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“Asymptomatic COVID-19 on LSUHSC’s Campus: Antibodies, PCR Tests, and Variants”

Background: Rapid spreading of the highly contagious severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) caused a pandemic of coronavirus disease 2019 (COVID-19) which has infected 188,128,952 people and resulted in 4,059,339 deaths worldwide (WHO COVID-19 Dashboard). Despite profound disease prevention measures and recent attempts at widespread vaccination, the virus continues to mutate and infect new people each day.

Objective: The goal of this study is to analyze the data collected from the COVID-19 screening and testing program at LSUHSC-New Orleans. This includes antibody testing data, exposure and symptom questionnaires, PCR viral testing, and viral RNA sequencing data from deidentified, asymptomatic staff and students of LSUHSC-NO.

Methods: From July 15, 2020, to November 15, 2020, LSUHSC-NO implemented a COVID-19 screening and testing program to track, document, and respond to cases of asymptomatic COVID-19 among its staff and students. A total of 1346 participants were screened. After an online questionnaire determined them to be asymptomatic for COVID-19, participants were tested for IgM and IgG antibodies to the SARS-CoV-2 nucleocapsid protein. Those with positive antibody results or recent exposure were referred to the LSUHSC/HCN clinic for RT-PCR testing. PCR results were recorded, and the viral genomes of PCR-positive samples were later sequenced by LSUHSC’s Precision Medicine lab. The participants were given an artificial identifier, and data from these sources was analyzed using Excel and Stata statistical software.

Results: The study found intriguing correlations between the antibody profiles of the participants, race and ethnicity, and PCR results. Additionally, genetic sequencing of the viral samples revealed that B.1.2, B.1.311, and B.1.234 lineages were most prominent on LSUHSC’s campus during this time. Interestingly, the B.1.429 (California lineage) was also found among our samples. In addition, the Precision Medicine Lab’s recent sequencing results from UMC’s summer 2021 patients can be juxtaposed with the sequencing results of the original asymptomatic 2020 participants for an interesting comparison of variant distributions.

Conclusion: The compelling findings of this study, in addition to other similar studies, can be used to observe changes in COVID-19 prevalence, antibody status, and lineage patterns over time. These additions to the rapidly developing field of COVID-19 research can help institutions like LSUHSC learn from the results of past disease control measures and more efficiently minimize similar outbreaks in the future.

Citation: WHO COVID-19 Dashboard. Geneva: World Health Organization, 2020. Available online: <https://covid19.who.int/> (last cited: July 15, 2021).