 days regional for leakiness 32% and R0=1.14). We find a strong correlation between the population size of each region and the experienced restriction time. For countries with large counties, this can result in only a mild reduction in restriction time for regional containment, which can only be partly compensated by lower thresholds for initiating local measures and increasing their duration. In contrast, further subdividing large counties into smaller units can ensure a strong reduction of the restriction time for the regional strategy.

Interpretation: The leakiness, i.e. the proportion of cross-regional contacts, and the regional structure itself were crucial parameters for the performance of the regional strategy. Therefore, regional strategies could offer an adaptive way to contain the epidemic with fewer overall restrictions, if cross-regional infections can be kept below the critical level, which could be achieved without affecting local socioeconomic freedom. Maintaining general hygiene and contact tracing, testing should be intensified to ensure regional measures can be initiated at low infection thresholds, preventing the spread of

the disease to other regions before local elimination. While such tight control could lead to more restrictions in the short run, restrictions necessary for long-term containment could be reduced by up to a factor of 10. Our open-source simulation code is freely available and can be readily adapted to other countries.

Reference

https://www.thelancet.com/journals/eclinm/article/PIIS2589-5370(20)30462-4/fulltext

Immunological memory to SARS-CoV-2 assessed for up to 8 months after infection

Abstract

Understanding immune memory to SARS-CoV-2 is critical for improving diagnostics and vaccines, and for assessing the likely future course of the COVID-19 pandemic. We analyzed multiple compartments of circulating immune memory to SARS-CoV-2 in 254 samples from 188 COVID-19 cases, including 43 samples at ≥ 6 months post-infection. IgG to the Spike protein was relatively stable over 6+ months. Spike-specific memory B cells were more abundant at 6 months than at 1 month post symptom onset. SARS-CoV-2-specific CD4+ T cells and CD8+ T cells declined with a half-life of 3-5 months. By studying antibody, memory B cell, CD4+ T cell, and CD8+ T cell memory to SARS-CoV-2 in an integrated manner, we observed that each component of SARS-CoV-2 immune memory exhibited distinct kinetics.

Reference

https://science.sciencemag.org/content/early/2021/01/05/science.abf4063

Publication Date: Jan 05, 2021

SARS-CoV-2 infection is associated with a pro-thrombotic platelet phenotype

Abstract

Novel coronavirus disease 2019 (COVID-19) is associated with a hypercoagulable state, characterized by abnormal coagulation parameters and by increased incidence of cardiovascular complications. With this study, we aimed to investigate the activation state and the expression of transmembrane proteins in platelets of hospitalized COVID-19 patients. We investigated transmembrane proteins expression with a customized mass

cytometry panel of 21 antibodies. Platelets of 8 hospitalized COVID-19 patients not requiring intensive care support and without pre-existing conditions were compared to platelets of healthy controls (11 donors) with and without in vitro stimulation with thrombin receptor-activating peptide (TRAP). Mass cytometry of non-stimulated platelets detected an increased surface expression of activation markers P-Selectin (0.67 vs. 1.87 median signal intensity for controls vs. patients, $p = 0.0015$) and LAMP-3 (CD63, 0.37 vs. 0.81, $p = 0.0004$), the GPIIb/IIIa complex (4.58 vs. 5.03, $p < 0.0001$) and other adhesion molecules involved in platelet activation and platelet–leukocyte interactions. Upon TRAP stimulation, mass cytometry detected a higher expression of P-selectin in COVID-19 samples compared to controls ($p < 0.0001$). However, we observed a significantly reduced capacity of COVID-19 platelets to increase the expression of activation markers LAMP-3 and P-Selectin upon stimulation with TRAP. We detected a hyperactivated phenotype in platelets during SARS-CoV-2 infection, consisting of highly expressed platelet activation markers, which might contribute to the hypercoagulopathy observed in COVID-19. In addition, several transmembrane proteins were more highly expressed compared to healthy controls. These findings support research projects investigating antithrombotic and antiplatelet treatment regimes in COVID-19 patients, and provide new insights on the phenotypical platelet expression during SARS-CoV-2 infection.

Reference

https://www.nature.com/articles/s41419-020-03333-9

The neutrophil-to-lymphocyte ratio determines clinical efficacy of corticosteroid therapy in patients with COVID-19

Abstract

Corticosteroid therapy is now recommended as a treatment in patients with severe COVID-19. But one key question is how to objectively identify severely ill patients who may benefit from such therapy. Here, we assigned 12,862 COVID-19 cases from 21 hospitals in Hubei Province equally to a training and a validation cohort. It was found that a neutrophil-to-lymphocyte ratio (NLR) > 6.11 at admission discriminated a higher risk for mortality. Importantly, however, corticosteroid treatment in such individuals was associated with a lower risk of 60-day all-cause mortality. Conversely, in individuals with an NLR ≤ 6.11 or with type 2 diabetes, corticosteroid treatment was not associated with

reduced mortality, but rather increased risks of hyperglycemia and infections. These results show that in the studied cohort corticosteroid treatment is associated with beneficial outcomes in a subset of COVID-19 patients who are non-diabetic and with severe symptoms as defined by NLR.

Reference

https://www.cell.com/cell-metabolism/fulltext/S1550-4131(21)00002-4

Estimating and explaining the spread of COVID-19 at the county level in the USA

Abstract

The basic reproduction number, R_0, determines the rate of spread of a communicable disease and therefore gives fundamental information needed to plan public health interventions. Using mortality records, we estimated the rate of spread of COVID-19 among 160 counties and county-aggregates in the USA at the start of the epidemic. We show that most of the high among-county variance is explained by four factors ($R^2 = 0.70$): the timing of outbreak, population size, population density, and spatial location. For predictions of future spread, population density and spatial location are important, and for the latter we show that SARS-CoV-2 strains containing the G614 mutation to the spike gene are associated with higher rates of spread. Finally, the high predictability of R_0 allows extending estimates to all 3109 counties in the conterminous 48 states. The high variation of R_0 argues for public health policies enacted at the county level for controlling COVID-19.

Reference

https://www.nature.com/articles/s42003-020-01609-6

Cold sensitivity of the SARS-CoV-2 spike ectodomain

Abstract

The SARS-CoV-2 spike (S) protein, a primary target for COVID-19 vaccine development, presents its receptor binding domain in two conformations, the receptor-accessible ‘up’ or receptor-inaccessible ‘down’ states. Here we report that the commonly used stabilized S ectodomain construct ‘2P’ is sensitive to cold temperatures, and this cold sensitivity is

abrogated in a ‘down’ state-stabilized ectodomain. Our findings will impact structural, functional and vaccine studies that use the SARS-CoV-2 S ectodomain.

Reference

https://www.nature.com/articles/s41594-020-00547-5

Publication Date: Jan 04, 2021

Standardization of ELISA protocols for serosurveys of the SARS-CoV-2 pandemic using clinical and at-home blood sampling

Abstract

The extent of SARS-CoV-2 infection throughout the United States population is currently unknown. High quality serology is key to avoiding medically costly diagnostic errors, as well as to assuring properly informed public health decisions. Here, we present an optimized ELISA-based serology protocol, from antigen production to data analyses, that helps define thresholds for IgG and IgM seropositivity with high specificities. Validation of this protocol is performed using traditionally collected serum as well as dried blood on mail-in blood sampling kits. Archival (pre-2019) samples are used as negative controls, and convalescent, PCR-diagnosed COVID-19 patient samples serve as positive controls. Using this protocol, minimal cross-reactivity is observed for the spike proteins of MERS, SARS1, OC43 and HKU1 viruses, and no cross reactivity is observed with anti-influenza A H1N1 HAI. Our protocol may thus help provide standardized, population-based data on the extent of SARS-CoV-2 seropositivity, immunity and infection.

Reference

https://www.nature.com/articles/s41467-020-20383-x

A multi-pronged approach targeting SARS-CoV-2 proteins using ultra-large virtual screening

Abstract

The unparalleled global effort to combat the continuing severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic over the last year has resulted in promising prophylactic measures. However, a need still exists for cheap, effective therapeutics and targeting multiple points in the viral life cycle could help tackle the current as well as future coronaviruses. Here we leverage our recently developed, ultra-large

scale in silico screening platform, VirtualFlow, to search for inhibitors that target SARS-CoV-2. In this unprecedented structure-based virtual campaign, we screened roughly 1 billion molecules against each of 40 different target sites on 17 different potential viral and host targets. In addition to targeting the active sites of viral enzymes, we also targeted critical auxiliary sites such as functionally important protein-protein interactions.

Reference

https://www.cell.com/iscience/fulltext/S2589-0042(20)31218-9

Acute immune signatures and their legacies in severe acute respiratory syndrome coronavirus-2 infected cancer patients

Abstract

Given the immune system's importance for cancer surveillance and treatment, we have investigated how it may be affected by SARS-CoV-2 infection of cancer patients. Across some heterogeneity in tumour type, stage and treatment, virus-exposed solid cancer patients display a dominant impact of SARS-CoV-2, apparent from the resemblance of their immune signatures to those for COVID-19+ non-cancer patients. This is not the case for haematological malignancies, with virus-exposed patients collectively displaying heterogeneous humoral responses, an exhausted T cell phenotype and a high prevalence of prolonged virus shedding. Furthermore, while recovered solid cancer patients' immunophenotypes resemble those of non-virus-exposed cancer patients, recovered haematological cancer patients display distinct, lingering immunological legacies. Thus, while solid cancer patients, including those with advanced disease, seem no more at risk of SARS-CoV-2-associated immune dysregulation than the general population, haematological cancer patients show complex immunological consequences of SARS-CoV-2 exposure that might usefully inform their care.

Reference

https://www.cell.com/cancer-cell/fulltext/S1535-6108(21)00001-5

The aging transcriptome and cellular landscape of the human lung in relation to SARS-CoV-2

Abstract

Age is a major risk factor for severe coronavirus disease-2019 (COVID-19). Here, we interrogate the transcriptional features and cellular landscape of the aging human lung.

By intersecting these age-associated changes with experimental data on SARS-CoV-2, we identify several factors that may contribute to the heightened severity of COVID-19 in older populations. The aging lung is transcriptionally characterized by increased cell adhesion and stress responses, with reduced mitochondria and cellular replication. Deconvolution analysis reveals that the proportions of alveolar type 2 cells, proliferating basal cells, goblet cells, and proliferating natural killer/T cells decrease with age, whereas alveolar fibroblasts, pericytes, airway smooth muscle cells, endothelial cells and IGSF21^{+} dendritic cells increase with age. Several age-associated genes directly interact with the SARS-CoV-2 proteome. Age-associated genes are also dysregulated by SARS-CoV-2 infection in vitro and in patients with severe COVID-19. These analyses illuminate avenues for further studies on the relationship between age and COVID-19.

Reference

https://www.nature.com/articles/s41467-020-20323-9

Analysis of SARS-CoV-2 antibodies in COVID-19 convalescent blood using a coronavirus antigen microarray

Abstract

The current practice for diagnosis of COVID-19, based on SARS-CoV-2 PCR testing of pharyngeal or respiratory specimens in a symptomatic patient at high epidemiologic risk, likely underestimates the true prevalence of infection. Serologic methods can more accurately estimate the disease burden by detecting infections missed by the limited testing performed to date. Here, we describe the validation of a coronavirus antigen microarray containing immunologically significant antigens from SARS-CoV-2, in addition to SARS-CoV, MERS-CoV, common human coronavirus strains, and other common respiratory viruses. A comparison of antibody profiles detected on the array from control sera collected prior to the SARS-CoV-2 pandemic versus convalescent blood specimens from virologically confirmed COVID-19 cases demonstrates near complete discrimination of these two groups, with improved performance from use of antigen combinations that include both spike protein and nucleoprotein. This array can be used as a diagnostic tool, as an epidemiologic tool to more accurately estimate the disease burden of COVID-19, and as a research tool to correlate antibody responses with clinical outcomes.

Reference

https://www.nature.com/articles/s41467-020-20095-2

Machine learning-based prediction of COVID-19 diagnosis based on symptoms

Abstract

Effective screening of SARS-CoV-2 enables quick and efficient diagnosis of COVID-19 and can mitigate the burden on healthcare systems. Prediction models that combine several features to estimate the risk of infection have been developed. These aim to assist medical staff worldwide in triaging patients, especially in the context of limited healthcare resources. We established a machine-learning approach that trained on records from 51,831 tested individuals (of whom 4769 were confirmed to have COVID-19). The test set contained data from the subsequent week (47,401 tested individuals of whom 3624 were confirmed to have COVID-19). Our model predicted COVID-19 test results with high accuracy using only eight binary features: sex, age ≥60 years, known contact with an infected individual, and the appearance of five initial clinical symptoms. Overall, based on the nationwide data publicly reported by the Israeli Ministry of Health, a model was developed that detects COVID-19 cases by simple features accessed by asking basic questions. Our framework can be used, among other considerations, to prioritize testing for COVID-19 when testing resources are limited.

Reference

https://www.nature.com/articles/s41746-020-00372-6

Psychological characteristics associated with COVID-19 vaccine hesitancy and resistance in Ireland and the United Kingdom

Abstract

Identifying and understanding COVID-19 vaccine hesitancy within distinct populations may aid future public health messaging. Using nationally representative data from the general adult populations of Ireland (N = 1041) and the United Kingdom (UK; N = 2025), we found that vaccine hesitancy/resistance was evident for 35% and 31% of these populations respectively. Vaccine hesitant/resistant respondents in Ireland and the UK differed on a number of sociodemographic and health-related variables but were similar across a broad array of psychological constructs. In both populations, those resistant to

a COVID-19 vaccine were less likely to obtain information about the pandemic from traditional and authoritative sources and had similar levels of mistrust in these sources compared to vaccine accepting respondents. Given the geographical proximity and socio-economic similarity of the populations studied, it is not possible to generalize findings to other populations, however, the methodology employed here may be useful to those wishing to understand COVID-19 vaccine hesitancy elsewhere.

Reference

https://www.nature.com/articles/s41467-020-20226-9

Fast automated detection of COVID-19 from medical images using convolutional neural networks

Abstract

Coronavirus disease 2019 (COVID-19) is a global pandemic posing significant health risks. The diagnostic test sensitivity of COVID-19 is limited due to irregularities in specimen handling. We propose a deep learning framework that identifies COVID-19 from medical images as an auxiliary testing method to improve diagnostic sensitivity. We use pseudo-coloring methods and a platform for annotating X-ray and computed tomography images to train the convolutional neural network, which achieves a performance similar to that of experts and provides high scores for multiple statistical indices (F1 scores > 96.72% (0.9307, 0.9890) and specificity >99.33% (0.9792, 1.0000)). Heatmaps are used to visualize the salient features extracted by the neural network. The neural network-based regression provides strong correlations between the lesion areas in the images and five clinical indicators, resulting in high accuracy of the classification framework. The proposed method represents a potential computer-aided diagnosis method for COVID-19 in clinical practice.

Reference

https://www.nature.com/articles/s42003-020-01535-7

Neutralizing antibody titres in SARS-CoV-2 infections

Abstract

The SARS-CoV-2 pandemic poses the greatest global public health challenge in a century. Neutralizing antibody is a correlate of protection and data on kinetics of virus neutralizing antibody responses are needed. 293 Sera was tested from an observational cohort of 195 reverse transcription polymerase chain reaction (RT-PCR) confirmed SARS-CoV-2 infections collected from 0 to 209 days after onset of symptoms. Of 115 sera collected ≥61 days after onset of illness tested using plaque reduction neutralization (PRNT) assays, 99.1% remained seropositive for both 90% ($PRNT_{90}$) and 50% ($PRNT_{50}$) neutralization endpoints. It was estimated that it takes at least 372, 416 and 133 days for $PRNT_{50}$ titres to drop to the detection limit of a titre of 1:10 for severe, mild and asymptomatic patients, respectively. At day 90 after onset of symptoms (or initial RT-PCR detection in asymptomatic infections), it took 69, 87 and 31 days for $PRNT_{50}$ antibody titres to decrease by half (T1/2) in severe, mild and asymptomatic infections, respectively. Patients with severe disease had higher peak $PRNT_{90}$ and $PRNT_{50}$ antibody titres than patients with mild or asymptomatic infections. Age did not appear to compromise antibody responses, even after accounting for severity. It was concluded that SARS-CoV-2 infection elicits robust neutralizing antibody titres in most individuals.

Reference

https://www.nature.com/articles/s41467-020-20247-4

Dose-dependent response to infection with SARS-CoV-2 in the ferret model and evidence of protective immunity

Abstract

There is a vital need for authentic COVID-19 animal models to enable the pre-clinical evaluation of candidate vaccines and therapeutics. Here we report a dose titration study of SARS-CoV-2 in the ferret model. After a high (5×10^6 pfu) and medium (5×10^4 pfu) dose of virus is delivered, intranasally, viral RNA shedding in the upper respiratory tract (URT) is observed in 6/6 animals, however, only 1/6 ferrets show similar signs after low dose (5×10^2 pfu) challenge. Following sequential culls pathological signs of mild multifocal bronchopneumonia in approximately 5–15% of the lung is seen on day 3, in high and medium dosed groups. Ferrets re-challenged, after virus shedding ceased, are

fully protected from acute lung pathology. The endpoints of URT viral RNA replication & distinct lung pathology are observed most consistently in the high dose group. This ferret model of SARS-CoV-2 infection presents a mild clinical disease.

Reference

https://www.nature.com/articles/s41467-020-20439-y

COVIDiSTRESS global survey dataset on psychological and behavioural consequences of the COVID-19 outbreak

Abstract

This N = 173,426 social science dataset was collected through the collaborative COVIDiSTRESS Global Survey – an open science effort to improve understanding of the human experiences of the 2020 COVID-19 pandemic between 30th March and 30th May, 2020. The dataset allows a cross-cultural study of psychological and behavioural responses to the Coronavirus pandemic and associated government measures like cancellation of public functions and stay at home orders implemented in many countries. The dataset contains demographic background variables as well as measures of Asian Disease Problem, perceived stress (PSS-10), availability of social provisions (SPS-10), trust in various authorities, trust in governmental measures to contain the virus (OECD trust), personality traits (BFF-15), information behaviours, agreement with the level of government intervention, and compliance with preventive measures, along with a rich pool of exploratory variables and written experiences. A global consortium from 39 countries and regions worked together to build and translate a survey with variables of shared interests, and recruited participants in 47 languages and dialects. Raw plus cleaned data and dynamic visualizations are available.

Reference

https://www.nature.com/articles/s41597-020-00784-9

Human stem cell models to study host–virus interactions in the central nervous system

Abstract

Advancements in human pluripotent stem cell technology offer a unique opportunity for the neuroimmunology field to study host–virus interactions directly in disease-relevant

cells of the human central nervous system (CNS). Viral encephalitis is most commonly caused by herpesviruses, arboviruses and enteroviruses targeting distinct CNS cell types and often leading to severe neurological damage with poor clinical outcomes. Furthermore, different neurotropic viruses will affect the CNS at distinct developmental stages, from early prenatal brain development to the aged brain. With the unique flexibility and scalability of human pluripotent stem cell technology, it is now possible to examine the molecular mechanisms underlying acute infection and latency, determine which CNS subpopulations are specifically infected, study temporal aspects of viral susceptibility, perform high-throughput chemical or genetic screens for viral restriction factors and explore complex cell-non-autonomous disease mechanisms. Therefore, human pluripotent stem cell technology has the potential to address key unanswered questions about antiviral immunity in the CNS, including emerging questions on the potential CNS tropism of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).

Reference

https://www.nature.com/articles/s41577-020-00474-y

Epicutaneous immunization with modified vaccinia Ankara viral vectors generates superior T cell immunity against a respiratory viral challenge

Abstract

Modified Vaccinia Ankara (MVA) was recently approved as a smallpox vaccine. Variola is transmitted by respiratory droplets and MVA immunization by skin scarification (s.s.) protected mice far more effectively against lethal respiratory challenge with vaccinia virus (VACV) than any other route of delivery, and at lower doses. Comparisons of s.s. with intradermal, subcutaneous, or intramuscular routes showed that MVAOVA s.s.-generated T cells were both more abundant and transcriptionally unique. MVAOVA s.s. produced greater numbers of lung Ova-specific $CD8^+$ TRM and was superior in protecting mice against lethal VACVOVA respiratory challenge. Nearly as many lung TRM were generated with MVAOVA s.s. immunization compared to intra-tracheal immunization with MVAOVA and both routes vaccination protected mice against lethal pulmonary challenge with VACVOVA. Strikingly, MVAOVA s.s.-generated effector T cells exhibited overlapping gene transcriptional profiles to those generated via intra-tracheal immunization. Overall, our data suggest that heterologous MVA vectors immunized via s.s. are uniquely well-

suited as vaccine vectors for respiratory pathogens, which may be relevant to COVID-19. In addition, MVA delivered *via* s.s. could represent a more effective dose-sparing smallpox vaccine.

Reference

https://www.nature.com/articles/s41541-020-00265-5

Publication Date: Jan 01, 2021

Comprehensive *in-vivo* secondary structure of the SARS-CoV-2 genome reveals novel regulatory motifs and mechanisms

Abstract

SARS-CoV-2 is the positive-sense RNA virus that causes COVID-19 disease. The genome of SARS-CoV-2 is unique among viral RNAs in its vast potential to form RNA structures and yet, as much as 97% of its 30 kilobases have not been structurally explored. Here, we apply a novel long amplicon strategy to determine for the first time the secondary structure of the SARS-CoV-2 RNA genome at single-nucleotide resolution in infected cells. Our in-depth structural analysis reveals networks of well-folded RNA structures throughout Orf1ab, and reveals aspects of SARS-CoV-2 genome architecture that distinguish it from other RNA viruses. Evolutionary analysis shows that several features of the SARS-CoV-2 genomic structure are conserved across beta coronaviruses and we pinpoint regions of well-folded RNA structure that merit downstream functional analysis. The native, secondary structure of SARS-CoV-2 presented here is a roadmap that will facilitate focused studies on the viral life cycle, facilitate primer design, and guide the identification of RNA drug targets against COVID-19.

Reference

https://www.cell.com/molecular-cell/fulltext/S1097-2765(20)30962-X

SARS-CoV-2 leads to a small vessel endotheliitis in the heart

Abstract

Background: SARS-CoV-2 infection (COVID-19 disease) can induce systemic vascular involvement contributing to morbidity and mortality. SARS-CoV-2 targets epithelial and endothelial cells through the ACE2 receptor. The anatomical involvement of the coronary tree is not explored yet.

Methods: Cardiac autopsy tissue of the entire coronary tree (main coronary arteries, epicardial arterioles/venules, epicardial capillaries) and epicardial nerves were analyzed in COVID-19 patients (n = 6). All anatomical regions were immunohistochemically tested for ACE2, TMPRSS2, CD147, CD45, CD3, CD4, CD8, CD68 and IL-6. COVID-19 negative patients with cardiovascular disease (n = 3) and influenza A (n = 6) served as controls.

Findings: COVID-19 positive patients showed strong ACE2 / TMPRSS2 expression in capillaries and less in arterioles/venules. The main coronary arteries were virtually devoid of ACE2 receptor and had only mild intimal inflammation. Epicardial capillaries had a prominent lympho-monocytic endotheliitis, which was less pronounced in arterioles/venules. The lymphocytic-monocytic infiltrate strongly expressed CD4, CD45, CD68. Peri/epicardial nerves had strong ACE2 expression and lympho-monocytic inflammation. COVID-19 negative patients showed minimal vascular ACE2 expression and lacked endotheliitis or inflammatory reaction.

Interpretation: ACE2 / TMPRSS2 expression and lymphomonocytic inflammation in COVID-19 disease increases crescentically towards the small vessels suggesting that COVID-19-induced endotheliitis is a small vessel vasculitis not involving the main coronaries. The inflammatory neuropathy of epicardial nerves in COVID-19 disease provides further evidence of an angio- and neurotrophic affinity of SARS-COV2 and might potentially contribute to the understanding of the high prevalence of cardiac complications such as myocardial injury and arrhythmias in COVID-19.

Reference

https://www.thelancet.com/journals/ebiom/article/PIIS2352-3964(20)30558-2/fulltext

Publication Date: Dec 31, 2020

Deposition distribution of the new coronavirus (SARS-CoV-2) in the human airways upon exposure to cough-generated droplets and aerosol particles

Abstract

The new coronavirus disease 2019 (COVID-19) has been emerged as a rapidly spreading pandemic. The disease is thought to spread mainly from person-to-person through

respiratory droplets produced when an infected person coughs, sneezes, or talks. The pathogen of COVID-19 is the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). It infects the cells binding to the angiotensin-converting enzyme 2 receptor (ACE2) which is expressed by cells throughout the airways as targets for cellular entry. Although the majority of persons infected with SARS-CoV-2 experience symptoms of mild upper respiratory tract infection, in some people infections of the acinar airways result in severe, potentially fatal pneumonia. However, the induction of COVID-19 pneumonia requires that SARS-CoV-2 reaches the acinar airways. While huge efforts have been made to understand the spread of the disease as well as the pathogenesis following cellular entry, much less attention is paid to how SARS-CoV-2 from the environment reach the receptors of the target cells. The aim of the present study is to characterize the deposition distribution of SARS-CoV-2 in the airways upon exposure to cough-generated droplets and aerosol particles. For this purpose, the Stochastic Lung Deposition Model has been applied. Particle size distribution, breathing parameters supposing normal breathing through the nose, and viral loads were taken from the literature. We found that the probability of direct infection of the acinar airways due to inhalation of particles emitted by a bystander cough is very low. As the number of viruses deposited in the extrathoracic airways is about 7 times higher than in the acinar airways, we concluded that in most cases COVID-19 pneumonia must be preceded by SARS-CoV-2 infection of the upper airways. Our results suggest that without the enhancement of viral load in the upper airways, COVID-19 would be much less dangerous. The period between the onset of initial symptoms and the potential clinical deterioration could provide an opportunity for prevention of pneumonia by blocking or significantly reducing the transport of viruses towards the acinar airways. Therefore, even non-specific treatment forms like disinfection of the throat and nasal and oral mucosa may effectively keep the viral load of the upper airways low enough to avoid or prolong the progression of the disease. In addition, using a tissue or cloth in order to absorb droplets and aerosol particles emitted by own coughs of infected patients before re-inhalation is highly recommended even if they are alone in quarantine.

Reference

https://www.nature.com/articles/s41598-020-79985-6

Risk assessment and seroprevalence of SARS-CoV-2 infection in healthcare workers of COVID-19 and non-COVID-19 hospitals in Southern Switzerland

Abstract

Background: Hospital healthcare workers (HCW), in particular those involved in the clinical care of COVID-19 cases, are presumably exposed to a higher risk of acquiring the disease than the general population.

Methods: Between April 16 and 30, 2020 we conducted a prospective, SARS-CoV-2 seroprevalence study in HCWs in Southern Switzerland. Participants were hospital personnel with varying COVID-19 exposure risk depending on job function and working site. They provided personal information (including age, sex, occupation, and medical history) and self-reported COVID-19 symptoms. Odds ratio (OR) of seropositivity to IgG antibodies was estimated by univariate and multivariate logistic regressions.

Findings: Among 4726 participants, IgG antibodies to SARS-CoV-2 were detected in 9.6% of the HCWs. Seropositivity was higher among HCWs working on COVID-19 wards (14.1% (11.9–16.5)) compared to other hospital areas at medium (10.7% (7.6–14.6)) or low risk exposure (7.3% (6.4–8.3)). OR for high vs. medium wards risk exposure was 1.42 (0.91–2.22), P = 0.119, and 1.98 (1.55–2.53), P<0.001 for high vs. low wards risk exposure. The same was for true for doctors and nurses (10.1% (9.0–11.3)) compared to other employees at medium (7.1% (4.8–10.0)) or low risk exposure (6.6% (5.0–8.4)). OR for high vs. medium profession risk exposure was 1.37 (0.89–2.11), P = 0.149, and 1.75 (1.28–2.40), P = 0.001 for high vs. low profession risk exposure. Moreover, seropositivity was higher among HCWs who had household exposure to COVID-19 cases compared to those without (18.7% (15.3–22.5) vs. 7.7% (6.9–8.6), OR 2.80 (2.14–3.67), P<0.001).

Interpretation: SARS-CoV-2 antibodies are detectable in up to 10% of HCWs from acute care hospitals in a region with high incidence of COVID-19 in the weeks preceding the study. HCWs with exposure to COVID-19 patients have only a slightly higher absolute risk of seropositivity compared to those without, suggesting that the use of PPE and other measures aiming at reducing nosocomial viral transmission are effective. Household contact with known COVID-19 cases represents the highest risk of seropositivity.

Reference

https://www.thelancet.com/journals/lanepe/article/PIIS2666-7762(20)30013-2/fulltext

A model to rate strategies for managing disease due to COVID-19 infection

Abstract

Considering looming fatality and economic recession, effective policy making based on ongoing COVID-19 pandemic is an urgent and standing issue. Numerous issues for controlling infection have arisen from public discussion led by medical professionals. Yet understanding of these factors has been necessarily qualitative and control measures to correct unfavorable trends specific to an infection area have been lacking. The logical implement for control is a large scale stochastic model with countless parameters lacking robustness and requiring enormous data. This paper presents a remedy for this vexing problem by proposing an alternative approach. Machine learning has come to play a widely circulated role in the study of complex data in recent times. It was demonstrated that when machine learning is employed together with the mechanistic framework of a mathematical model, there can be a considerably enhanced understanding of complex systems. A mathematical model describing the viral infection dynamics reveals two transmissibility parameters influenced by the management strategies in the area for the control of the current pandemic. Both parameters readily yield the peak infection rate and means for flattening the curve, which is correlated to different management strategies by employing machine learning, enabling comparison of different strategies and suggesting timely alterations. Treatment of population data with the model shows that restricted non-essential business closure, school closing and strictures on mass gathering influence the spread of infection. While a rational strategy for initiation of an economic reboot would call for a wider perspective of the local economics, the model can speculate on its timing based on the status of the infection as reflected by its potential for an unacceptably renewed viral onslaught.

Reference

https://www.nature.com/articles/s41598-020-79817-7

Clinically distinct COVID-19 cases share notably similar immune response progression: A follow-up analysis

Abstract

Inflammatory responses to the novel coronavirus SARS-CoV-2, which causes COVID-19, range from asymptomatic to severe. Here, a follow-up analysis of a longitudinal study was presented characterizing COVID-19 immune responses from a father and son with distinctly different clinical courses. The father required a lengthy hospital stay for severe symptoms, whereas his son had mild symptoms and no fever yet tested positive for SARS-CoV-2 for 29 days. Father and son, as well as another unrelated COVID-19 patient, displayed a robust increase of SERPING1, the transcript encoding C1 esterase inhibitor (C1–INH). It was further bolstered this finding by incorporating a serum proteomics dataset and found that serum C1–INH was consistently increased in COVID-19 patients. C1–INH is a central regulator of the contact and complement systems, potentially linking COVID-19 to complement hyperactivation, fibrin clot formation, and immune depression. Furthermore, despite distinct clinical cases, significant parallels were observed in transcripts involved in interferon and B cell signaling. As symptoms were resolving, widespread decreases were seen in immune-related transcripts to levels below those of healthy controls. The study provides insight into the immune responses of likely millions of people with extremely mild symptoms who may not be aware of their infection with SARS-CoV-2 and implies a potential for long-lasting consequences that could contribute to reinfection risk.

Reference

https://www.cell.com/heliyon/fulltext/S2405-8440(20)32719-5

Epidemic area contact history and sleep quality associated with posttraumatic stress symptoms in the first phase of COVID-19 outbreak in China

Abstract

The impact of 2019 coronavirus disease (COVID-19) outbreak on mental health was of widespread concern recently. The present study aimed to exam sleep quality and posttraumatic stress symptoms (PTSS) and potential influence factors in the first phases of COVID-19 massive outbreak in China. A snowball sampling technique was used and

a total of 2027 Chinese participated in the present study. Demographic information, epidemic area contact history, sleep quality and PTSS data were collected with an internet-based cross-sectional survey. Results suggested that 59.7% participants were not fully satisfied with their sleep quality, and 50.9% participants had various degrees of short sleep duration problems. 44.1% and 33.0% participants had sleep disturbance and sleep onset latency problems. Also, the prevalence of PTSS reached 4.7% in the self-rating survey. Epidemic area contact history affected PTSS and latency onset of sleep under the influence of COVID-19. Epidemic area contact history and sleep quality had interaction effects on PTSS. The present study was one of the first to evaluate acute psychological responses and possible risk factors during the peak of COVID-19 in China and results indicate that keeping good sleep quality in individuals with pandemic exposure experiences is a way to prevent PTSS.

Reference

https://www.nature.com/articles/s41598-020-80649-8

PERSPECTIVE

Publication Date: Jan 06, 2021

The impact of COVID-19 on rare and complex connective tissue diseases: The experience of ERN ReCONNET

During the COVID-19 pandemic, the need to provide high-level care for a large number of patients with COVID-19 has affected resourcing for, and limited the routine care of, all other conditions. The impact of this health emergency is particularly relevant in the rare connective tissue diseases (rCTDs) communities, as discussed in this Perspective article by the multi-stakeholder European Reference Network on Rare and Complex Connective Tissue and Musculoskeletal Diseases (ERN ReCONNET). The clinical, organizational and health economic challenges faced by health-care providers, institutions, patients and their families during the SARS-CoV-2 outbreak have demonstrated the importance of ensuring continuity of care in the management of rCTDs, including adequate diagnostics and monitoring protocols, and highlighted the need for a structured emergency strategy. The vulnerability of patients with rCTDs needs to be taken into account when planning future health policies, in preparation for not only the post-COVID era, but also any possible new health emergencies. For more details, read the link given below.

Reference

https://www.nature.com/articles/s41584-020-00565-z

Publication Date: Jan 05, 2021

Scientists criticize ‘rushed’ approval of Indian COVID-19 vaccine without efficacy data

India’s drug regulator approved two COVID-19 vaccines on 3 January, a decision Prime Minister Narendra Modi hailed on Twitter as “a decisive turning point to strengthen a spirited fight!” against the pandemic and a testament to the Indian scientific community’s self reliance. But some scientists and patient advocates are sharply critical of the move—in particular, the decision to greenlight Covaxin, a vaccine developed in India by Bharat Biotech, without awaiting the results of a phase III trial to determine efficacy and safety.

At a Sunday press conference, the drugs controller general of India, V. G. Somani, said that even though Covaxin's efficacy study is still recruiting participants, he was approving the vaccine as an "abundant precaution," in case it was needed to curb the spread of a highly transmissible variant of SARS-CoV-2 first found in the United Kingdom. Somani said it and the other vaccine, the Indian version of a vaccine developed by the University of Oxford and AstraZeneca, were approved for "restricted use" in an emergency situation and that their manufacturers would have to continue the clinical trials that have begun. For more details, read the link given below.

Reference

https://www.sciencemag.org/news/2021/01/scientists-criticize-rushed-approval-indian-covid-19-vaccine-without-efficacy-data

Publication Date: Jan 01, 2021

The puzzle of the COVID-19 pandemic in Africa

The COVID-19 pandemic has been puzzling to many public health experts because Africa has reported far fewer cases and deaths from COVID-19 than predicted. As of 22 November 2020, the continent of Africa, comprising 1.3 billion people, had recorded 2,070,953 cases of COVID-19 and 49,728 deaths, representing ~3.6% of total global cases. Because of the continent's overstrained and weak health systems, inadequate financing of health care, paucity in human resources, and challenges posed by existing endemic diseases—including HIV, tuberculosis, and malaria—earlier predictions suggested that up to 70 million Africans may be infected with severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) by June, with more than 3 million deaths. On page 79 of this issue, Uyoga et al. report a serosurvey study (measuring the occurrence of SARS-CoV-2 antibodies) of blood donors in Kenya that suggested that the incidence of SARS-CoV-2 infection is much higher than expected from case numbers. Using blood donor samples as a proxy, Uyoga et al. estimated that SARS-CoV-2 infections occurred in 5.5% of the population in Kisumu, 7.3% in Nairobi, and 8.0% in Mombasa, with an overall average of 4.3%. This translates to ~2.2 million total possible infections compared with the reported 77,585 infections in the country as of 23 November 2020. Similarly, in October 2020, Mozambique reported less than 3000 confirmed cases of COVID-19; however, serosurveys found that 5% of households in the city of Nampula and 2.5% of

households in the city of Pemba had been exposed to the virus. This suggests that there may be more infections than recorded.

There are several factors that may influence the trajectory of the COVID-19 pandemic in Africa. These include limited testing (which limits detection and isolation, and thus public health measures), a much younger population (and thus fewer severe cases and deaths), climatic differences (which could affect transmission), preexisting immunity, genetic factors, early implementation of public health measures, and timely leadership. Two key aspects that may contribute to our understanding of the pandemic puzzle in Africa include scaling up of testing and use of serosurveys. For more details, read the link given below.

Reference

https://science.sciencemag.org/content/371/6524/27

NEWSLETTER

Publication Date: Jan 05, 2021

New variant of SARS-CoV-2 in UK causes surge of COVID-19

For most of November, 2020, England was in lockdown to force down the incidence of COVID-19 cases that had steadily increased in the late summer and autumn. Other countries in the UK (Wales, Scotland, and Northern Ireland) had also been reimposing and subsequently lifting restrictions, since each of the four nations is in charge of its own COVID-19 control plans. For a while, the strategy in England appeared to have worked, with many areas that previously had high case incidence seeing rates drop sharply in November, including northwest England and Yorkshire, areas which had previously seen some of the highest incidence rates in the UK. However, it soon became apparent that the English lockdown had not had the same effect in every region. In Kent, a large county in the southeast, cases actually continued to increase during the lockdown, despite having the same restrictions as other regions. When, on Dec 2, 2020, England lifted its lockdown and moved back into a three-level tiered restrictions system, cases continued to increase sharply in Kent and then rapidly in Greater London and other parts of the southeast. And despite the approval of two vaccines in recent weeks, the UK now faces a race against time to vaccinate as many vulnerable and elderly people as possible. For more details, read the link given below.

Reference

https://www.thelancet.com/journals/lanres/article/PIIS2213-2600(21)00005-9/fulltext

Publication Date: Jan 04, 2021

The game-changing COVID-19 antibody test

BioSURE COVID-19 Triple Antibody Rapid Test is simple, quick and effective COVID-19 test to perform and only requires 5ul of capillary blood to deliver results in just 10 minutes. It was developed and manufactured in the UK, and comes in a box, with a price of £750 excluding VAT, that contains sufficient product for 25 tests (£30 per test). For more details, read the link given below.

Reference

https://www.nature.com/articles/s41404-020-0640-0

HIGHLIGHTS

Publication Date: Jan 04, 2021

SARS-CoV-2 detected in olfactory neurons

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is present in the neurons of the olfactory mucosa in some individuals who died with COVID-19, according to new research published in Nature Neuroscience. The finding suggests that the virus could invade the CNS via the olfactory nerve and possibly other cranial nerves.

The researchers analyzed post-mortem tissue from 33 individuals with COVID-19, including samples from the olfactory mucosa, olfactory bulb, uvula, trigeminal ganglion and medulla oblongata. They used real-time quantitative PCR (rt-qPCR), and in-situ hybridization to detect SARS-CoV-2 RNA, as well as immunohistochemistry and electron microscopy to detect the protein. The results of the rt-qPCR revealed that viral RNA was most common in the olfactory mucosa, where it was detected in 20 of 30 participants. The next most common locations were the uvula and the medulla oblongata, both of which were SARS-CoV-2 RNA-positive in six participants. Electron microscopy analysis of tissue from one individual with a high viral RNA load revealed intact viral particles in the olfactory mucosa.

These new findings add to our understanding of the interactions between SARS-CoV-2 and the brain, but whether viral invasion of the CNS via the olfactory system is responsible for the neurological symptoms observed in patients with COVID-19 is not entirely clear. For more details, read the link given below.

Reference

https://www.nature.com/articles/s41582-020-00449-6

COMMENT

Publication Date: Jan 06, 2021

Understanding the pharmacokinetics of Favipiravir: Implications for treatment of influenza and COVID-19

Favipiravir (T-705; 6-fluoro-3-hydroxy-2-pyrazinecarboxamide) is an orally bioavailable nucleoside analog that selectively inhibits the PB1 subunit of the RNA-dependent RNA polymerases of influenza with activity against a range of other RNA viruses. Favipiravir has been studied in humans initially for influenza and subsequently for emerging pathogens, including Ebola and COVID-19.

Given *in vitro* data against SARS-CoV-2 and the ability to dose orally, there has been interest in the use of favipirivir for the treatment of COVID-19. In the first study, 3 arms (1800 mg BID x 2 doses then 800 mg BID (high dose) vs. 1600 mg BID x 2 doses then 600 mg BID (low dose) vs. placebo) were studied in hospitalized COVID-19 patients in Russia. Favipiravir was associated with more rapid clearance of PCR and resolution of fever. In the second open-label study, 89 Japanese patients were randomized to early vs late therapy for asymptomatic or mild COVID-19 using high dose favipirivir. Therapy was not associated with a difference in viral clearance (n = 69 evaluable patients) or a trend to faster defervescence (n = 30 evaluable patients). In the last study, 156 Japanese hospitalized COVID-19 patients were randomized to receive high dose favipirivir vs. placebo. Favipiriavir was associated with more rapid alleviation of symptoms and PCR negativity (11.9 vs. 14.7 days). None of the studies included PK assessments of favipiravir. For more details, read the link given below.

Reference

https://www.thelancet.com/journals/ebiom/article/PIIS2352-3964(20)30580-6/fulltext

A breath of fresh air – the potential for COVID-19 breath diagnostics

As the world continues to grapple with the ongoing SARS-CoV-2 pandemic, it remains clear that frequent and widespread virus testing is a valuable tool to understand disease spread and to guide public health actions by communities and governments. To date, most traditional diagnostic tests continue to rely on established polymerase chain reaction

(PCR) technologies, which have proven to be quite robust as a tool for mass screening and remain the gold standard within modern medicine. When employed using standardized protocols, PCR typically has a high accuracy and high specificity (eg, low false positives and low false negatives). Early in the pandemic, there were challenges to quickly establish and distribute the best testing methods. Once resolved, the test was widely and successfully rolled out in protocols across the world. However, other challenges have emerged when using this as a tool to combat COVID-19 spread. For one, there are known sampling issues with nasopharyngeal PCR tests. While PCR itself is incredibly robust, it relies on collecting samples of actively amplifying viral genetic material. Though uncommon, it is possible to “miss” swabbing an area with active viral loads, which leads to a false-negative test result. There have been many more issues with the operational logistics and product supply chains that have strained testing systems during this public health crisis. The liquid reagents needed for the PCR test and the nasal swabs are in high demand, thus limiting availability in some locations causing alterations to planned testing protocols. Finally, although PCR is very reliable, there can be a significant time delay between sampling and when the results are available – hours-to-days, depending on processing capabilities of the test site. For more details, read the link given below.

Reference

https://www.thelancet.com/journals/ebiom/article/PIIS2352-3964(20)30559-4/fulltext

Publication Date: Jan 05, 2021

Endemic SARS-CoV-2 will maintain post-pandemic immunity

COVID-19 vaccinations have started, and will stop the pandemic. Citing recent data that are in line with immunological knowledge and predictions, combined with insights of common cold coronaviruses, we here set out the case that the maintenance of population immunity will not depend on continued vaccinations but on the endemic presence of SARS-CoV-2. For more details, read the link given below.

Reference

https://www.nature.com/articles/s41577-020-00493-9

Publication Date: Jan 04, 2021

SARS-CoV-2 structural features may explain limited neutralizing-antibody responses

Neutralizing antibody responses of SARS-CoV-2-infected patients may be low and of short duration. It was proposed here that coronaviruses employ a structural strategy to avoid strong and enduring antibody responses. Other viruses induce optimal and long-lived neutralizing antibody responses, thanks to 20 or more repetitive, rigid antigenic epitopes, spaced by 5–10 nm, present on the viral surface. Such arrays of repetitive and highly organized structures are recognized by the immune system as pathogen-associated structural patterns (PASPs), which are characteristic for pathogen surfaces. In contrast, coronaviruses are large particles with long spikes (S protein) embedded in a fluid membrane. Therefore, the neutralizing epitopes (which are on the S protein) are loosely “floating” and widely spaced by an average of about 25 nm. Consequently, recruitment of complement is poor and stimulation of B cells remains suboptimal, offering an explanation for the inefficient and short-lived neutralizing antibody responses. For more details, read the link given below.

Reference

https://www.nature.com/articles/s41541-020-00264-6