COVID-19 Evidence Support Team
EVIDENCE SEARCH REPORT

Review Question: What is the epidemiology of the omicron variant and its impact on health care?
Context: Split from variant ongoing search/review
Review Code: EOC211220v010 ESR  Complete Date: March 4, 2022

Librarian Notes & Comments

Hello,

Attached are search results for the omicron epidemiology alerts dated February 25 to March 4 2022.

In addition to the 91 references gathered by alerts this past week, we found an additional 16 references not picked up by the alerts (handsearched).

Also, we are noticing a decline in the number of articles and grey literature sources continuing to provide timely information on this topic.

Let us know if there are any questions or concerns,
Lukas & Mark

Disclaimer
This information is provided as a service by the Saskatchewan Health Authority and University of Saskatchewan Libraries. Professional librarians conduct searches of the literature. Results are subject to the limitations of the databases and the specificity, broadness and appropriateness of the search parameters presented by the requester. The Libraries do not represent in any matter that retrieved citations are complete, accurate or otherwise to be relied upon. The search results are only valid as of the date and time at which the search is conducted. The Libraries do not accept responsibility for any loss or damage arising from the use of, or reliance on, search results.
Search Results: Guidelines, Summaries & Other Grey Literature

Manitoba Government | Ministry of Health


Yukon Government | Ministry of Health


Ontario Government | Public Health Ontario


Health Canada

  - Variants of Concern: https://health-infobase.canada.ca/covid-19/epidemiological-summary-covid-19-cases.html#VOC

COVID-19 Critical Intelligence Unit


UK Health Security Agency


WHO.int


Yale Medicine (Blog)

CIDRAP


CTV News

- Four cases of BA.2 Omicron subvariant found in Manitoba. 25 February 2022. https://winnipeg.ctvnews.ca/four-cases-of-ba-2-omicron-subvariant-found-in-manitoba-1.5796544

Search Results: Journal Articles (includes preprints) – HANDSEARCHED

Sorted by newest-oldest.

   ABSTRACT: The loosening of COVID-19 policies and shortening duration of precautions signal the emergence of what some call the "inevitability camp": those who believe everyone will contract the rapidly spreading omicron variant, thereby generating herd immunity. There is one major problem with this view. It is becoming increasingly apparent that 14% (estimated range 2%-30%) of those infected with omicron will develop long COVID, a prolonged set of neurological and physical maladies that have haunted some people since the pandemic began in 2020.

   URL: https://doi.org/10.1056/NEJMoa2119451
   DOI: 10.1056/NEJMoa2119451

   10.1093/jtm/taac021.
   ABSTRACT: We identified the U.S. airports and metropolitan areas, particularly New York City, Miami, and Los Angeles, that were the most likely locations of importation and domestic spread of Omicron from South Africa. Vaccination coverage suggested that several cities in Georgia, Texas, and Utah were particularly vulnerable to public health impacts.
   URL: https://www.ncbi.nlm.nih.gov/pubmed/35234894
   DOI: 10.1093/jtm/taac021
   10.1093/jtm/taac021.

   DOI: 10.15585/mmwr.mm7109e1
10.1002/uog.24893.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35229932
DOI: 10.1002/uog.24893
10.1002/uog.24893.


ABSTRACT: BACKGROUND The SARS-CoV-2 Omicron (B.1.1.529) variant has two main sub-lineages, BA.1 and BA.2 with significant genetic distance between them. This study investigated protection of infection with one sub-lineage against reinfection with the other sub-lineage in Qatar during a large BA.1 and BA.2 Omicron wave, from December 19, 2021 to February 21, 2022.METHODS Two national matched, retrospective cohort studies were conducted to estimate effectiveness of BA.1 infection against reinfection with BA.2 (N=20,197; BA.1-against-BA.2 study), and effectiveness of BA.2 infection against reinfection with BA.1 (N=100,925; BA.2-against-BA.1 study). Associations were estimated using Cox proportional-hazards regression models.RESULTS In the BA.1-against-BA.2 study, cumulative incidence of infection was estimated at 0.03% (95% CI: 0.01-0.07%) for the BA.1-infected cohort and at 0.62% (95% CI: 0.51-0.75%) for the uninfected-control cohort, 15 days after the start of follow-up. Effectiveness of BA.1 infection against reinfection with BA.2 was estimated at 94.9% (95% CI: 88.4-97.8%). In the BA.2-against-BA.1 study, cumulative incidence of infection was estimated at 0.03% (95% CI: 0.02-0.04%) for the BA.2-infected cohort and at 0.17% (95% CI: 0.15-0.21%) for the uninfected-control cohort, 15 days after the start of follow-up. Effectiveness of BA.2 infection against reinfection with BA.1 was estimated at 85.6% (95% CI: 77.4-90.9%).CONCLUSIONS Infection with an Omicron sub-lineage appears to induce strong, but not full protection against reinfection with the other sub-lineage, for at least several weeks after the initial infection.Competing Interest StatementThe authors have declared no competing interest.Funding StatementThe authors are grateful for institutional salary support from the Biomedical Research Program and the Biostatistics, Epidemiology, and Biomathematics Research Core, both at Weill Cornell Medicine-Qatar, as well as for institutional salary support provided by the Ministry of Public Health, Hamad Medical Corporation, and Sidra Medicine. The authors are also grateful for the Qatar Genome Programme and Qatar University Biomedical Research Center for institutional support for the reagents needed for the viral genome sequencing. The funders of the study had no role in study design, data collection, data analysis, data interpretation, or writing of the article. Statements made herein are solely the responsibility of the authors.Author DeclarationsI confirm all relevant ethical guidelines have been followed, and any necessary IRB and/or ethics committee approvals have been obtained.YesThe details of the IRB/oversight body that provided approval or exemption for the research described are given below: Hamad Medical Corporation and Weill Cornell Medicine-Qatar Institutional Review Boards approved this retrospective study with a waiver of informed consent.I confirm that all necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived, and that any patient/participant/sample identifiers included were not known to anyone (e.g., hospital staff, patients or participants themselves) outside the research group so cannot be used to identify individuals.YesI understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance).YesI have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable.YesThe dataset of this study is a property of the Qatar Ministry of Public Health that was provided to the researchers through a restricted-access agreement that prevents sharing the dataset with a third party or publicly. Future access to this dataset can be considered through a direct application for data access to Her Excellency the Minister of Public Health.
Evidence Search Report: EOC211220v010 ESR

(https://www.moph.gov.qa/english/Pages/default.aspx). Aggregate data are available within the manuscript and its Supplementary information.

URL: http://medrxiv.org/content/early/2022/02/25/2022.02.24.22271440.abstract
DOI: 10.1101/2022.02.24.22271440


Evidence Search Report: EOC211220v010 ESR

URL: https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2022.27.9.2200121


ABSTRACT: IMPORTANCE: Prior infection and vaccination both contribute to population-level SARS-CoV-2 immunity. Population-level immunity will influence future transmission and disease burden. OBJECTIVE: To estimate population immunity to prevalent SARS-CoV-2 variants in the United States over the course of the epidemic until December 1, 2021, and how this changed with the introduction of the Omicron variant. Design, settings, participants: We used daily SARS-CoV-2 infection estimates and vaccination coverage data for each US state and county. We estimated relative rates of vaccination conditional on previous infection status using the Census Bureaus Household Pulse Survey. We used published evidence on natural and vaccine-induced immunity, including waning and immune escape. We used a Bayesian model to synthesize evidence and estimate population immunity outcomes. Main Outcomes and Measures: The fraction of the population with (i) immunological exposure to SARS-CoV-2 (ever infected with SARS-CoV-2 and/or received one or more doses of a COVID-19 vaccine), (ii) effective protection against infection, and (iii) effective protection against severe disease, for each US state and county from January 1, 2020, to December 1, 2021. RESULTS: The estimated percentage of the US population with a history of SARS-CoV-2 infection or vaccination as of December 1, 2021, was 88.2% (95%CrI: 83.6%-93.5%), compared to 24.9% (95%CrI: 18.5%-34.1%) on January 1, 2021. State-level estimates for December 1, 2021, ranged between 76.9% (95%CrI: 67.6%-87.6%, West Virginia) and 94.4% (95%CrI: 91.2%-97.3%, New Mexico). Accounting for waning and immune escape, the effective protection against the Omicron variant on December 1, 2021, was 21.8% (95%CrI: 20.7%-23.4%) nationally and ranged between 14.4% (95%CrI: 13.2%-15.8%, West Virginia), to 26.4% (95%CrI: 25.3%-27.8%, Colorado). Effective protection against severe disease from Omicron was 61.2% (95%CrI: 59.1%-64.0%) nationally and ranged between 53.0% (95%CrI: 47.3%-60.0%, Vermont) and 65.8% (95%CrI: 64.9%-66.7%, Colorado). CONCLUSIONS AND RELEVANCE: While over three-quarters of the US population had prior immunological exposure to SARS-CoV-2 via vaccination or infection on December 1, 2021 only a fifth of the population was estimated to have effective protection to infection with the immune- evading Omicron variant.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34981078
DOI: 10.1101/2021.12.23.21268272


ABSTRACT: The SARS-CoV-2 Omicron variant (B.1.1.529), classified as Variant of Concern by the World Health Organization on 26 November 2021, emerged in South Africa in November 2021, and has later been identified worldwide, raising serious concerns. A real-time RT-PCR assay was designed for the rapid screening of the Omicron variant, targeting characteristic mutations of the spike gene. After assessing the specificity of the assay, the real-time PCR was used to test 737 sewage samples collected throughout Italy (19/21 Regions) between 11 November and 25 December 2021, with the aim of assessing the spread of the new variant in Italy. Positive samples were also tested with a real-time RT-PCR developed by the European Commission, Joint Research Centre (JRC), and through nested RT-PCR followed by Sanger
sequencing. Overall, 115 samples tested positive for Omicron SARS-CoV-2 variant. The first occurrence of Omicron in sewage was detected on 7 December, in Veneto, North Italy. Later on, the variant spread extremely fast, with prevalence of positive wastewater samples rising from 1.0% (1/104 samples) in the week 5-11 December, to 17.5% (25/143 samples) in the week 12-18, to 65.9% (89/135 samples) in the week 19-25, in line with the increase in cases of infection with the Omicron variant observed during December in Italy. Similarly, the number of Regions/Autonomous Provinces in which the variant was detected increased from one in the first week, to 11 in the second, and to 17 in the last one. The presence of the Omicron variant was confirmed by the JRC real-time RT-PCR in 79.1% of the positive samples and by Sanger sequencing thorough detection of key variant mutations. In conclusion, we designed an RT-qPCR assay capable to distinguish Omicron variant from other SARS-CoV-2 variants which can be successfully used for clinical samples, as well as for the purpose of wastewater-based epidemiology.

DOI: 10.2139/ssrn.4044451


10.1038/d41586-022-00510-y.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35228738
DOI: 10.1038/d41586-022-00510-y
10.1038/d41586-022-00510-y.

14. Niemann CU, da Cunha-Bang C, Helleberg M, et al. Patients with CLL have similar high risk of death upon the omicron variant of COVID-19 as previously during the pandemic. medRxiv. 2022:2022.03.01.22271685. DOI: 10.1101/2022.03.01.22271685

ABSTRACT: Previous studies have shown that patients with chronic lymphocytic leukemia (CLL) and coronavirus disease 2019 (COVID-19) have high mortality rates. The omicron variant has been reported to give milder disease in the general population, but outcomes of infections with the omicron variant among immunocompromised patients have not previously been reported. In a population-based cohort we assessed rates of hospitalizations, ICU-admissions, and 30-day all-cause mortality among all patients with CLL from Eastern Denmark testing positive for severe adult respiratory syndrome coronavirus 2 (SARS-CoV-2) in time periods before and after dominance of the omicron variant. Rates of hospitalizations and ICU-admissions declined significantly, whereas 30-day mortality remained as high as 23% in the period with dominance of the omicron sublineage BA.2 variant. Thus, patients with CLL in general and in particular those above 70 years of age with one or more comorbidities should be considered for closer monitoring and pre-emptive antiviral therapy upon a positive SARS-CoV-2 test. Competing Interest Statement CUN received research funding and/or consultancy fees outside this work from Abbvie, Janssen, AstraZeneca, Beigene, Roche, CSL Behring, Takeda and Octapharma. CB received consultancy fees outside of this work from AstraZeneca. The remaining authors declare no conflicts of interest. Funding Statement The study was supported by a COVID-19 grant from the Ministry of Higher Education and Science (0238-00006B) and the Danish National Research Foundation (DNRF126) by the Danish Cancer Society and the EU funded CLL-CLUE for CUN. CB received funding from Weimanns Legat. The Capital Region of Denmark, Center for Economy, provided data extracts from the EHR system. Author Declarations I confirm all relevant ethical guidelines have been followed, and any necessary IRB and/or ethics committee approvals have been obtained. Yes The details of the IRB/oversight body that provided approval or exemption for the research described are given below: The Ethics Committee of the Capital Region of Denmark gave ethical approval for this work, Journal-nr.: H-20026502.1 I confirm that all necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived, and that any patient/participant/sample identifiers included were not known to anyone (e.g., hospital staff, patients or participants themselves) outside the research group so cannot be used to identify individuals. Yes I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes I have followed all appropriate research
reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes All data produced in the present study are available upon reasonable request to the authors with the restrictions that data privacy regulations put on the data set.

URL: http://medrxiv.org/content/early/2022/03/02/2022.03.01.22271685.abstract
DOI: 10.1101/2022.03.01.22271685

15. Sidik SM. Had Omicron? You're unlikely to catch its rising variant. Nature. 2022. DOI: 10.1038/d41586-022-00558-w
10.1038/d41586-022-00558-w.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35217841
DOI: 10.1038/d41586-022-00558-w.
10.1038/d41586-022-00558-w.


ABSTRACT: Objective To assess the risk of death involving COVID-19 following infection from Omicron (B.1.1.539/BA.1) relative to Delta (B.1.617.2). Design Retrospective cohort study. Setting England, UK, 1 December 2021 to 25 January 2022. Participants 1,035,163 people aged 18-100 years who tested positive for SARS-CoV-2 in the national surveillance programme, and had an infection identified as either Omicron- or Delta compatible. Main outcome measures Death involving COVID-19 as identified from death certification records. The exposure of interest was the SARS-CoV-2 variant identified from NHS Test and Trace PCR positive tests taken in the community (pillar 2) and analysed by Lighthouse laboratories. Cause-specific Cox proportional hazard regression models were adjusted for sex, age, vaccination status, previous infection, calendar time, ethnicity, Index of Multiple Deprivation rank, household deprivation, university degree, keyworker status, country of birth, main language, region, disability, and comorbidities. Additionally, we tested for interactions between variant and sex, age, vaccination status and comorbidities. Results The risk of death involving COVID-19 was 67% lower for Omicron compared to Delta and the reduction in the risk of death involving COVID-19 for Omicron compared to Delta was more pronounced in males than in females and in people under 70 years old than in people aged 70 years or over. Regardless of age, reduction of the risk of death from Omicron relative to Delta more was more pronounced in people who had received a booster than in those having received only two doses. Conclusions Our results support early work showing the relative reduction in severity of Omicron compared to Delta in terms of hospitalisation and extends this research to assess COVID-19 mortality. Our work also highlights the importance of the vaccination booster campaign, where the reduction in risk of death involving COVID-19 is most pronounced in individuals who had received a booster. What is already known on this topic The Omicron variant, which refers to the whole lineage (BA.1, BA.2, BA.3) had already been shown to be more transmissible than the Delta variant, but there is emerging evidence suggests that the risk of hospitalisation and risk of death within 28 days after a SARS-CoV-2 test is lower. However, with a highly transmissible infection and high levels of population testing, definition of death within 28 days is more likely to be susceptible to misclassification bias due to asymptomatic or co- incidental infection. There is no study so far comparing the risk of COVID-19 death as identified from death certification records, with the cause of death assessed by the physician who attended the patient in the last illness. What this study adds Using data from a large cohort of COVID-19 infections that occurred in December 2021, we examined the difference in the risk COVID-19 death, as identified from death certification records, between the Delta and Omicron BA.1 variant. Our study shows that risk of death involving COVID-19 was reduced by 67% following infection with the Omicron BA.1 variant relative to the Delta variant after adjusting for a wide range of potential confounders, including vaccination status and comorbidities. Importantly, we found that the relative risk of COVID-19 mortality following Omicron versus Delta infection varied by age and sex, with lower relative risk in younger individuals and for males than females. The reduction in risk of death involving COVID-19 was also most pronounced in individuals who had received a booster. Competing Interest Statement The authors have declared no competing interests.
Evidence Search Report

Interest. Funding Statement

No funding

Author Declarations

I confirm all relevant ethical guidelines have been followed, and any necessary IRB and/or ethics committee approvals have been obtained. Yes

The details of the IRB/oversight body that provided approval or exemption for the research described are given below: Ethical approval was obtained from the National Statistician’s Data Ethics Advisory Committee (NSDEC(20)12). I confirm that all necessary patient/participant consent has been obtained and the appropriate institutional forms have been archived, and that any patient/participant/sample identifiers included were not known to anyone (e.g., hospital staff, patients or participants themselves) outside the research group so cannot be used to identify individuals. Yes

I understand that all clinical trials and any other prospective interventional studies must be registered with an ICMJE-approved registry, such as ClinicalTrials.gov. I confirm that any such study reported in the manuscript has been registered and the trial registration ID is provided (note: if posting a prospective study registered retrospectively, please provide a statement in the trial ID field explaining why the study was not registered in advance). Yes

I have followed all appropriate research reporting guidelines and uploaded the relevant EQUATOR Network research reporting checklist(s) and other pertinent material as supplementary files, if applicable. Yes

Information on data availability and access is available via the Secure Research Service: https://www.ons.gov.uk/aboutus/whatwedo/statistics/requestingstatistics/approvedresearcherscheme

URL: http://medrxiv.org/content/early/2022/02/25/2022.02.24.22271466.abstract

DOI: 10.1101/2022.02.24.22271466

Search Results: Results from Ovid Alerts: 25 February 2022 – 04 March 2022

Sorted by newest-oldest.


ABSTRACT: INTRODUCTION: The coronavirus disease 2019 (COVID-19) first reported in Wuhan, China in December 2019 is a global pandemic that is threatening the health and wellbeing of people worldwide. To date there have been more than 274 million reported cases and 5.3 million deaths. The Omicron variant first documented in the City of Tshwane, Gauteng Province, South Africa on 9 November 2021 led to exponential increases in cases and a sharp rise in hospital admissions. The clinical profile of patients admitted at a large hospital in Tshwane is compared with previous waves. METHODS: 466 hospital COVID-19 admissions since 14 November 2021 were compared to 3962 admissions since 4 May 2020, prior to the Omicron outbreak. Ninety-eight patient records at peak bed occupancy during the outbreak were reviewed for primary indication for admission, clinical severity, oxygen supplementation level, vaccination and prior COVID-19 infection. Provincial and city-wide daily cases and reported deaths, hospital admissions and excess deaths data were sourced from the National Institute for Communicable Diseases, the National Department of Health and the South African Medical Research Council. RESULTS: For the Omicron and previous waves, deaths and ICU admissions were 4.5% vs 21.3% (p<0.00001), and 1% vs 4.3% (p<0.00001) respectively; length of stay was 4.0 days vs 8.8 days; and mean age was 39 years vs 49.8 years. Admissions in the Omicron wave peaked and declined rapidly with peak bed occupancy at 51% of the highest previous peak during the Delta wave. Sixty two (63%) patients in COVID-19 wards had incidental COVID-19 following a positive SARS-CoV-2 PCR test . Only one third (36) had COVID-19 pneumonia, of which 72% had mild to moderate disease. The remaining 28% required high care or ICU admission. Fewer than half (45%) of patients in COVID-19 wards required oxygen supplementation compared to 99.5% in the first wave. The death rate in the face of an exponential increase in cases during the Omicron wave at the city and provincial levels shows a decoupling of cases and deaths compared to previous waves, corroborating the clinical findings of decreased severity of disease seen in patients admitted to the Steve Biko Academic Hospital. CONCLUSION: There was decreased severity of COVID-19 disease in the Omicron-driven fourth wave in the City of Tshwane, its first global epicentre.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34971823


ABSTRACT: Herein, we report a case of an Italian male infected by Delta sublineage AY.4 harboring an atypical deletion, leading to a N gene target failure (NGTF) by a commercial molecular assay for SARS-CoV-2 diagnosis (Allplex(TM) SARS-CoV-2 Assay, Seegene). A 59-year-old unvaccinated patient was hospitalized for pulmonary embolism, with first negative results obtained by both molecular and antigen tests. After several days of viral negativity, he presented positive results for E and RdRP/S genes, but negative in N gene. Negativity in N gene was repeatedly confirmed in the following days. Suspecting an infection by the Omicron variant, SARS-CoV-2 genome sequencing was rapidly performed from nasopharyngeal swab by MiSeq and revealed the presence of the Delta sublineage AY.4 variant with an atypical deletion of six nucleotides, leading to G214-G215 deletion in the Nucleocapsid, thus responsible for NGTF. The analysis of GISAI D sequences (N = 2,618,373 12 January 2022) showed that G214-G215 deletion is rarely occurring in most circulating Delta lineages and sublineages in the globe and Europe, with an overall prevalence never exceeding 0.2%. Hence, this study highlights the importance to perform SARS-CoV-2 sequencing and to characterize novel mutations/deletions that could jeopardize the proper interpretation of molecular diagnostic tests. Based on these assumptions, the role of deletions in the recently identified Omicron variant deserves further investigation.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35208724
DOI: 10.3390/microorganisms10020268


ABSTRACT: Coronavirus disease 2019 (COVID-19) first emerged in Wuhan city in December 2019, and became a grave global concern due to its highly infectious nature. The Severe Acute Respiratory Coronavirus-2, with its predecessors (i.e., MERS-CoV and SARS-CoV) belong to the family of Coronaviridae. Reportedly, COVID-19 has infected 344,710,576 people around the globe and killed nearly 5,598,511 persons in the short span of two years. On November 24, 2021, B.1.1.529 strain, later named Omicron, was classified as a Variant of Concern (VOC). SARS-CoV-2 has continuously undergone a series of unprecedented mutations and evolved to exhibit varying characteristics. These mutations have largely occurred in the spike (S) protein (site for antibody binding), which attribute high infectivity and transmissibility characteristics to the Omicron strain. Although many studies have attempted to understand this new challenge in the COVID-19 strains race, there is still a lot to be demystified. Therefore, the purpose of this review was to summarize the structural or virologic characteristics, burden, and epidemiology of the Omicron variant and its potential to evade the immune response.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35208905
DOI: 10.3390/microorganisms10020451


ABSTRACT: The SARS-CoV-2 Omicron variant has a growth advantage over the Delta variant because of higher transmissibility, immune evasion or shorter serial interval. Using S gene target failure (SGTF) as indication for Omicron BA.1, we identified 908 SGTF and 1,621 non-SGTF serial intervals in the same period. Within households, the mean serial interval for SGTF cases was 0.2-0.6 days shorter than for non-SGTF cases. This suggests that the growth advantage of Omicron is partly due to a shorter serial interval.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35144721
DOI: 10.2807/1560-7917.ES.2022.27.6.2200042

ABSTRACT: In 2019, the Canadian Government released a national dementia strategy that identified the need to address the health inequity (e.g., avoidable, unfair, and unjust differences in health outcomes) and improve the human rights of people living with dementia. However, the novel coronavirus disease 2019 (COVID-19) pandemic is having an inequitable impact on people with dementia in terms of mortality and human rights violations. As the new Omicron COVID-19 variant approaches its peak, our commentary highlights the need for urgent action to support people living with dementia and their care partners. More specifically, we argue that reducing COVID-19 inequities requires addressing underlying population-level factors known as the social determinants of health. Health disparities cannot be rectified merely by looking at mortality rates of people with dementia. Thus, we believe that improving the COVID-19 outcomes of people with dementia requires addressing key determinants such as where people live, their social supports, and having equitable access to healthcare services. Drawing on Canadian-based examples, we conclude that COVID-19 policy responses to the pandemic must be informed by evidence-informed research and collaborative partnerships that embrace the lived experience of diverse people living with dementia and their care partners.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35239172
DOI: 10.17269/s41997-022-00618-8


ABSTRACT: The B.1.1.529 (Omicron) variant, first detected in November 2021, was responsible for a surge in U.S. infections with SARS-CoV-2, the virus that causes COVID-19, during December 2021-January 2022 (1). To investigate the effectiveness of prevention strategies in household settings, CDC partnered with four U.S. jurisdictions to describe Omicron household transmission during November 2021-February 2022. Persons with sequence-confirmed Omicron infection and their household contacts were interviewed. Omicron transmission occurred in 124 (67.8%) of 183 households. Among 431 household contacts, 227 were classified as having a case of COVID-19 (attack rate [AR] = 52.7%).(dagger) The ARs among household contacts of index patients who had received a COVID-19 booster dose, of fully vaccinated index patients who completed their COVID-19 primary series within the previous 5 months, and of unvaccinated index patients were 42.7% (47 of 110), 43.6% (17 of 39), and 63.9% (69 of 108), respectively. The AR was lower among household contacts of index patients who isolated (41.2%, 99 of 240) compared with those of index patients who did not isolate (67.5%, 112 of 166) (p-value <0.01). Similarly, the AR was lower among household contacts of index patients who ever wore a mask at home during their potentially infectious period (39.5%, 88 of 223) compared with those of index patients who never wore a mask at home (68.9%, 124 of 180) (p-value <0.01). Multicomponent COVID-19 prevention strategies, including up-to-date vaccination, isolation of infected persons, and mask use at home, are critical to reducing Omicron transmission in household settings.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35238860
DOI: 10.15585/mmwr.mm7109e1


ABSTRACT: Omicron is an emerging SARS-CoV-2 variant, evolved from the Indian delta variant B.1.617.2, which is currently infecting worldwide. The spike glycoprotein, an important molecule in the pathogenesis and transmissions of SARS-CoV-2 variants, especially omicron B.1.1.529, shows 37 mutations distributed over the trimeric protein domains. Notably, fifteen of these mutations reside in the receptor-binding domain of the spike glycoprotein, which may alter transmissibility and infectivity. Additionally, the omicron spike evades neutralization more efficiently than the delta spike. Most of the therapeutic antibodies are ineffective against the omicron variant, and double immunization with BioNTech-Pfizer (BNT162b2) might not adequately protect against severe disease induced by omicron B.1.1.529. So far, no efficient antiviral drugs are available against omicron. The present study identified the promising inhibitors from seaweed's bioactive compounds to inhibit the omicron variant B.1.1.529. We have also compared the seaweed's
compounds with the standard drugs ceftriaxone and cefuroxime, which were suggested as beneficial antiviral drugs in COVID-19 treatment. Our molecular docking analysis revealed that caffeic acid hexoside (-6.4 kcal/mol; RMSD = 2.382 Å) and phloretin (-6.3 kcal/mol; RMSD = 0.061 Å) from Sargassum wightii (S. wightii) showed the inhibitory effect against the crucial residues ASN417, SER496, TYR501, and HIS505, which are supported for the inviolable omicron and angiotensin-converting enzyme II (ACE2) receptor interaction. Cholestan-3-ol, 2-methylene-, (3beta, 5 alpha) (CMBA) (-6.0 kcal/mol; RMSD = 3.074 Å) from Corallina officinalis (C. officinalis) manifested the strong inhibitory effect against the omicron RBD mutated residues LEU452 and ALA484, was magnificently observed as the essential residues in Indian delta variant B.1.617.2 previously. The standard drugs (ceftriaxone and cefuroxime) showed no or less inhibitory effect against RBD of omicron B.1.1.529. The present study also emphasized the pharmacological properties of the considered chemical compounds. The results could be used to develop potent seaweed-based antiviral drugs and/or dietary supplements to treat omicron B.1.1529-infected patients.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35200677
DOI: 10.3390/md20020148

URL: https://www.ncbi.nlm.nih.gov/pubmed/35108465
DOI: 10.1056/NEJMp2119682

ABSTRACT: In line with previous instalments of analysis from this ongoing study to monitor 'Covid Seroprevalence' among blood donors in South Africa, we report on analysis of 3395 samples obtained from 8 to 12 November 2021 in all provinces of South Africa except the Western Cape. As in our previous analyses, we see no evidence of age and sex dependence of prevalence, but substantial variation by province, and by race within each province, from which we generated provincial total point estimates (EC-74%; FS-75%; GP-68%; ZN-73%; LP-66; MP-73%; NC-63%; NW-81%) and a 'South Africa minus Western Cape' national prevalence estimate of 71% (95%CI 69-74%). We note that sample collection occurred just before the omicron variant driven wave in South Africa, but otherwise present these results without significant interpretation.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35194594
DOI: 10.21203/rs.3.rs-1359658/v1

URL: https://www.ncbi.nlm.nih.gov/pubmed/35177843
DOI: 10.1038/d41586-022-00471-2

ABSTRACT: Many people want to know when the COVID-19 pandemic will end and life will return to normal. This question is highly elusive and distinct predictions have been proposed. In this study, the global mortality and case fatality rate of COVID-19 were analyzed using nonlinear regression. The analysis showed that the COVID-19 pandemic could terminate in 2022, but COVID-19 could be one or two times more deadly than seasonal influenza by 2023. The prediction considered the possibility of the emergence of new variants of SARS-CoV-2 and was supported by the features of the Omicron variant and other facts. As the herd immunity against COVID-19 established through natural infections and mass vaccination is distinct among countries, COVID-19 could be more or less deadly in some countries in the coming years than the prediction. Although the future of COVID-19 will have multiple possibilities, this statistics-based prediction could aid to make proper decisions and establish an example on the prediction of infectious diseases.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35150458

**ABSTRACT:** Mass COVID-19 vaccination, as the last resort to bring society to a new normal, has been rapidly rolled out in the US. However, because of the lifting of international travel restrictions, amid the many uncertainties induced by the emerging B.1.1.529 variant, it remains unclear about the timeline of reaching herd immunity and when our daily life will return to normalcy. Since access to a vaccine is an important predicate to the achievement of herd immunity, we articulate the vaccine access issue as the degree of fit between patients and the healthcare system in five dimensions: availability, accessibility, accommodation, affordability, and acceptability. These five dimensions can be adopted in existing health practice and policy to elucidate effective strategies for raising COVID-19 vaccination rates and improving vaccine equity in the fight against the new variant.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/34922789

**DOI:** 10.1016/j.vaccine.2021.11.096


**ABSTRACT:** Airborne transmission of SARS-CoV-2 has been increasingly recognized in the outbreak of COVID-19, especially with the Omicron variant. We investigated an outbreak due to Omicron variant in a restaurant. Besides epidemiological and phylogenetic analyses, the secondary attack rates of customers of restaurant-related COVID-19 outbreak before (Outbreak R1) and after enhancement of indoor air dilution (Outbreak R2) were compared. On 27th December 2021, an index case stayed in restaurant R2 for 98 min. Except for 1 sitting in the same table, six other secondary cases sat in 3 corners at 3 different zones, which were served by different staff. The median exposure time was 34 min (range: 19-98 min). All 7 secondary cases were phylogenetically related to the index. Smoke test demonstrated that the airflow direction may explain the distribution of secondary cases. Compared with an earlier COVID-19 outbreak in another restaurant R1 (19th February 2021), which occurred prior to the mandatory enhancement of indoor air dilution, the secondary attack rate among customers in R2 was significantly lower than that in R1 (3.4%, 7/207 vs 28.9%, 22/76, p<0.001). Enhancement of indoor air dilution through ventilation and installation of air purifier could minimize the risk of SARS-CoV-2 transmission in the restaurants. Copyright © 2022 Elsevier B.V.

**DOI:** 10.1016/j.jhazmat.2022.128504


**ABSTRACT:** Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), has spread worldwide. Many variants of SARS-CoV-2 have been reported, some of which have increased transmissibility and/or reduced susceptibility to vaccines. There is an urgent need for variant phenotyping for epidemiological surveillance of circulating lineages. Whole-genome sequencing is the gold standard for identifying SARS-CoV-2 variants, which constitutes a major bottleneck in developing countries. Methodological simplification could increase epidemiological surveillance feasibility and efficiency. We designed a novel multiplex real-time reverse transcriptase PCR (RT-PCR) to detect SARS-CoV-2 variants with 5 gene mutations. This multiplex PCR typing method was established to detect 9 mutations with specific primers and probes (DeltaHV 69/70, K417T, K417N, L452R, E484K, E484Q, N501Y, P681H, and P681R) against the receptor-binding domain of the spike protein of SARS-CoV-2 variants. In silico analyses showed high specificity of the assays. Variants of concern (VOC) typing results were found to be highly specific for our intended targets, with no cross-reactivity observed with other upper respiratory viruses. The PCR-based typing methods were further validated using whole-genome sequencing and a commercial kit that was applied to clinical samples of 250 COVID-19 patients from Taiwan. The screening of these samples allowed the identification of epidemic trends by time intervals,
Evidence Search Report: EOC211220v010 ESR


patients. We now emphasise that timing of surgery should include the assessment of baseline and increased risk, optimising vaccination and functional status, and shared decision-making. While these recommendations focus on the omicron variant and current evidence, the principles may also be of relevance to future variants. As further data emerge, these recommendations may be revised.

**ABSTRACT**


**ABSTRACT:** SARS-CoV-2 lineages have diverged into highly prevalent variants termed "variants of concern" (VOCs). Here, we characterized emerging SARS-CoV-2 spike polymorphisms in vitro and in vivo to understand their impact on transmissibility and virus pathogenicity and fitness. We demonstrate that the substitution S:655Y, represented in the gamma and omicron VOCs, enhances viral replication and spike protein cleavage. The S:655Y substitution was transmitted more efficiently than its ancestor S:655H in the hamster infection model and was able to outcompete S:655H in the hamster model and in a human primary airway system. Finally, we analyzed a set of emerging SARS-CoV-2 variants to investigate how different sets of mutations may impact spike processing. All VOCs tested exhibited increased spike cleavage and fusogenic capacity. Taken together, our study demonstrates that the spike mutations present in VOCs that become epidemiologically prevalent in humans are linked to an increase in spike processing and virus transmission.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35150638

**DOI:** 10.1016/j.chom.2022.01.006


**ABSTRACT:** Background: The increase in SARS-CoV-2 infections in December 2021 in the United States was driven primarily by the Omicron variant which largely displaced the Delta over a three week span. Outcomes from infection with the Omicron remain uncertain. We evaluate whether clinical outcomes and viral loads differ between Delta and Omicron infections during the period when both variants were co-circulating.

**Methods:** Remnant clinical specimens from patients that tested positive for SARS-CoV-2 after standard of care testing between the last week of November and the end of December 2021 were used for whole viral genome sequencing. Cycle threshold values (Ct) for viral RNA, the presence of infectious virus, and levels of respiratory IgG were measured, and clinical outcomes were obtained. Differences in each measure were compared between variants stratified by vaccination status. Results: The Omicron variant displaced the Delta during the study period and constituted 95% of the circulating lineages by the end of December 2021. Patients with Omicron infections (N= 1121) were more likely to be vaccinated compared to patients with Delta (N = 910), but were less likely to be admitted, require ICU level care, or succumb to infection regardless of vaccination status. There was no significant difference in Ct values based on the lineage regardless of the vaccination status. Recovery of infectious virus in cell culture was reduced in boosted patients compared to fully vaccinated without a booster and unvaccinated when infected with the Delta lineage. However, in patients with Omicron infections, recovery of infectious virus was not affected by vaccination. Conclusions: Omicron infections of vaccinated individuals are expected, yet admissions are less frequent. Admitted patients might develop severe disease comparable to Delta. Efforts for reducing the Omicron transmission are required as even though the admission risk is lower, the numbers of infections continue to be high. Research in context Evidence before this study: The unprecedented increase in COVID-19 cases in the month of December 2021, associated with the displacement of the Delta variant with the Omicron, triggered a lot of concerns. An understanding of the disease severity associated with infections with Omicron is essential as well as the virological determinants that contributed to its widespread predominance. We searched PubMed for articles published up to January 23, 2022, using the search terms ("Omicron") AND ("Disease severity") as well as ("Omicron") AND ("Viral load") AND/ or ("Cell culture"). Our search yielded 3 main studies that directly assessed the omicron's clinical severity in South Africa, its infectious viral load compared to Delta, and the dynamics of viral RNA
shedding. In South Africa, compared to Delta, Omicron infected patients showed a significant reduction in severe disease. In this study, Omicron and non-Omicron variants were characterized based on S gene target failure using the TaqPath COVID-19 PCR (Thermo Fisher Scientific). In the study from Switzerland that assessed the infectious viral load in Omicron versus Delta, the authors analyzed only 18 Omicron samples that were all from vaccinated individuals to show that compared to Delta, Omicron had equivalent infectious viral titers. The third study that assessed the Omicron viral dynamics showed that the peak viral RNA in Omicron infections is lower than Delta. No published studies assessed the clinical discrepancies of Omicron and Delta infected patients from the US, nor comprehensively assessed, by viral load and cell culture studies, the characteristics of both variants stratified by vaccination status. Added value of this study: To the best of our knowledge, this is the only study to date to compare the clinical characteristics and outcomes after infection with the Omicron variant compared to Delta in the US using variants characterized by whole genome sequencing and a selective time frame when both variant co-circulated. It is also the first study to stratify the analysis based on the vaccination status and to compare fully vaccinated patients who didn't receive a booster vaccination to patients who received a booster vaccination. In addition, we provide a unique viral RNA and infectious virus load analyses to compare Delta and Omicron samples from unvaccinated, fully vaccinated, and patients with booster vaccination. Implications of all the available evidence: Omicron associated with a significant increase in infections in fully and booster vaccinated individuals but with less admissions and ICU level care. Admitted patients showed similar requirements for supplemental oxygen and ICU level care when compared to Delta admitted patients. Viral loads were similar in samples from Omicron and Delta infected patients regardless of the vaccination status. The recovery of infectious virus on cell culture was reduced in samples from patients infected with Delta who received a booster dose, but this was not the case with Omicron. The recovery of infectious virus was equivalent in Omicron infected unvaccinated, fully vaccinated, and samples from patients who received booster vaccination. Funding: NIH/NIAID Center of Excellence in Influenza Research and Surveillance contract HHS N2772201400007C, Johns Hopkins University, Maryland department of health, Centers for Disease Control and Prevention contract 75D30121C11061.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35118480
DOI: 10.1101/2022.01.26.22269927


ABSTRACT: The Omicron variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has high transmissibility and recently swept the globe. Due to the extensive number of mutations, this variant has high level of immune evasion, which drastically reduced the efficacy of existing antibodies and vaccines. Thus, it is important to test an Omicron-specific vaccine, evaluate its immune response against Omicron and other variants, and compare its immunogenicity as boosters with existing vaccine designed against the reference wildtype virus (WT). Here, we generated an Omicron-specific lipid nanoparticle (LNP) mRNA vaccine candidate, and tested its activity in animals, both alone and as a heterologous booster to existing WT mRNA vaccine. Our Omicron-specific LNP-mRNA vaccine elicited strong and specific antibody response in vaccination-naive mice. Mice that received two-dose WT LNP-mRNA, the one mimicking the commonly used Pfizer/Moderna mRNA vaccine, showed a >40-fold reduction in neutralization potency against Omicron variant than that against WT two weeks post second dose, which further reduced to background level >3 months post second dose. As a booster shot for two-dose WT mRNA vaccinated mice, a single dose of either a homologous booster with WT LNP-mRNA or a heterologous booster with Omicron LNP-mRNA restored the waning antibody response against Omicron, with over 40-fold increase at two weeks post injection as compared to right before booster. Interestingly, the heterologous Omicron LNP-mRNA booster elicited neutralizing titers 10-20 fold higher than the homologous WT booster against the Omicron variant, with comparable titers against the Delta variant. All three types of vaccination, including Omicron mRNA alone, WT mRNA homologous booster, and Omicron heterologous booster, elicited broad binding antibody responses against SARS-CoV-2 WA-1, Beta, and Delta variants, as well as other Betacoronavirus species such as SARS-CoV, but not Middle East respiratory syndrome coronavirus (MERS-
CoV). These data provided direct proof-of-concept assessments of an Omicron-specific mRNA vaccination in vivo, both alone and as a heterologous booster to the existing widely-used WT mRNA vaccine form.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35194606
DOI: 10.1101/2022.02.14.480449


ABSTRACT: Emerging SARS-CoV-2 variants of concern (VOC) have been associated with enhanced transmissibility and immune escape. Next-generation sequencing (NGS) of the whole genome is the gold standard for variant identification for surveillance but is time-consuming and costly. Rapid and cost-effective assays that detect SARS-CoV-2 variants are needed. We evaluated Allplex SARS-CoV-2 Master Assay and Variants I Assay to detect HV69/70 deletion, Y144 deletion, E484K, N501Y, and P681H spike mutations in 248 positive samples collected in Kuala Lumpur, Malaysia, between January and May 2021. Spike variants were detected in 78/248 (31.5%), comprising 60 VOC B.1.351 (beta) and 18 B.1.1.7 (alpha). With NGS as reference for 115 samples, the sensitivity for detecting the spike mutations was 98.7% with the Master Assay and 100% with the Variants I Assay. The emergence of beta variants correlated with increasing COVID-19 infections in Malaysia. The prevalence of alpha VOC and lineage B.1.466.2 was low. These assays detect mutations present in alpha, beta and gamma VOCs. Of the VOCs which have subsequently emerged, the assays should detect omicron (B.1.1.529) but not B.1.617.2 (delta). In conclusion, spike variant PCR assays can be used to rapidly monitor selected SARS-CoV-2 VOCs in resource-limited settings, but require updates as new variants emerge.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35026305
DOI: 10.1016/j.jviromet.2022.114462


URL: https://www.ncbi.nlm.nih.gov/pubmed/34850421
DOI: 10.1002/jmv.27491


ABSTRACT: Since the inception of SARS-CoV-2 in December 2019, many variants have emerged over time. Some of these variants have resulted in transmissibility changes of the virus and may also have impact on diagnosis, therapeutics and even vaccines, thereby raising particular concerns in the scientific community. The variants which have mutations in Spike glycoprotein are the primary focus as it is the main target for neutralising antibodies. SARS-CoV-2 is known to infect human through Spike glycoprotein and uses receptor-binding domain (RBD) to bind to the ACE2 receptor in human. Thus, it is of utmost importance to study these variants and their corresponding mutations. Such 12 different important variants identified so far are B.1.1.7 (Alpha), B.1.351 (Beta), B.1.525 (Eta), B.1.427/B.1.429 (Epsilon), B.1.526 (Iota), B.1.617.1 (Kappa), B.1.617.2 (Delta), C.37 (Lambda), P.1 (Gamma), P.2 (Zeta), P.3 (Theta) and the recently discovered B.1.1.529 (Omicron). These variants have 84 unique mutations in Spike glycoprotein. To analyse such mutations, multiple sequence alignment of 77681 SARS-CoV-2 genomes of 98 countries over the period from January 2020 to July 2021 is performed followed by phylogenetic analysis. Also, characteristics of new emerging variants are elaborately discussed. The individual evolution of these mutation points and the respective variants are visualised and their characteristics are also reported. Moreover, to judge the characteristics of the non-synonymous mutation points (substitutions), their biological functions are evaluated by PolyPhen-2 while protein structural stability is evaluated using I-Mutant 2.0.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35123183
DOI: 10.1016/j.intimp.2022.108565

ABSTRACT: Our study focuses on free energy calculations of SARS-CoV-2 spike protein receptor binding motives (RBMs) from wild type and variants of concern (VOCs), with emphasis on SARS-CoV-2 Omicron. Our computational analysis underlines the occurrence of positive selection processes that specify Omicron host adaption and bring changes on the molecular level into context with clinically relevant observations. Our free energy calculation studies regarding the interaction of Omicron’s RBM with human angiotensin converting enzyme 2 (hACE2) indicate weaker binding to the receptor than Alpha’s or Delta’s RBMs. Upon weaker binding, fewer viruses are predicted to be generated in time per infected cell, resulting in a delayed induction of danger signals as a trade-off. Along with delayed immunogenicity and pathogenicity, more viruses may be produced in the upper respiratory tract, explaining enhanced transmissibility. Since in interdependence on the human leukocyte antigen type (HLA type), more SARS-CoV-2 Omicron viruses are assumed to be required to initiate inflammatory immune responses, and because of pre-existing partial immunity through previous infections and/or vaccinations, which mostly guard the lower respiratory tract, overall disease severity is expected to be reduced.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35208550
DOI: 10.3390/medicina58020226


ABSTRACT: Omicron, the novel highly mutated SARS-CoV-2 Variant of Concern (VOC, Pango lineage B.1.1.529) was first collected in early November 2021 in South Africa. By the end of November 2021, it had spread and approached fixation in South Africa, and had been detected on all continents. We analyzed the exponential growth of Omicron over four-week periods in the two most populated of South Africa’s provinces, Gauteng and KwaZulu-Natal, arriving at the doubling time estimates of, respectively, 3.3 days (95% CI: 3.2-3.4 days) and 2.7 days (95% CI: 2.3-3.3 days). Similar or even shorter doubling times were observed in other locations: Australia (3.0 days), New York State (2.5 days), UK (2.4 days), and Denmark (2.0 days). Log-linear regression suggests that the spread began in Gauteng around 11 October 2021; however, due to presumable stochasticity in the initial spread, this estimate can be inaccurate. Phylogenetics-based analysis indicates that the Omicron strain started to diverge between 6 October and 29 October 2021. We estimated that the weekly growth of the ratio of Omicron to Delta is in the range of 7.2-10.2, considerably higher than the growth of the ratio of Delta to Alpha (estimated to be in the range of 2.5-4.2), and Alpha to pre-existing strains (estimated to be in the range of 1.8-2.7). High relative growth does not necessarily imply higher Omicron infectivity. A two-strain SEIR model suggests that the growth advantage of Omicron may stem from immune evasion, which permits this VOC to infect both recovered and fully vaccinated individuals. As we demonstrated within the model, immune evasion is more concerning than increased transmissibility, because it can facilitate larger epidemic outbreaks.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35215887
DOI: 10.3390/v14020294


ABSTRACT: The coronavirus disease 2019 (COVID-19) pandemic continues worldwide with many variants arising, some of which are variants of concern (VOCs). A recent VOC, omicron (B.1.1.529), which obtains a large number of mutations in the receptor-binding domain (RBD) of the spike protein, has risen to intense scientific and public attention. Here, we studied the binding properties between the human receptor ACE2 (hACE2) and the VOC RBDs and resolved the crystal and cryoelectron microscopy structures of the omicron RBD-hACE2 complex as well as the crystal structure of the delta RBD-hACE2 complex. We found that, unlike alpha, beta, and gamma, omicron RBD binds to hACE2 at a similar affinity to that of the prototype RBD, which might be due to compensation of multiple mutations for both immune escape and transmissibility. The complex structures of omicron RBD-hACE2 and delta RBD-hACE2 reveal the structural basis of how RBD-specific mutations bind to hACE2.

ABSTRACT: BACKGROUND: In May, 2021, the delta (B.1.617.2) SARS-CoV-2 variant became dominant in the UK, superseded by the omicron (B.1.1.529) variant in December, 2021. The delta variant is associated with increased transmissibility compared with the alpha variant, which was the dominant variant in the UK between December, 2020, and May, 2021. To understand transmission and the effectiveness of interventions, we aimed to investigate whether the delta variant generation time (the interval between infections in infector-infectee pairs) is shorter—i.e., transmissions are happening more quickly—than that of the alpha variant. METHODS: In this epidemiological analysis, we analysed transmission data from an ongoing UK Health Security Agency (UKHSA) prospective household study. Households were recruited to the study after an index case had a positive PCR test and genomic sequencing was used to determine the variant responsible. By fitting a mathematical transmission model to the data, we estimated the intrinsic generation time (which assumes a constant supply of susceptible individuals throughout infection) and the household generation time (which reflects realised transmission in the study households, accounting for susceptible depletion) for the alpha and delta variants. FINDINGS: Between February and August, 2021, 227 households consisting of 559 participants were recruited to the UKHSA study. The alpha variant was detected or assumed to be responsible for infections in 131 households (243 infections in 334 participants) recruited in February-May, and the delta variant in 96 households (174 infections in 225 participants) in May-August. The mean intrinsic generation time was shorter for the delta variant (4.7 days, 95% credible interval [CI] 4.1-5.6) than the alpha variant (5.5 days, 4.7-6.5), with 92% posterior probability. The mean household generation time was 28% (95% CI 0-48%) shorter for the delta variant (3.2 days, 95% CI 2.5-4.2) than the alpha variant (4.5 days, 3.7-5.4), with 97.5% posterior probability. INTERPRETATION: The delta variant transmits more quickly in households than the alpha variant, which can be attributed to faster depletion of susceptible individuals in households and a possible decrease in the intrinsic generation time. Interventions such as contact tracing, testing, and isolation might be less effective if transmission of the virus occurs quickly. FUNDING: National Institute for Health Research, UK Health Security Agency, Engineering and Physical Sciences Research Council, and UK Research and Innovation.

**ABSTRACT:** The SARS-CoV-2 Omicron exhibits striking immune evasion and is spreading rapidly worldwide. Understanding the structural basis of the high transmissibility and enhanced immune evasion of Omicron is of high importance. Here through cryo-EM analysis, we present both the closed and open states of the Omicron spike (S), which appear more compact than the counterparts of the G614 strain(1), potentially related to Omicron residue substitutions-induced enhanced inter-protomer and S1-S2 interactions. The closed state showing dominant population may indicate a conformational masking mechanism for Omicron’s immune evasion. Moreover, we capture three states for the Omicron S-ACE2 complex, revealing that the substitutions on the Omicron RBM result in new salt bridges/H-bonds, more favorable electrostatic surface properties, and overall strengthened S-ACE2 interaction, in line with the observed higher ACE2 affinity of Omicron S relative to G614. Furthermore, we determine structures of Omicron S in complex with the Fab of S3H3, an antibody able to cross-neutralize major variants of concern including Omicron, elucidating the structural basis for S3H3-mediated broad-spectrum neutralization. Our findings shed new lights on the receptor engagement and antibody neutralization/evasion of Omicron and may also inform design of broadly effective SARS-CoV-2 vaccines.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35228716
DOI: 10.1038/s41586-022-04581-9


URL: https://www.ncbi.nlm.nih.gov/pubmed/35151383
DOI: 10.1016/S0140-6736(22)00266-5


**ABSTRACT:** The coronavirus is naturally mutating over time and producing new variants. Some of them are more contagious and destructive than previous strains. Also, some variants are capable of therapeutic escaping. Earlier SARS-CoV-2 variants proved that some are supercritical, and newly mutated strains are creating new challenges to the global healthcare systems. Here we aimed to evaluate different coronavirus variants and associated challenges for healthcare systems. We searched for information online and on the PubMed, Scopus, and Embase databases. We found the wild-type virus is more sensitive for neutralization and more controllable than newer variants. The Delta and Omicron variants are more highly transmissible than Alpha, Beta, and Gamma variants. Also, few strains are resistant to neutralization. Therefore, there is a chance of reinfection among the vaccinated population. The transmissibility and resistance of the recently identified Omicron variant is still unclear. The Delta variant is the most dangerous among all variants due to its high transmissibility, disease severity, and mortality rate. For poor and developing countries, oxygen supply, medication, vaccination, and device supply are challenging during epidemic waves. Slowing down the transmission, mass vaccination, vaccine redesign, re-compiling action plans, and following safety guidelines can be effective solutions to the new challenges.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35141522
DOI: 10.1177/2632010X221075584


**ABSTRACT:** COVID 19 is the disease caused by severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2; SC2) which has caused a world-wide pandemic with striking morbidity and mortality. Evaluation of SC2 strains demonstrated impressive genetic variability and many of these viral variants are now defined as variants of concern (VOC) that cause enhanced transmissibility, decreased susceptibility to antibody neutralization...
or therapeutics and or the ability to induce severe disease. Currently, the delta (delta) and omicron (o) variants are particularly problematic based on their impressive and unprecedented transmissibility and ability to cause break through infections. The delta variant also accumulates at high concentrations in host tissues and has caused waves of lethal disease. Because studies from our laboratory have demonstrated that chitinase 3-like-1 (CHI3L1) stimulates ACE2 and Spike (S) priming proteases that mediate SC2 infection, studies were undertaken to determine if interventions that target CHI3L1 are effective inhibitors of SC2 viral variant infection. Here we demonstrate that CHI3L1 augments epithelial cell infection by pseudoviruses that express the alpha, beta, gamma, delta or omicron S proteins and that the CHI3L1 inhibitors anti-CHI3L1 and kasugamycin inhibit epithelial cell infection by these VOC pseudovirus moieties. Thus, CHI3L1 is a universal, VOC-independent therapeutic target in COVID 19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35118470
DOI: 10.1101/2022.01.21.477274

ABSTRACT: In South Korea, a November 2021 outbreak caused by severe acute respiratory syndrome coronavirus 2 Omicron variant originated from 1 person with an imported case and spread to households, kindergartens, workplaces, restaurants, and hospitals, resulting in 11 clusters within 3 weeks. An epidemiologic curve indicated rapid community transmission of the Omicron variant.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35171760
DOI: 10.3201/eid2804.220006

ABSTRACT: BACKGROUND: Males ages 12-17 years have an elevated risk of mRNA vaccination-associated myo/pericarditis. A risk-benefit analysis of first and second doses of mRNA vaccination in adolescent boys by health status and history of SARS-CoV-2 infection has not been performed. METHODS: Using the Vaccine Adverse Event Reporting System (VAERS), we identified BNT162b2 [Pfizer-BioNTech] myo/pericarditis occurrence according to CDC criteria. Main outcomes were: 1) post-vaccination myo/pericarditis crude incidence in adolescents aged 12-15 and 16-17; and 2) two risk-benefit analyses by age, sex, comorbidity and history of infection. RESULTS: Cases of myo/pericarditis (n=253) included 129 after dose 1 and 124 after dose 2; 86.9% were hospitalized. Incidence per million after dose two in males aged 12-15 and 16-17 was 162.2 and 93.0, respectively. Weighing post-vaccination myo/pericarditis against COVID-19 hospitalization during delta, our risk benefit analysis suggests that among 12-17-year-olds, two-dose vaccination was uniformly favorable only in non-immune girls with a comorbidity. In boys with prior infection and no comorbidities, even one dose carried more risk than benefit according to international estimates. In the setting of omicron, one dose may be protective in non-immune children, but dose two does not appear to confer additional benefit at a population level. CONCLUSIONS: Our findings strongly support individualized pediatric COVID-19 vaccination strategies which weigh harms in this overall low-risk cohort.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35156705
DOI: 10.1111/eci.13759

URL: https://www.ncbi.nlm.nih.gov/pubmed/35063123
DOI: 10.1016/S0140-6736(22)00090-3

ABSTRACT: Emerging severe acute respiratory syndrome coronavirus type 2 (SARS-CoV-2) variants, especially those of concern, may have an impact on the virus's transmissibility and pathogenicity, as well as diagnostic equipment performance and vaccine effectiveness. Even though the SARS-CoV-2 Delta variant (B.1.617.2) emerged during India's second wave of infections, Delta variants have grown dominant internationally and are still evolving. On November 26, 2021, World Health Organization identified the variant B.1.1.529 as a variant of concern, naming it Omicron, based on evidence that Omicron contains numerous mutations that may influence its behavior. However, the mode of transmission and severity of the Omicron variant remains unknown. We used computational studies to examine the Delta and Omicron variants in this study and found that the Omicron variant had a higher affinity for human angiotensin-converting enzyme 2 (ACE2) than the Delta variant due to a significant number of mutations in the SARS-CoV-2 receptor-binding domain (RBD), indicating a higher potential for transmission. Based on docking studies, the Q493R, N501Y, S371L, S373P, S375F, Q498R, and T478K mutations contribute significantly to high binding affinity with human ACE2. In comparison to the Delta variant, both the entire spike protein and the RBD in Omicron include a high proportion of hydrophobic amino acids such as leucine and phenylalanine. These amino acids are located within the protein's core and are required for structural stability. We observed a disorder-order transition in the Omicron variant between spike protein RBD regions 468-473, and it may be significant in the influence of disordered residues/regions on spike protein stability and binding to ACE2. A future study might investigate the epidemiological and biological consequences of the Omicron variant.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34914115
DOI: 10.1002/jmv.27526

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URL: https://www.ncbi.nlm.nih.gov/pubmed/34990256
DOI: 10.1126/science.acz9928

ABSTRACT: Genomic surveillance is a critical tool for tracking emerging variants of SARS-CoV-2 (the virus that causes COVID-19), which can exhibit characteristics that potentially affect public health and clinical interventions, including increased transmissibility, illness severity, and capacity for immune escape. During June 2021-January 2022, CDC expanded genomic surveillance data sources to incorporate sequence data from public repositories to produce weighted estimates of variant proportions at the jurisdiction level and refined analytic methods to enhance the timeliness and accuracy of national and regional variant proportion estimates. These changes also allowed for more comprehensive variant proportion estimation at the jurisdictional level (i.e., U.S. state, district, territory, and freely associated state). The data in this report are a summary of findings of recent proportions of circulating variants that are updated weekly on CDC’s COVID Data Tracker website to enable timely public health action.(dagger) The SARS-CoV-2 Delta (B.1.617.2 and AY sublineages) variant rose from 1% to >50% of viral lineages circulating nationally during 8 weeks, from May 1-June 26, 2021. Delta-associated infections remained predominant until being rapidly overtaken by infections associated with the Omicron (B.1.1.529 and BA sublineages) variant in December 2021, when Omicron increased from 1% to >50% of circulating viral lineages during a 2-week period. As of the week ending January 22, 2022, Omicron was estimated to account for 99.2% (95% CI = 99.0%-99.5%) of SARS-CoV-2 infections nationwide, and Delta for 0.7% (95% CI = 0.5%-1.0%). The dynamic landscape of SARS-CoV-2 variants in 2021, including Delta- and Omicron-driven resurgences of SARS-CoV-2 transmission across the United States, underscores the importance of robust genomic surveillance efforts to inform public health planning and practice.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35143464
DOI: 10.15585/mmwr.mm7106a4

ABSTRACT: Explosively emerging SARS-CoV-2 variants challenge current nomenclature schemes based on genetic diversity and biological significance. Genomic composition-based machine learning methods have recently performed well in identifying phenotype-genotype relationships. We introduced a framework involving dinucleotide (DNT) composition representation (DCR) to parse the general human adaptation of RNA viruses and applied a three-dimensional convolutional neural network (3D CNN) analysis to learn the human adaptation of other existing coronaviruses (CoVs) and predict the adaptation of SARS-CoV-2 variants of concern (VOCs). A markedly separable, linear DCR distribution was observed in two major genes-receptor-binding glycoprotein and RNA-dependent RNA polymerase (RdRp)-of six families of single-stranded (ssRNA) viruses. Additionally, there was a general host-specific distribution of both the spike proteins and RdRps of CoVs. The 3D CNN based on spike DCR predicted a dominant type II adaptation of most Beta, Delta and Omicron VOCs, with high transmissibility and low pathogenicity. Type I adaptation with opposite transmissibility and pathogenicity was predicted for SARS-CoV-2 Alpha VOCs (77%) and Kappa variants of interest (58%). The identified adaptive determinants included D1118H and A570D mutations and local DNTs. Thus, the 3D CNN model based on DCR features predicts SARS-CoV-2, a major type II human adaptation and is qualified to predict variant adaptation in real time, facilitating the risk-assessment of emerging SARS-CoV-2 variants and COVID-19 control.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35233612
DOI: 10.1093/bib/bbac036


ABSTRACT: WHAT IS KNOWN AND OBJECTIVE: Omicron is a variant of the COVID-19 virus that is causing considerable concern worldwide, with an increasing number of countries re-imposing national lockdowns. Our objective is to comment on its impact and to suggest that, threatening as it is, Omicron may well contribute to a resolution of the current pandemic. COMMENT: On 31 December 2019, the World Health Organization (WHO) reported on a cluster of cases of pneumonia in Wuhan, China. Soon after, Chinese investigators who made the discovery identified the causative virus as a new coronavirus, now known as severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). An effective vaccine was licenced for emergency use within a year of its first sequencing. SARS-CoV-2, in common with many respiratory viruses, mutates rapidly, and the challenge for vaccine developers is to obtain vaccines that are effective against the new variants. The licenced first-generation vaccines were fortunately all highly effective against the variant known as Delta. The variant of greatest current concern is the Omicron variant, a highly infectious agent, which seems to show a significant vaccine escape with existing vaccines. Infection protects against further infection. If Omicron turns out to cause less severe disease, it may well be a contributor to ending the pandemic. WHAT IS NEW AND CONCLUSION: It is unlikely that the available vaccines will bring rapid control of the current pandemic, given their patchy availability worldwide and the residual pool of unvaccinated people. New vaccines take time to develop and to deploy even in the age of mRNA vaccines. If Omicron turns out to be relatively mild, it may well be that when we look back at the history of the current pandemic, the variant would be seen as a contributor to its solution. The hand of nature may well show more largesse than the developed nations in immunizing the world.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35128705
DOI: 10.1111/jcpt.13614


ABSTRACT: The B.1.1.529/Omicron variant of SARS-CoV-2 was only recently detected in southern Africa, but its subsequent spread has been extensive, both regionally and globally(1). It is expected to become dominant in the coming weeks(2), probably due to enhanced transmissibility. A striking feature of this variant is the large number of spike mutations(3) that pose a threat to the efficacy of current COVID-19 vaccines and antibody therapies(4). This concern is amplified by the findings of our study. Here we found that B.1.1.529
is markedly resistant to neutralization by serum not only from patients who recovered from COVID-19, but also from individuals who were vaccinated with one of the four widely used COVID-19 vaccines. Even serum from individuals who were vaccinated and received a booster dose of mRNA-based vaccines exhibited substantially diminished neutralizing activity against B.1.1.529. By evaluating a panel of monoclonal antibodies against all known epitope clusters on the spike protein, we noted that the activity of 17 out of the 19 antibodies tested were either abolished or impaired, including ones that are currently authorized or approved for use in patients. Moreover, we also identified four new spike mutations (S371L, N440K, G446S and Q493R) that confer greater antibody resistance on B.1.1.529. The Omicron variant presents a serious threat to many existing COVID-19 vaccines and therapies, compelling the development of new interventions that anticipate the evolutionary trajectory of SARS-CoV-2.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35016198
DOI: 10.1038/s41586-021-04388-0


ABSTRACT: The Omicron variant of concern (VOC), first detected in Italy at the end of November 2021, has since spread rapidly, despite high vaccine coverage in the Italian population, especially in healthcare workers (HCWs). This study describes an outbreak of SARS-CoV-2 Omicron infection in 15 booster-vaccinated HCWs. On 16 December 2021, two HCWs working in the same ward were infected with SARS-CoV-2. The Omicron VOC was suspected due to S gene target failure on molecular testing. Further investigation revealed that 15 (65%) of 23 HCWs attending a social gathering on 13 December were infected with Omicron, as shown by whole-genome sequencing, with a phylogenetic tree suggesting a common source of exposure. Five of these HCWs experienced mild symptoms. A patient with multiple chronic conditions hospitalized in the same ward was also infected by one of the HCWs involved in the outbreak. Despite being booster vaccinated, this patient required ICU treatment. Ten subjects achieved negativity in 10-19 days. The outbreak in booster-vaccinated subjects confirms the high transmissibility and immune evasion of the Omicron VOC. More stringent non-pharmaceutical interventions, administration of booster doses, and genomic surveillance are crucial long-term strategies to mitigate the consequences of the spread of the Omicron VOC.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35214741
DOI: 10.3390/vaccines10020283


ABSTRACT: INTRODUCTION: Coronavirus disease of 2019 (COVID-19) has resulted in millions of cases worldwide. As the pandemic has progressed, the understanding of this disease has evolved. OBJECTIVE: This first in a two-part series on COVID-19 updates provides a focused overview of the presentation and evaluation of COVID-19 for emergency clinicians. DISCUSSION: COVID-19, caused by Severe Acute Respiratory Syndrome coronavirus 2 (SARS-CoV-2), has resulted in significant morbidity and mortality worldwide. Several variants exist, including a variant of concern known as Delta (B.1.617.2 lineage) and the Omicron variant (B.1.1.529 lineage). The Delta variant is associated with higher infectivity and poor patient outcomes, and the Omicron variant has resulted in a significant increase in infections. While over 80% of patients experience mild symptoms, a significant proportion can be critically ill, including those who are older and those with comorbidities. Upper respiratory symptoms, fever, and changes in taste/smell remain the most common presenting symptoms. Extrapulmonary complications are numerous and may be severe, including the cardiovascular, neurologic, gastrointestinal, and dermatologic systems. Emergency department evaluation includes focused testing for COVID-19 and assessment of end-organ injury. Imaging may include chest radiography, computed tomography, or ultrasound. Several risk scores may assist in prognostication, including the 4C (Coronavirus Clinical Characterisation Consortium) score, quick COVID Severity Index (qCSI), NEWS2, and the PRIEST score, but these should only supplement and not replace clinical judgment. CONCLUSION: This review provides a focused update of the presentation and evaluation of COVID-19 for emergency clinicians.

ABSTRACT: AIM: Most children with COVID-19 have mild symptoms, but data on the Omicron variant are rare. This paper describes unexpected cases with convulsions during 1 week in January 2022. METHODS: Four children with COVID-19 were admitted with convulsions to the paediatric department in Orebro, Sweden, when Omicron accounted for more than 98% of the country’s COVID-19 cases. Three children tested positive for the virus, and one had clinical COVID-19. I was able to contact the parents of three boys, who gave consent for these case studies. RESULTS: Two boys aged 3 and 21 months tested positive for the virus and a 14-year-old boy tested negative, but had a cold and family members who had tested positive. The teenager had a history of urinary tract infections, but the younger boys had no earlier comorbidities. None had a history of epilepsy or febrile convulsions. The younger children had a fever and the teenager had upper respiratory symptoms. The 3-month-old child had repeated convulsions for several hours, the 21-month-old had continuous convulsions for 15-20 min, and the teenager had a convulsion for 30-60 s, followed by uncharacteristic aggression. CONCLUSION: Convulsions may be a sign of the Omicron variant in children with COVID-19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35098577
DOI: 10.1111/apa.16276


ABSTRACT: BACKGROUND: The B.1.1.529 (omicron) variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) was first identified on November 25, 2021, in Gauteng province, South Africa. Data regarding the seroprevalence of SARS-CoV-2 IgG in Gauteng before the fourth wave of coronavirus disease 2019 (Covid-19), in which the omicron variant was dominant, are needed. METHODS: We conducted a seroepidemiologic survey from October 22 to December 9, 2021, in Gauteng to determine the seroprevalence of SARS-CoV-2 IgG. Households included in a previous seroepidemiologic survey (conducted from November 2020 to January 2021) were contacted; to account for changes in the survey population, there was a 10% increase in the households contacted, with the use of the same sampling framework. Dried-blood-spot samples were tested for IgG against SARS-CoV-2 spike protein and nucleocapsid protein with the use of quantitative assays. We also evaluated Covid-19 epidemiologic trends in Gauteng, including cases, hospitalizations, recorded deaths, and excess deaths from the start of the pandemic through January 12, 2022. RESULTS: Samples were obtained from 7010 participants, of whom 1319 (18.8%) had received a Covid-19 vaccine. The seroprevalence of SARS-CoV-2 IgG ranged from 56.2% (95% confidence interval [CI], 52.6 to 59.7) among children younger than 12 years of age to 79.7% (95% CI, 77.6 to 81.5) among adults older than 50 years of age. Vaccinated participants were more likely to be seropositive for SARS-CoV-2 than unvaccinated participants (93.1% vs. 68.4%). Epidemiologic data showed that the incidence of SARS-CoV-2 infection increased and subsequently declined more rapidly during the fourth wave than it had during the three previous waves. The incidence of infection was decoupled from the incidences of hospitalization, recorded death, and excess death during the fourth wave, as compared with the proportions seen during previous waves. CONCLUSIONS: Widespread underlying SARS-CoV-2 seropositivity was observed in Gauteng before the omicron-dominant wave of Covid-19. Epidemiologic data showed a decoupling of hospitalizations and deaths from infections while omicron was circulating. (Funded by the Bill and Melinda Gates Foundation.).

URL: https://www.ncbi.nlm.nih.gov/pubmed/35196424
DOI: 10.1056/NEJMoa2119658


ABSTRACT: SARS-CoV-2 evolution threatens vaccine- and natural infection-derived immunity as well as the efficacy of therapeutic antibodies. To improve public health preparedness, we sought to predict which existing
Evidence Search Report: EOC211220v010 ESR


ABSTRACT: OBJECTIVES: We aimed to investigate the first Omicron cases detected in France in order to assess case characteristics and provide supporting information on the possible impact of this variant on the healthcare system. METHODS: A standardized questionnaire was used to collect information from confirmed and probable Omicron cases. RESULTS: Median age of 468 investigated cases was 35 years, 376 were symptomatic (89%); 64% were vaccinated with two doses and 7% had received three doses. Loss of smell and taste were reported by 8.3% and 9% of cases, respectively. Seven cases were hospitalized, three of those were unvaccinated (including two with reported precondition). No admissions to intensive care and no deaths were reported. CONCLUSIONS: Our results confirm a mild clinical presentation among the first Omicron cases detected in France and highlight the importance for the national COVID-19 surveillance system to quickly detect and adapt to the emergence of a new variant.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35167979
DOI: 10.1016/j.idnow.2022.02.003

48. Mallapaty S. Fourth dose of COVID vaccine offers only slight boost against Omicron infection. Nature. 2022. DOI: 10.1038/d41586-022-00486-9

URL: https://www.ncbi.nlm.nih.gov/pubmed/35197600
DOI: 10.1038/d41586-022-00486-9


ABSTRACT: The first U.S. case of COVID-19 attributed to the Omicron variant of SARS-CoV-2 (the virus that causes COVID-19) was reported on December 1, 2021 (1), and by the week ending December 25, 2021, Omicron was the predominant circulating variant in the United States.* Although COVID-19-associated hospitalizations are more frequent among adults,(dagger) COVID-19 can lead to severe outcomes in children and adolescents (2). This report analyzes data from the Coronavirus Disease 19-Associated Hospitalization Surveillance Network (COVID-NET)( section sign) to describe COVID-19-associated hospitalizations among U.S. children (aged 0-11 years) and adolescents (aged 12-17 years) during periods of Delta (July 1-December 18, 2021) and Omicron (December 19, 2021-January 22, 2022) predominance. During the Delta- and Omicron-predominant periods, rates of weekly COVID-19-associated hospitalizations per 100,000 children and adolescents peaked during the weeks ending September 11, 2021, and January 8, 2022, respectively. The Omicron variant peak (7.1 per 100,000) was four times that
of the Delta variant peak (1.8), with the largest increase observed among children aged 0-4 years. During December 2021, the monthly hospitalization rate among unvaccinated adolescents aged 12-17 years (23.5) was six times that among fully vaccinated adolescents (3.8). Strategies to prevent COVID-19 among children and adolescents, including vaccination of eligible persons, are critical. *

URL: https://www.ncbi.nlm.nih.gov/pubmed/35176003
DOI: 10.15585/mmwr.mm7107e4


ABSTRACT: Although accumulating data have investigated the effect of SARS-CoV-2 mutations on antibody neutralizing activity, less is known about T cell immunity. In this work, we found that the ancestral (Wuhan strain) Spike protein can efficaciously reactivate CD4+ T cell memory in subjects with previous Alpha variant infection. This finding has practical implications, as in many countries only one vaccine dose is currently administered to individuals with previous COVID-19, independently of which SARS-CoV-2 variant was responsible of the infection. We also found that only a minority of Spike-specific CD4+ T cells targets regions mutated in Alpha, Beta and Delta variants, both after natural infection and vaccination. Finally, we found that the vast majority of Spike-specific CD4+ T cell memory response induced by natural infection or mRNA vaccination is conserved also against Omicron variant. This is of importance, as this newly emerged strain is responsible for a sudden rise in COVID-19 cases worldwide due to its increased transmissibility and ability to evade antibody neutralization. Collectively, these observations suggest that most of the memory CD4+ T cell response is conserved against SARS-CoV-2 variants of concern, providing an efficacious line of defense that can protect from the development of severe forms of COVID-19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35154116
DOI: 10.3389/fimmu.2022.801431

51. Menasria T, Aguilera M. Genomic Diversity of SARS-CoV-2 in Algeria and North African Countries: What We Know So Far and What We Expect? Microorganisms. 2022;10(2). DOI: 10.3390/microorganisms10020467

ABSTRACT: Here, we report a first comprehensive genomic analysis of SARS-CoV-2 variants circulating in North African countries, including Algeria, Egypt, Libya, Morocco, Sudan and Tunisia, with respect to genomic clades and mutational patterns. As of December 2021, a total of 1669 high-coverage whole-genome sequences submitted to EpiCoV GISAID database were analyzed to infer clades and mutation annotation compared with the wild-type variant Wuhan-Hu-1. Phylogenetic analysis of SARS-CoV-2 genomes revealed the existence of eleven GISAID clades with GR (variant of the spike protein S-D614G and nucleocapsid protein N-G204R), GH (variant of the ORF3a coding protein ORF3a-Q57H) and GK (variant S-T478K) being the most common with 25.9%, 19.9%, and 19.6%, respectively, followed by their parent clade G (variant S-D614G) (10.3%). Lower prevalence was noted for GRY (variant S-N501Y) (5.1%), S (variant ORF8-L84S) (3.1%) and GV (variant of the ORF3a coding protein NS3-G251V) (2.0%). Interestingly, 1.5% of total genomes were assigned as GRA (Omicron), the newly emerged clade. Across the North African countries, 108 SARS-CoV-2 lineages using the Pangolin assignment were identified, whereby most genomes fell within six major lineages and variants of concern (VOC) including B.1, the Delta variants (AY.X, B.1.617.2), C.36, B.1.1.7 and B.1.1. The effect of mutations in SAR-CoV-2 genomes highlighted similar profiles with D614G spike (S) and ORF1b-P314L variants as the most changes found in 95.3% and 87.9% of total sequences, respectively. In addition, mutations affecting other viral proteins appeared frequently including; N:RG203KR, N:G212V, NSP3:T428I, ORF3a-Q57H, S:N501Y, M:I82T and E:V5F. These findings highlight the importance of genomic surveillance for understanding the SARS-CoV-2 genetic diversity and its spread patterns, leading to a better guiding of public health intervention measures. The know-how analysis of the present work could be implemented worldwide in order to overcome this health crisis through harmonized approaches.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35208920
DOI: 10.3390/microorganisms10020467
URL: https://www.ncbi.nlm.nih.gov/pubmed/34989785
DOI: 10.1001/jama.2021.24168


ABSTRACT: The Omicron variant features enhanced transmissibility and antibody escape. Here, we describe the Omicron receptor-binding domain (RBD) mutational landscape using amino acid interaction (AAI) networks, which are well suited for interrogating constellations of mutations that function in an epistatic manner. Using AAI, we map Omicron mutations directly and indirectly driving increased escape breadth and depth in class 1-4 antibody epitopes. Further, we present epitope networks for authorized therapeutic antibodies and assess perturbations to each antibody's epitope. Since our initial modeling following the identification of Omicron, these predictions have been realized by experimental findings of Omicron neutralization escape from therapeutic antibodies ADG20, AZD8895, and AZD1061. Importantly, the AAI predicted escape resulting from indirect epitope perturbations was not captured by previous sequence or point mutation analyses. Finally, for several Omicron RBD mutations, we find evidence for a plausible role in enhanced transmissibility via disruption of RBD-down conformational stability at the RBDdown-RBDdown interface.
URL: https://www.ncbi.nlm.nih.gov/pubmed/35233548
DOI: 10.1016/j.xcrm.2022.100527


ABSTRACT: In mid-December 2021, the B.1.1.529 (Omicron) variant of SARS-CoV-2, the virus that causes COVID-19, surpassed the B.1.617.2 (Delta) variant as the predominant strain in California. Initial reports suggest that the Omicron variant is more transmissible and resistant to vaccine neutralization but causes less severe illness compared with previous variants (1-3). To describe characteristics of patients hospitalized with SARS-CoV-2 infection during periods of Delta and Omicron predominance, clinical characteristics and outcomes were retrospectively abstracted from the electronic health records (EHRs) of adults aged >/=18 years with positive reverse transcription-polymerase chain reaction (RT-PCR) SARS-CoV-2 test results admitted to one academic hospital in Los Angeles, California, during July 15-September 23, 2021 (Delta predominant period, 339 patients) and December 21, 2021-January 27, 2022 (Omicron predominant period, 737 patients). Compared with patients during the period of Delta predominance, a higher proportion of adults admitted during Omicron predominance had received the final dose in a primary COVID-19 vaccination series (were fully vaccinated) (39.6% versus 25.1%), and fewer received COVID-19-directed therapies. Although fewer required intensive care unit (ICU) admission and invasive mechanical ventilation (IMV), and fewer died while hospitalized during Omicron predominance, there were no significant differences in ICU admission or IMV when stratified by vaccination status. Fewer fully vaccinated Omicron-period patients died while hospitalized (3.4%), compared with Delta-period patients (10.6%). Among Omicron-period patients, vaccination was associated with lower likelihood of ICU admission, and among adults aged >/=65 years, lower likelihood of death while hospitalized. Likelihood of ICU admission and death were lowest among adults who had received a booster dose. Among the first 131 Omicron-period hospitalizations, 19.8% of patients were clinically assessed as admitted for non-COVID-19 conditions. Compared with adults considered likely to have been admitted because of COVID-19, these patients were younger (median age = 38 versus 67 years) and more likely to have received at least one dose of a COVID-19 vaccine (84.6% versus 61.0%). Although 20% of SARS-CoV-2-associated hospitalizations during the period of Omicron predominance might be driven by non-COVID-19 conditions, large numbers of hospitalizations place a strain on health systems. Vaccination, including a
booster dose for those who are fully vaccinated, remains critical to minimizing risk for severe health outcomes among adults with SARS-CoV-2 infection.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35143466
DOI: 10.15585/mmwr.mm7106e2


ABSTRACT: The ongoing COVID-19 pandemic caused by SARS-CoV-2 is associated with high morbidity and mortality. This zoonotic virus has emerged in Wuhan of China in December 2019 from bats and pangolins probably and continuing the human-to-human transmission globally since last two years. As there is no efficient approved treatment, so, a number of vaccines was developed at an unprecedented speed to counter the pandemic. Moreover, vaccine hesitancy is observed which may be another possible reason for this never ending pandemic. In the meantime, several variants and mutations were identified and causing multiple waves globally. Now the safety and efficacy of these vaccines are debatable and recommended to determine if vaccines are able to interrupt transmission of SARS-CoV-2 variant of concern (VOC). Moreover, the VOCs continue to emerge that appear more transmissible and less sensitive to virus-specific immune responses. In this overview, we have highlighted various drugs and vaccines used to counter this pandemic along with their reported side effects. Moreover, the preliminary data for the novel VOC "Omicron" is discussed with the existing animal models.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35184391
DOI: 10.1111/cbdd.14035


ABSTRACT: The emergence of Omicron (B.1.1.529) variant of SARS-CoV-2 has resulted into a very massive surge in COVID-19 cases worldwide. Due to continuous emergence of multiple variants of SARS-CoV-2, the ongoing pandemic has caused severe morbidity and mortality in last two years. The rate of infectivity of Omicron variant is much higher than Delta variant and in a very quick time Omicron has displaced the Delta variant and now become a dominant variant across the globe. The twin combination of Omicron and Delta variant is triggering a Tsunami wave of ever high surges in COVID-19 cases worldwide. This article highlights the global threats and challenges posed by Omicron, and strategies to counter it with a particular focus on Indian sub-continent.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35014038
DOI: 10.1002/jmv.27585


ABSTRACT: BACKGROUND: Two doses of mRNA vaccination have shown >94% efficacy at preventing COVID-19 mostly in naive adults, but it is not clear if the second dose is needed to maximize effectiveness in those previously exposed to SARS-CoV-2 and what other factors affect responsiveness. METHODS: We measured IgA, IgG and IgM levels against SARS-CoV-2 spike (S) and nucleocapsid (N) antigens from the wild-type and S from the Alpha, Beta and Gamma variants of concern, after BNT162b2 (Pfizer/BioNTech) or mRNA-1273 (Moderna) vaccination in a cohort of health care workers (N=578). Neutralizing capacity and antibody avidity were evaluated. Data were analyzed in relation to COVID-19 history, comorbidities, vaccine doses, brand and adverse events. FINDINGS: Vaccination induced robust IgA and IgG levels against all S antigens. Neutralization capacity and S IgA and IgG levels were higher in mRNA-1273 vaccinees, previously SARS-CoV-2 exposed, particularly if symptomatic, and in those experiencing systemic adverse effects (p<0.05). A second dose in pre-exposed did not increase antibody levels. Smoking and comorbidities were associated with 43% (95% CI, 19-59) and 45% (95% CI, 63-18) lower neutralization, respectively, and 35% (95% CI, 3-57%) and 55% (95% CI, 33-70%) lower antibody levels, respectively. Among fully vaccinated, 6.3% breakthroughs were detected up to 189 days post-vaccination. Among pre-

**ABSTRACT:** Predictive scores are important tools for the triage of patients with coronavirus disease 2019. The PRIORITY score is advantageous because it does not require laboratory and radiologic information. However, the original development and validation cohorts studied only unvaccinated patients in early 2020. We aimed to externally validate the PRIORITY score in a cohort of patients with the exposed non-vaccinated, 90% were IgG seropositive more than 300 days post-infection. **INTERPRETATION:** Our data support administering a single-dose in pre-exposed healthy individuals as primary vaccination. However, heterogeneity of responses suggests that personalized recommendations may be necessary depending on COVID-19 history and life-style. Higher mRNA-1273 immunogenicity would be beneficial for those expected to respond worse to vaccination and in face of variants that escape immunity such as Omicron. Persistence of antibody levels in pre-exposed unvaccinated indicates maintenance of immunity up to one year. **FUNDING:** This work was supported by Institut de Salut Global de Barcelona (ISGlobal) internal funds, in-kind contributions from Hospital Clinic de Barcelona, the Fundacio Privada Daniel Bravo Andreu, and European Institute of Innovation and Technology (EIT) Health (grant number 20877), supported by the European Institute of Innovation and Technology, a body of the European Union receiving support from the H2020 Research and Innovation Programme. We acknowledge support from the Spanish Ministry of Science and Innovation and State Research Agency through the "Centro de Excelencia Severo Ochoa 2019-2023" Program (CEX2018-000806-S), and support from the Generalitat de Catalunya through the CERCA Program. L. I. work was supported by PID2019-110810RB-I00 grant from the Spanish Ministry of Science & Innovation. Development of SARS-CoV-2 reagents was partially supported by the National Institute of Allergy and Infectious Diseases Centers of Excellence for Influenza Research and Surveillance (contract number HHSN272201400008C). The funders had no role in study design, data collection and analysis, the decision to publish, or the preparation of the manuscript.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35032961

**DOI:** 10.1016/j.cmi.2022.01.031


**ABSTRACT:** SARS-CoV-2, the causative virus for COVID-19 has now super-mutated into the Omicron (Om) variant. On its spike (S) glycoprotein alone, more than 30 substitutions have been characterized with 15 within the receptor binding domain (RBD); It therefore calls to question the transmissibility and antibody escapability of Omicron. This study was setup to investigate the Omicron RBD’s interaction with ACE2 (host receptor) and a SARS-CoV-2 neutralizing monoclonal antibody (mAb). In-silico mutagenesis was used to generate the Om-RBD in complex with ACE2 or mAb from the wildtype. HDOCK server was used to redock and score the mAbs in Om-RBD bound state relative to the wildtype. Stability of interaction between all complexes were investigated using all-atom molecular dynamics (MD). Analyses of trajectories showed that Om-RBD has evolved into an efficient ACE2 binder, via pi-pi (Om-RBD-Y501/ACE2-Y41) and salt-bridge (Om-RBD-K493/ACE2-Y41) interactions. Conversely, in binding mAb, it has become less efficient (Center of mass distance of RBD from mAb complex, wildtype approximately 30 A, Omicron approximately 41 A). Disruption of Om-RBD/mAb complex resulted from loose interaction between Om-RBD and the light chain complementarity-determining region residues. Omicron is expected to be better transmissible and less efficiently interacting with neutralizing convalescent mAbs with consequences on transmissibility provided other mutations within the S protein similarly promote cell fusion and viral entry.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35066447

**DOI:** 10.1016/j.compbiomed.2022.105226


**DOI:** 10.1016/s0140-6736(22)00056-3
novel delta and omicron variants of coronavirus disease 2019 and mixed vaccination status. METHODS: A total of 410 patients were included in a cross-sectional sampling of all patients admitted to the National Centre of Infectious Diseases on October 27, 2021. A further 102 and 136 patients with vaccine-breach Delta and Omicron variant infection from April to August and December 2021, respectively, were also included. Variables at the time of admission were collected retrospectively from medical records and used to calculate the probability of deterioration using the PRIORITY model. RESULTS: Of the total 648 included patients, 447 (69.0%) were vaccinated. The mean age was 61.6 years (standard deviation +/- 19.0 years), and 268 patients (41.4%) were female. A total of 112 patients (17.3%) met the primary outcome of developing critical illness or mortality. The performance of the score in this cohort was comparable with the original cohorts, with an area under the receiver operating characteristic curve for all patients of 0.794 (95% CI, 0.752-0.835; p < 0.001), regression coefficient of 1.069, and intercept of 0.04. Subgroup analysis of unvaccinated and vaccinated patients showed that performance was superior in vaccinated individuals, with an area under the receiver operating characteristic curve of 0.684 (95% CI, 0.608-0.760; p < 0.0001) and 0.831 (95% CI, 0.772-0.891; p < 0.0001), respectively. DISCUSSION: Our data support the continued use of the PRIORITY score in this era of novel variants and increased vaccination uptake.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35150879
DOI: 10.1101/2021.09.29.21264272


ABSTRACT: Background: The COVID-19 pandemic is dominated by variant viruses; the resulting impact on disease severity remains unclear. Using a retrospective cohort study, we assessed the hospitalization risk following infection with seven SARS-CoV-2 variants. Methods: Our study includes individuals with positive SARS-CoV-2 RT-PCR in the Washington Disease Reporting System with available viral genome data, from December 1, 2020 to January 14, 2022. The analysis was restricted to cases with specimens collected through sentinel surveillance. Using a Cox proportional hazards model with mixed effects, we estimated hazard ratios (HR) for hospitalization risk following infection with a variant, adjusting for age, sex, calendar week, and vaccination. Findings: 58,848 cases were sequenced through sentinel surveillance, of which 1705 (2.9%) were hospitalized due to COVID-19. Higher hospitalization risk was found for infections with Gamma (HR 3.20, 95%CI 2.40-4.26), Beta (HR 2.85, 95%CI 1.56-5.23), Delta (HR 2.28 95%CI 1.56-3.34) or Alpha (HR 1.64, 95%CI 1.29-2.07) compared to infections with ancestral lineages; Omicron (HR 0.92, 95%CI 0.56-1.52) showed no significant difference in risk. Following Alpha, Gamma, or Delta infection, unvaccinated patients show higher hospitalization risk, while vaccinated patients show no significant difference in risk, both compared to unvaccinated, ancestral lineage cases. Hospitalization risk following Omicron infection is lower with vaccination. Conclusion: Infection with Alpha, Gamma, or Delta results in a higher hospitalization risk, with vaccination attenuating that risk. Our findings support hospital preparedness, vaccination, and genomic surveillance. Summary: Hospitalization risk following infection with SARS-CoV-2 variant remains unclear. We find a higher hospitalization risk in cases infected with Alpha, Beta, Gamma, and Delta, but not Omicron, with vaccination lowering risk. Our findings support hospital preparedness, vaccination, and genomic surveillance.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34729567
DOI: 10.1101/2021.09.29.21264272


ABSTRACT: The COVID-19 pandemic has had a significant global impact, with more than 280,000,000 people infected and 5,400,000 deaths. The use of personal protective equipment and the anti-SARS-CoV-2 vaccination campaigns have reduced infection and death rates worldwide. However, a recent increase in infection rates has been observed associated with the appearance of SARS-CoV-2 variants, including the more recently described lineage B.1.617.2 (Delta variant) and lineage B.1.1.529/BA.1 (Omicron variant). These new variants put the effectiveness of international vaccination at risk, with the appearance of new
outbreaks of COVID-19 throughout the world. This emergence of new variants has been due to multiple predisposing factors, including molecular characteristics of the virus, geographic and environmental conditions, and the impact of social determinants of health that favor the genetic diversification of SARS-CoV-2. We present a literature review on the most recent information available on the emergence of new variants of SARS-CoV-2 in the world. We analyzed the biological, geographical, and sociocultural factors that favor the development of these variants. Finally, we evaluate the surveillance strategies for the early detection of new variants and prevent their distribution outside these regions.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35207482
DOI: 10.3390/life12020194


ABSTRACT: The omicron variant of SARS-CoV-2, B.1.1.529, was included in the World Health Organization (WHO) list of variants of concerns (VOC) on 26 November 2021. Within only three months, omicron has spread rapidly to become the dominant variant in many countries. Studies have begun to evaluate the virulence, transmissibility, and degree of immune protection from current SARS-CoV-2 vaccines or previous infection with the omicron variant. On 21 January 2022, the WHO published its seventh technical update and recommendations for priority actions in response to the omicron SARS-CoV-2 variant and cautioned that the overall risk from omicron remains high. At the start of this third year of the global COVID-19 pandemic, this editorial aims to summarize the evidence that supports the current priority recommendations and response from the WHO regarding the omicron variant of SARS-CoV-2, B.1.1.529.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35102132
DOI: 10.12659/MSM.936199


URL: https://www.ncbi.nlm.nih.gov/pubmed/35150632
DOI: 10.1016/S2542-5196(22)00009-2


ABSTRACT: Seroprevalence surveys suggest that more than a third and possibly more than half of the global population has been infected with SARS-CoV-2 by early 2022. As large numbers of people continue to be infected, the efficacy and duration of natural immunity in terms of protection against SARS-CoV-2 reinfections and severe disease is of crucial significance for the future. This narrative review provides an overview on epidemiological studies addressing this issue. National surveys covering 2020-2021 documented that a previous SARS-CoV-2 infection is associated with a significantly reduced risk of reinfections with efficacy lasting for at least one year and only relatively moderate waning immunity. Importantly, natural immunity showed roughly similar effect sizes regarding protection against reinfection across different SARS-CoV-2 variants, with the exception of the Omicron variant for which data are just emerging before final conclusions can be drawn. Risk of hospitalizations and deaths was also reduced in SARS-CoV-2 reinfections versus primary infections. Observational studies indicate that natural immunity may offer equal or greater protection against SARS-CoV-2 infections compared to individuals receiving two doses of an mRNA vaccine, but data are not fully consistent. The combination of a previous SARS-CoV-2 infection and a respective vaccination, termed hybrid immunity, seems to confer the greatest protection against SARS-CoV-2 infections, but several knowledge gaps remain regarding this issue. Natural immunity should be considered for public health policy regarding SARS-CoV-2.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35149106
DOI: 10.1016/j.envres.2022.112911

ABSTRACT: Severe acute respiratory syndrome coronavirus-2 (SARS CoV-2) is the causative agent of coronavirus disease-19 (Covid-19) which has been designated a worldwide pandemic by the World Health Organization on March 11, 2020. Since that time, the virus has mutated and an assortment of variants have been successful at establishing themselves in the human population. This review article describes the SARS CoV-2 genome, hot spot mutations, variants, and then focuses on the Delta variant, finishing up with an update on the Omicron variant. The genome encompasses 11 open reading frames, one of which encodes the spike or S protein that has been the target for vaccines and some of the drugs because of its role in attachment to the human host cell, as well as antibodies. Mutations in the S protein that are common among several of the variants include D614G that increases transmissibility and viral load and is often associated with P323L on the RNA dependent RNA polymerase. N501Y is a mutation in the receptor binding domain of the S protein that increases binding to the ACE-2 receptor on the human host cells by 10 fold. The discussed variants carry combinations of these and other mutations and are classified by the World Health Organization as variants of concern, variants of interest, and variants under monitoring. All variants are characterized by increased transmissibility (relative to the original SARS CoV-2), which is the reason for their ability to establish themselves. Several but not all variants are more resistant to antiviral drugs and less susceptible to antibodies/vaccines. The Delta variant that dominated the world until November 2021 causes an increased risk for hospitalization and death, but is still very susceptible to the current vaccines. The most recent variant, Omicron, is characterized by increased transmissibility and decreased antibody susceptibility.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35227008
DOI: 10.31083/j.fbl2702065


URL: https://www.ncbi.nlm.nih.gov/pubmed/35165664
DOI: 10.1016/j.genrep.2022.101549


ABSTRACT: As severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) evolves, it accumulates mutations, which are changes in the genetic code. Because this virus has built-in RNA repair mechanisms, it generates mutations more slowly than some other RNA viruses. Thousands of mutations have emerged since the beginning of the pandemic throughout all virus genomes sequenced to date, resulting in thousands of distinct variants. However, some variants have recently been discovered that appear to increase transmissibility and may affect illness pervasiveness. In this study, we investigated SARS-CoV-2 variants and how countries intervene with them. We also depicted the top 25 countries where the Omicron variant is prevalent, with the UK, US, Denmark, France, and Australia having the top five places as of January 13, 2022. The perception of SARS-CoV-2 variants was investigated in those five countries, and the propagation rate of the Omicron variant was determined to be 51%, 29%, 26%, 15%, and 44%, respectively, indicating that the Omicron variant is the most prevalent among the others. Then, a study of SARS-CoV-2 infection test rate based on tests conducted per one million populations with a number of sequences in those five countries reveals that 25%, 73%, 1.6%, 4.8%, and 1.5%, respectively, it suggests that viral testing should be increased in all five countries since it will help to determine the precise distribution of variants and aid governments in making policy decisions for public safety. We anticipated the production of new variants strains. This study implies that limiting disease transmissions, such as acquiring a coronavirus disease 2019 vaccine and booster doses for those aged 18 and older, as well as wearing the mask in public places, is the best strategy to prevent the emergence of new variants.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35112734
DOI: 10.1002/jmv.27634
ABSTRACT: There is a growing concern that ongoing evolution of SARS-CoV-2 could lead to variants of concern (VOC) that are capable of avoiding some or all of the multifaceted immune response generated by both prior infection or vaccination, with the recently described B.1.1.529 (Omicron) VOC being of particular interest. Peripheral blood mononuclear cell samples from PCR-confirmed, recovered COVID-19 convalescent individuals (n = 30) infected with SARS-CoV-2 in the United States collected in April and May 2020 who possessed at least one or more of six different HLA haplotypes were selected for examination of their anti-SARS-CoV-2 CD8(+) T-cell responses using a multiplexed peptide-major histocompatibility complex tetramer staining approach. This analysis examined if the previously identified viral epitopes targeted by CD8(+) T cells in these individuals (n = 52 distinct epitopes) are mutated in the newly described Omicron VOC (n = 50 mutations). Within this population, only one low-prevalence epitope from the Spike protein, restricted to two HLA alleles and found in 2/30 (7%) individuals, contained a single amino acid change associated with the Omicron VOC. These data suggest that virtually all individuals with existing anti-SARS-CoV-2 CD8(+) T-cell responses should recognize the Omicron VOC and that SARS-CoV-2 has not evolved extensive T-cell escape mutations at this time. IMPORTANCE The newly identified Omicron variant of concern contains more mutations than any of the previous variants described to date. In addition, many of the mutations associated with the Omicron variant are found in areas that are likely bound by neutralizing antibodies, suggesting that the first line of immunological defense against COVID-19 is compromised. However, both natural infection and vaccination develop T-cell-based responses in addition to antibodies. This study examined if the parts of the virus, or epitopes, targeted by the CD8(+) T-cell response in 30 individuals who recovered from COVID-19 in 2020 were mutated in the Omicron variant. Only one of 52 epitopes identified in this population contained an amino acid that was mutated in Omicron. These data suggest that the T-cell immune response in previously infected, and most likely vaccinated, individuals should still be effective against Omicron.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35229637
DOI: 10.1128/mbio.03617-21

ABSTRACT: As the latest identified novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variant of concern (VOC), the influence of Omicron on our globe grows promptly. Compared with the last VOC (Delta variant), more mutations were identified, which may address the characteristics of Omicron. Considering these crucial mutations and their implications including an increase in transmissibility, COVID-19 severity, and reduction of efficacy of currently available diagnostics, vaccines, and therapeutics, Omicron has been classified as one of the VOC. Notably, 15 of these mutations reside in the receptor-binding domain of spike glycoprotein, which may alter transmissibility, infectivity, neutralizing antibody escape, and vaccine breakthrough cases of COVID-19. Therefore, our present study characterizes the mutational hotspots of the Omicron variant in comparison with the Delta variant of SARS-CoV-2. Furthermore, detailed information was analyzed to characterize the global perspective of Omicron, including transmission dynamic, effect on testing, and immunity, which shall promote the progress of the clinical application and basic research. Collectively, our data suggest that due to continuous variation in the spike glycoprotein sequences, the use of coronavirus-specific attachment inhibitors may not be the current choice of therapy for emerging SARS-CoV-2 VOCs. Hence, we need to proceed with a sense of urgency in this matter.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34905235
DOI: 10.1002/jmv.27524

ABSTRACT: In 2019, the world faced a serious health challenge, the rapid spreading of a life-threatening viral pneumonia, coronavirus disease 2019 (COVID-19) caused by a betacoronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). As of January 2022 WHO statistics show more than 5.6 million death and about 350 million infection by SARS-CoV-2. One of the life-threatening aspects of COVID-19 is secondary infections and reduced efficacy of antibiotics against them. Since the beginning of COVID-19 many researches have been done on identification, treatment, and vaccine development. Bacterial viruses (bacteriophages) could offer novel approaches to detect, treat and control COVID-19. Phage therapy and in particular using phage cocktails can be used to control or eliminate the bacterial pathogen as an alternative or complementary therapeutic agent. At the same time, phage interaction with the host immune system can regulate the inflammatory response. In addition, phage display and engineered synthetic phages can be utilized to develop new vaccines and antibodies, stimulate the immune system, and elicit a rapid and well-appropriate defense response. The emergence of SARS-CoV-2 new variants like delta and omicron has proved the urgent need for precise, efficient and novel approaches for vaccine development and virus detection techniques in which bacteriophages may be one of the plausible solutions. Therefore, phages with similar morphology and/or genetic content to that of coronaviruses can be used for ecological and epidemiological modeling of SARS-CoV-2 behavior and future generations of coronavirus, and in general new viral pathogens. This article is a comprehensive review/perspective of potential applications of bacteriophages in the fight against the present pandemic and the post-COVID era.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35151823
DOI: 10.1016/j.micpath.2022.105442


ABSTRACT: BACKGROUND: The purpose of this study was to evaluate the necessity of COVID-19 vaccination in persons who have already had COVID-19. METHODS: Employees of Cleveland Clinic working in Ohio on Dec 16, 2020, the day COVID-19 vaccination was started, were included. Anyone who tested positive for COVID-19 at least once before the study start date was considered previously infected. One was considered vaccinated 14 days after receiving the second dose of a COVID-19 mRNA vaccine. The cumulative incidence of COVID-19, symptomatic COVID-19, and hospitalizations for COVID-19, were examined over the next year. RESULTS: Among 52238 employees, 4718 (9%) were previously infected, and 36922 (71%) were vaccinated by the study’s end. Cumulative incidence of COVID-19 was substantially higher throughout for those previously uninfected who remained unvaccinated than for all other groups, lower for the vaccinated than unvaccinated, and lower for those previously infected than those not. Incidence of COVID-19 increased dramatically in all groups after the Omicron variant emerged. In multivariable Cox proportional hazards regression, both prior COVID-19 and vaccination were independently associated with significantly lower risk of COVID-19. Among previously infected subjects, a lower risk of COVID-19 overall was not demonstrated, but vaccination was associated with a significantly lower risk of symptomatic COVID-19 in both the pre-Omicron (HR 0.60, 95% CI 0.40-0.90) and Omicron (HR 0.36, 95% CI 0.23-0.57) phases. CONCLUSIONS: Both previous infection and vaccination provide substantial protection against COVID-19. Vaccination of previously infected individuals does not provide additional protection against COVID-19 for several months, but after that provides significant protection at least against symptomatic COVID-19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34927270
DOI: 10.1002/jmv.27532


ABSTRACT: BACKGROUND: The purpose of this study was to evaluate the necessity of COVID-19 vaccination in persons with prior COVID-19. METHODS: Employees of Cleveland Clinic working in Ohio on Dec 16, 2020, the day COVID-19 vaccination was started, were included. Anyone who tested positive for COVID-19 at least once before the study start date was considered previously infected. One was considered vaccinated 14 days after receiving the second dose of a COVID-19 mRNA vaccine. The cumulative incidence of COVID-19, symptomatic COVID-19, and hospitalizations for COVID-19, were examined over the next year. RESULTS: Among 52238 employees, 4718 (9%) were previously infected, and 36922 (71%) were vaccinated by the study’s end. Cumulative incidence of COVID-19 was substantially higher throughout for those previously uninfected who remained unvaccinated than for all other groups, lower for the vaccinated than unvaccinated, and lower for those previously infected than those not. Incidence of COVID-19 increased dramatically in all groups after the Omicron variant emerged. In multivariable Cox proportional hazards regression, both prior COVID-19 and vaccination were independently associated with significantly lower risk of COVID-19. Among previously infected subjects, a lower risk of COVID-19 overall was not demonstrated, but vaccination was associated with a significantly lower risk of symptomatic COVID-19 in both the pre-Omicron (HR 0.60, 95% CI 0.40-0.90) and Omicron (HR 0.36, 95% CI 0.23-0.57) phases. CONCLUSIONS: Both previous infection and vaccination provide substantial protection against COVID-19. Vaccination of previously infected individuals does not provide additional protection against COVID-19 for several months, but after that provides significant protection at least against symptomatic COVID-19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35028662
DOI: 10.1093/cid/ciac022

**ABSTRACT:** The Omicron (B.1.1.529) variant of SARS-CoV-2 emerged in November 2021 and is rapidly spreading among the human population(1). Although recent reports reveal that the Omicron variant robustly escapes vaccine-associated and therapeutic neutralization antibodies(2-10), the pathogenicity of the virus remains unknown. Here we show that the replication of Omicron is substantially attenuated in human Calu3 and Caco2 cells. Further mechanistic investigations reveal that Omicron is inefficient in its use of transmembrane serine protease 2 (TMPRSS2) compared with wild-type SARS-CoV-2 (HKU-001a) and previous variants, which may explain its reduced replication in Calu3 and Caco2 cells. The replication of Omicron is markedly attenuated in both the upper and lower respiratory tracts of infected K18-hACE2 mice compared with that of the wild-type strain and Delta (B.1.617.2) variant, resulting in its substantially ameliorated lung pathology. Compared with wild-type SARS-CoV-2 and the Alpha (B.1.1.7), Beta (1.351) and Delta variants, infection by Omicron causes the lowest reduction in body weight and the lowest mortality rate. Overall, our study demonstrates that the replication and pathogenicity of the Omicron variant of SARS-CoV-2 in mice is attenuated compared with the wild-type strain and other variants.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35062016
**DOI:** 10.1038/s41586-022-04442-5


**ABSTRACT:** The Severe Acute Respiratory Syndrome-associated Coronavirus 2 (SARS-CoV-2) was an outbreak in December, 2019 and rapidly spread to the world. All variants of SARS-CoV-2, including the globally and currently dominant Delta variant (Delta-SARS-CoV-2), caused severe disease and mortality. Among all variants, Delta-SARS-CoV-2 had the highest transmissibility, growth rate, and secondary attack rate than other variants except for the new variant of Omicron that still exists with many unknown effects. In Taiwan, the pandemic Delta-SARS-CoV-2 began in Pingtung from 14 June 2021 and ceased at 11 July 2021. Seventeen patients were infected by Delta-SARS-CoV-2 and 1 person died during the Pingtung outbreak. The Public Health Bureau of Pingtung County Government stopped the Delta-SARS-CoV-2 outbreak within 1 month through measures such as epidemic investigation, rapid gene sequencing, rapidly expanding isolation, expanded screening of the Delta-SARS-CoV-2 antigen for people who lived in regional villages, and indirect intervention, including rapid vaccination, short lockdown period, and travel restrictions. Indirect environmental factors, such as low levels of air pollution, tropic weather in the summer season, and rural areas might have accelerated the ability to control the Delta-SARS-CoV-2 spread. This successful experience might be recommended as a successful formula for the unvaccinated or insufficiently vaccinated regions.

**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35162443
**DOI:** 10.3390/ijerph19031421


**URL:** https://www.ncbi.nlm.nih.gov/pubmed/35151048
**DOI:** 10.1016/j.jcv.2022.105101


**ABSTRACT:** Multiple variants of SARS-CoV-2 have emerged and are now prevalent at the global level. Currently designated variants of concern (VOCs) are B.1.1.7, B.1.351, P.1, B.1.617.2 variants and B.1.1.529. Possible options for VOC are urgently required as they carry mutations in the virus spike protein that allow them to spread more easily and cause more serious illness. The primary targets for most therapeutic methods against SARS-CoV-2 are the S (Spike) protein and RBD (Receptor-Binding Domain), which alter the binding to ACE2 (Angiotensin-Converting Enzyme 2). The most popular of these strategies involves the use of drug
development targeting the RBD and the NTD (N-terminal domain) of the spike protein and multiple epitopes of the S protein. Various types of mutations have been observed in the RBDs of B.1.1.7, B.1.351, P, and B.1.620. The incidence of RBD mutations increases the binding affinity to the ACE2 receptor. The high binding affinity of RBD and ACE2 has provided a structural basis for future evaluation of antibodies and drug development. Here we discuss the variants of SARS-CoV-2 and recent updates on the clinical evaluation of antibody-based treatment options. Presently, most of the antibody-based treatments have been effective in patients with SARS-CoV-2. However, there are still significant challenges in verifying independence, and the need for further clinical evaluation.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35237535
DOI: 10.3389/fcimb.2022.839170


ABSTRACT: On December 2, 2021, the Minnesota Department of Health (MDH) notified CDC of a COVID-19 case caused by sequence-confirmed SARS-CoV-2 B.1.1.529 (Omicron) variant in a Minnesota resident (patient A), the first such case identified in the state and one of the earliest identified in the United States. Patient A had attended a large indoor convention in New York, New York with approximately 53,000 attendees from 52 U.S jurisdictions and 30 foreign countries during November 19-21, 2021, and had close contact(dagger) during 5 days with 29 fellow attendees. The convention required attendees to have received >/=1 COVID-19 vaccine dose and enforced mask-use while indoors. On November 22, these close contact attendees were directly and immediately notified by patient A of their exposure to SARS-CoV-2, and they sought testing over the next few days while quarantined or isolated. As part of the larger investigation into SARS-CoV-2 transmission at the convention, a subinvestigation was conducted during December by CDC, MDH, and respective state and local health departments to characterize the epidemiology of Omicron variant infection among this group of close contacts and determine the extent of secondary household transmission. Among 30 convention attendees that included patient A (the index patient) and the 29 other close contacts, 23 were interviewed, among whom all were fully vaccinated, including 11 (48%) who had received a booster dose; all 23 sought testing, and 16 (70%) received a positive SARS-CoV-2 test result. Fewer attendees who had received a booster dose before the convention received a positive test result (six of 11) compared with those who had not received a booster dose (10 of 12). The 16 attendees with positive test results had a total of 20 household contacts, 18 of whom sought testing after exposure; six received a positive test result for SARS-CoV-2. None of the persons with positive test results was hospitalized or died. There was limited convention-associated transmission identified outside of this cluster; the larger investigation included cases of both SARS-CoV-2 B.1.617.2 (Delta) and Omicron, and all Omicron cases were associated with this group (1). Data from this investigation reinforces the importance of COVID-19 booster doses in combination with early notification and other multicomponent prevention measures to limit transmission and prevent severe illness from Omicron and other SARS-CoV-2 variants.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35176004
DOI: 10.15585/mmwr.mm7107a3


ABSTRACT: To clarify transmissibility of the severe acute respiratory syndrome coronavirus 2 Omicron variant, we determined serial intervals and secondary attack rates among household contacts in South Korea. Mean serial interval for 12 transmission pairs was 2.9 days, and secondary attack rate among 25 households was 50.0%, raising concern about a rapid surge in cases.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35107418
DOI: 10.3201/eid2803.212607

ABSTRACT: The occurrence of the omicron variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has importantly impacted surveillance and diagnosis, and has changed the therapeutic landscape of coronavirus disease 2019 (COVID-19). We present the first documented case of locally acquired SARS-CoV-2 omicron variant in Romania in a patient with no recent travel outside the country. We also present the full results of the epidemiological investigation that led to the identification of the index case in a co-worker who had developed mild symptoms shortly after returning from the UK and who had undergone multiple rapid antigen tests with negative results prior to being tested by RT-PCR. We highlight potential lessons learned and describe further directions for actionable research and development in the field of COVID-19.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35204439
DOI: 10.3390/diagnostics12020348


ABSTRACT: The Beijing, 2022 Olympics will be the second Games held amid the COVID-19 pandemic. Due to the unique circumstances the 2022 Games face-the Omicron spread, high virus transmissibility in winters, and uncertainties about vaccine efficacy and future variants of concern, safety measures amid the Beijing, 2022 Games will be one of the most intricate among large international events held during the pandemic. To ensure athletes' health, safety, and ability to participate in the Games, the organizers have introduced the Olympic COVID-free "bubble" protection ecosystem, in which COVID-free athletes could stay and be protected from potential infections that could upend their Games plans, if not their career as well. However, while staying in the "bubble" is key for athletes' health and success, there is a lack of insights on factors that might prevent athletes from continuing their scheduled Olympic journey as scheduled. To shed light on the issue, based on Beijing, 2022 Olympic Playbooks and most up-to-date guidance issued, this article and its accompanying infographic were developed to illustrate factors that could influence athletes' ability to join and stay in the "bubble", participate in the Games, and further build their career. Furthermore, we also adapted and integrated easy-to-adopt mental health de-stress techniques recommended by the World Health Organization to help athletes better thrive amid the Beijing, 2022 Winter Olympics, in or outside of the "bubble".

URL: https://www.ncbi.nlm.nih.gov/pubmed/35128490
DOI: 10.1016/j.bbih.2022.100424


URL: https://www.ncbi.nlm.nih.gov/pubmed/35128386
DOI: 10.1016/j.clinpr.2022.100134


URL: https://www.ncbi.nlm.nih.gov/pubmed/35175280
DOI: 10.1001/jama.2022.2274


ABSTRACT: Background: SARS-CoV-2 infections and hospitalizations are rising in the US and other countries after the emergence of the Omicron variant. Currently, data on infection rates, severity and racial/ethnic and gender disparities from Omicron in the US is limited. Method: We performed a retrospective cohort study of a large, geographically diverse database of patient electronic health records (EHRs) in the US. The study population comprised 881,473 patients who contracted SARS-CoV-2 infection for the first time between
Evidence Search Report: EOC211220v010 ESR

9/1/2021-1/16/2022, including 147,964 patients infected when Omicron predominated (Omicron cohort), 633,581 when Delta predominated (Delta cohort) and another 99,928 infected when the Delta predominated but just before the Omicron variant was detected in the US (Delta-2 cohort). We examined monthly incidence rates of COVID-19 infections stratified by age groups, gender, race and ethnicity, compared severe clinical outcomes including emergency department (ED) visits, hospitalizations, intensive care unit (ICU) admissions, and mechanical ventilation use between propensity-score matched Omicron and Delta cohorts stratified by age groups (0-4, 5-17, 18-64 and a per thousand yen 65 years), and examined racial/ethnic and gender differences in severe clinical outcomes. Findings: Among 147,964 infected patients in the Omicron cohort (average age: 39.1 years), 56.7% were female, 2.4% Asian, 21.1% Black, 6.2% Hispanic, and 51.8% White. The monthly incidence rate of COVID infections (new cases per 1000 persons per day) was 0.5-0.7 when Delta predominated, and rapidly increased to 3.8-5.2 when Omicron predominated. In January 2022, the infection rate was highest in children under 5 years (11.0) among all age groups, higher in Black than in White patients (14.0 vs. 3.8), and higher in Hispanic than in non-Hispanic patients (8.9 vs. 3.1). After propensity-score matching for demographics, socio-economic determinants of health, comorbidities and medications, risks for severe clinical outcomes in the Omicron cohort were significantly lower than in the Delta cohort: ED visits: 10.2% vs. 14.6% (risk ratio or RR: 0.70 [0.68-0.71]); hospitalizations: 2.6% vs. 4.4% (RR: 0.58 [0.55-0.60]); ICU admissions: 0.47% vs. 1.00% (RR: 0.47 [0.43-0.51]); mechanical ventilation: 0.08% vs. 0.3% (RR: 0.25 [0.20-0.31]). Similar reduction in disease severity was observed for all age groups. There were significant racial/ethnic and gender disparities in severe clinical outcomes in the Omicron cohort, with Black, Hispanic patients having more ED visits and ICU admissions than White and non-Hispanic patients, respectively and women had fewer hospitalization and ICU admission than men. Interpretation: The incidence rate of COVID infection during the omicron predominant period (prevalence >92%) was 6-8 times higher than during the Delta predominant period that preceded it consistent with greater infectivity. The incidence rate was highest among those less than 5 years of age, and in Black and Hispanic patients. COVID infections occurring when the Omicron predominated were associated with significantly less frequent severe outcomes than in matched patients when the Delta variant predominated. There were significant racial, ethnic and gender disparities in severe clinical outcomes, with Black and Hispanic patients and men disproportionately impacted.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35233579
DOI: 10.1101/2022.02.21.22271300

86. Yang W, Shaman J. Viral replication dynamics could critically modulate vaccine effectiveness and should be accounted for when assessing new SARS-CoV-2 variants. Influenza Other Respir Viruses. 2022;16(2):366-7. DOI: 10.1111/irv.12961

URL: https://www.ncbi.nlm.nih.gov/pubmed/35014184
DOI: 10.1111/irv.12961


ABSTRACT: With the increased prevalence of new SARS-CoV-2 variants of concern, such as Delta and Omicron, the COVID-19 pandemic has become an ongoing human health disaster, killing millions worldwide. SARS-CoV-2 invades its host through the interaction of its spike (S) protein with a host cell receptor, angiotensin-converting enzyme 2 (ACE2). In addition, heparan sulfate (HS) on the surface of host cells plays an important role as a co-receptor for this viral pathogen-host cell interaction. Our previous studies demonstrated that many sulfated glycans, such as heparin, fucoidans, and rhamnan sulfate have anti-SARS-CoV-2 activities. In the current study, a small library of sulfated glycans and highly negatively charged compounds, including pentosan polysulfate (PPS), mucopolysaccharide polysulfate (MPS), sulfated lactobionic acid, sulodexide, and defibrotide, was assembled and evaluated for binding to the S-proteins and inhibition of viral infectivity in vitro. These compounds inhibited the interaction of the S-protein receptor-binding domain (RBD) (wild type and different variants) with immobilized heparin, a highly sulfated HS, as determined using surface plasmon resonance (SPR). PPS and MPS showed the strongest inhibition of interaction of heparin and S-protein RBD. The competitive binding studies showed
that the IC50 of PPS and MPS against the S-protein RBD binding to immobilized heparin was ~35 nM and ~9 nM, respectively, much lower than the IC50 for soluble heparin (IC50 = 56 nM). Both PPS and MPS showed stronger inhibition than heparin on the S-protein RBD or spike pseudotyped lentiviral particles binding to immobilized heparin. Finally, in an in vitro cell-based assay, PPS and MPS exhibited strong antiviral activities against pseudotyped viral particles of SARS-CoV-2 containing wild-type or Delta S-proteins.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35215371
DOI: 10.3390/ph15020258


ABSTRACT: Monoclonal antibody therapy for the treatment of SARS-CoV-2 infection has been highly successful in decreasing disease severity; however, the recent emergence of the heavily mutated Omicron variant has posed a challenge to this treatment strategy. The Omicron variant BA.1 has been found to evade neutralization by several of the therapeutic monoclonal antibodies authorized for emergency use, while Vir-7831 and a cocktail consisting of monoclonal antibodies AZD8895+AZD1061 retain significant neutralizing activity. A newly emerged variant, Omicron BA.2, containing some of the BA.1 mutations plus an additional 6 mutations and 3 deletions, 3 of which lie in the receptor binding domain, has been found to be spreading with increased transmissibility. We report here, using spike protein-pseudotyped lentiviruses, decreased neutralization of BA.2 by several therapeutic monoclonal antibodies but that the mixture of AZD8895+AZD1061 retained substantial neutralizing activity against BA.2.

URL: https://www.ncbi.nlm.nih.gov/pubmed/35194604
DOI: 10.1101/2022.02.15.480166


ABSTRACT: Recently a new variant of SARS-CoV-2 was reported from South Africa. World Health Organization (WHO) named this mutant as a variant of concern - Omicron (B.1.1.529) on 26th November 2021. This variant exhibited more than thirty amino acid mutations in the spike protein. This mutation rate is exceeding the other variants by approximately 5-11 times in the receptor-binding motif of the spike protein. Omicron (B.1.1.529) variant might have enhanced transmissibility and immune evasion. This new variant can reinfect individuals previously infected with other SARS-CoV-2 variants. Scientists expressed their concern about the efficacy of already existing COVID-19 vaccines against Omicron (B.1.1.529) infections. Some of the crucial mutations that are detected in the receptor-binding domain of the Omicron variant have been shared by previously evolved SARS-CoV-2 variants. Based on the Omicron mutation profile in the receptor-binding domain and motif, it might have collectively enhanced or intermediary infectivity relative to its previous variants. Due to extensive mutations in the spike protein, the Omicron variant might evade the immunity in the vaccinated individuals.

URL: https://www.ncbi.nlm.nih.gov/pubmed/34982466
DOI: 10.26355/eurrev_202112_27653

90. Kupferschmidt K. Scientists see a 'really, really tough winter' with Omicron. Science. 2021;374(6574):1421-2. DOI: 10.1126/science.acz9834

URL: https://www.ncbi.nlm.nih.gov/pubmed/34914506
DOI: 10.1126/science.acz9834


URL: https://www.ncbi.nlm.nih.gov/pubmed/34882443
DOI: 10.1126/science.acx9782
### Appendix 1: Evidence Search Details

| Filters, Limits & Exclusions: | English only  
| [February 25, 2022 – March 04, 2022] |
| Sources Searched: | Alberta Health Services  
| BCCDC  
| CDC  
| CINAHL  
| City of Toronto  
| Cochrane  
| COVID-End  
| ECDC  
| Embase (Ovid)  
| Evidence Check Australia  
| FDA  
| Google  
| Google Scholar  
| Government of Ireland  
| Health Canada/ PHAC  
| Health Information and Quality Authority  
| HSE Ireland  
| Imperial College London  
| LitCOVID  
| L-OVE  
| McMaster Plus Evidence Alerts  
| MEDLINE (Ovid)  
| MedRxiv  
| NCCMT  
| Public Health Ontario  
| PubMed  
| TRIP Pro  
| UK Health Security Agency  
| United Nations, PAHO  
| Veteran’s Affairs Database  
| WHO Global Coronavirus Research Database  
| WHO  |

Librarian(s):  
Mark Mueller, Clinical Librarian, Saskatchewan Health Authority  
Lukas Miller, Clinical Librarian, Saskatchewan Health Authority

### Appendix 2: Search Strategies

#### Embase, Ovid MEDLINE(R)

<table>
<thead>
<tr>
<th># Searches</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 (coronavirus/ or betacoronavirus/ or coronavirus infections/ or sars-related coronavirus/) and (disease outbreaks/ or epidemics/ or epidemic/ or pandemics/ or pandemic/)</td>
<td>51074</td>
</tr>
<tr>
<td>2 (nCoV* or 2019nCoV or 19nCoV or COVID19* or COVID or SARS-COV-2 or SARS-CoV-2 or SARS-CoV2 or Severe Acute Respiratory Syndrome Coronavirus 2 or Severe Acute Respiratory Syndrome Coronavirus 2).ti,ab,kw,hw,ot.</td>
<td>465666</td>
</tr>
<tr>
<td>3 ((new or novel or &quot;19&quot; or &quot;2019&quot; or Wuhan or Hubei or China or Chinese) adj3 (coronavirus* or corona virus* or betacoronavirus* or CoV or HCoV)).ti,ab,kw,hw,ot.</td>
<td>268844</td>
</tr>
<tr>
<td>4 ((coronavirus* or corona virus* or betacoronavirus* or COVID*) adj3 (pandemic* or epidemic* or outbreak* or crisis)).ti,ab,kw,hw,ot.</td>
<td>192756</td>
</tr>
</tbody>
</table>
(longCOVID* or postCOVID* or postcoronavirus* or postSARS*).ti,ab,kf,kw,hw. 106
or/1-5 489896
("B.1.1.529" or "B11529" or "GR/484A" or omicron).ti,ab,kw,hw,kf,ot. 2038
6 and 7 1372
exp Epidemiology/ or exp Morbidity/ or exp Mortality/ 4978465
(epidemiolog* or morbidit* or mortalit* or "cause of death" or causation or etiolog* or disease outcome? or fatal outcome? or survival or incidence? or prevalence? or attack rate or basic reproduction or "R0" or "R 0" or transmissibility or severity).ti,ab,kf,kw,hw. 12114602
119 or 10 12835047
128 and 11 409
13 limit 12 to updaterange="oemezd[20220225-],medall[20220225-]" 119
14 remove duplicates from 13 94

Keywords Used in Other Resources
- "B.1.1.529" or "B11529" or "GR/484A" or "BA.2" or omicron

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