



# Asymptomatic COVID-19 on LSUHSC's Campus: Antibodies, PCR Testing, and Variants

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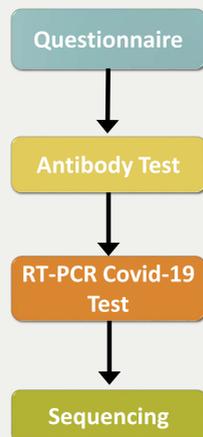
Crabtree Laboratory  
LSUHSC Genetics

## Introduction

- 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 resulted in 751,874 cases and 14,321 deaths in Louisiana.<sup>1</sup>
- From June 15 to November 15, 2020, LSUHSC - New Orleans implemented a screening and testing program to help track and manage the spread of COVID-19 on campus.

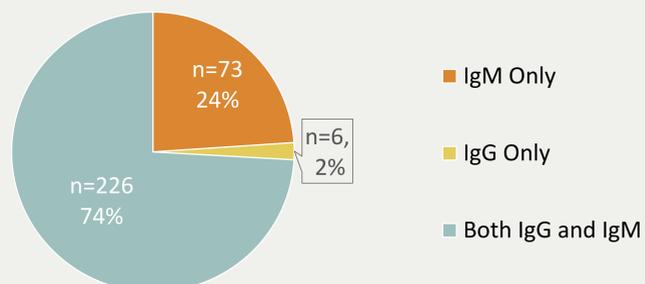
## Methods

- After an online questionnaire determined participants to be asymptomatic for COVID-19, they 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.
- The viral genomes of PCR-positive samples were later sequenced by the Precision Medicine lab.
- The participants were given an artificial identifier, and data from these sources was analyzed using Excel and Stata statistical software.
- A total of 1346 asymptomatic participants were screened via antibody testing, PCR testing, or both.



## Antibody Distribution

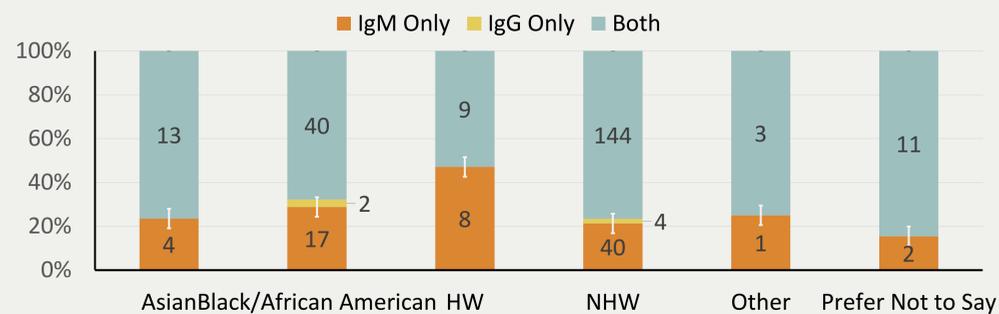
### Distribution of First-Time Seropositive Cases



**Figure 1.** Out of 1269 people who were tested for antibodies, 305 were positive for some antibody at some time. The distribution of only the first positive antibody result for each participant is represented in this graph.

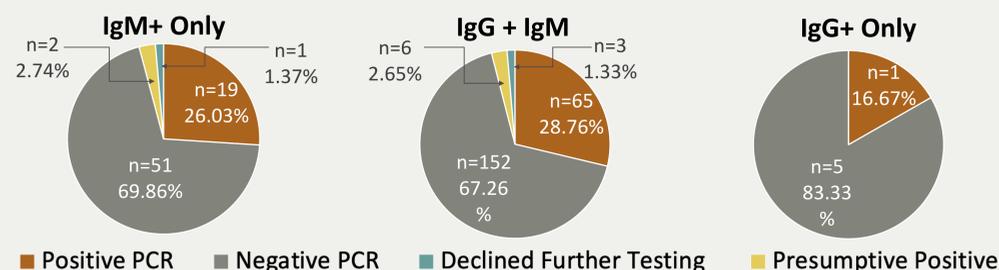
## Antibodies and Race/Ethnicity

### Distribution of Positive Antibody Results According to Race/Ethnicity



**Figure 2.** Participants who took an antibody test also submitted demographic information. The distribution of first-time seropositive results are shown according to race/ethnicity. n=305.

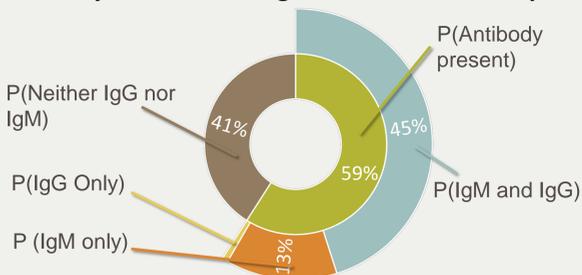
## PCR Results and Antibody Status



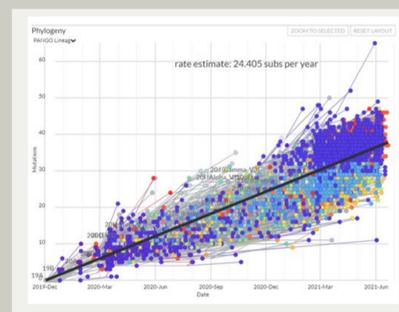
**Figure 3.** Results of PCR viral testing within five days of first-time seropositive antibody test, according to immunoglobulin distributions. Raw numbers are shown.

## COVID-Positive Patterns

### Antibody Results Among PCR-Positive Participants



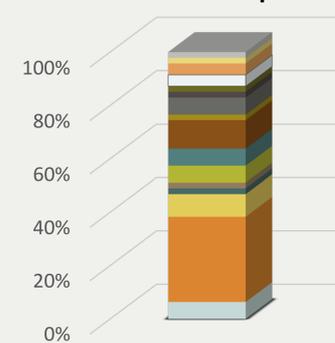
**Figure 4.** The probability of various antibody statuses among PCR-positive participants within five days of first antibody test. n=144.



**Figure 5.** Mutations over time according to PANGOLIN Lineage.<sup>2</sup>

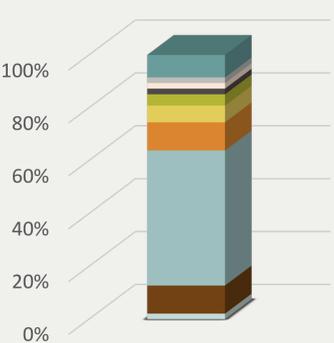
## Variants

### Variants Among LSUHSC Summer 2020 samples



B.1, B.1.239, B.1.306, B.1.361, B.1.577, B.1.612, B.1.2, B.1.240, B.1.311, B.1.429, B.1.595, B.1.234, B.1.243, B.1.349, B.1.564, B.1.595.1

### Variants Among UMC Summer 2021 Samples



B.1, B.1.1.7, B.1.234, B.1.429, B.1.612, B.1.1.519, B.1.2, B.1.243, B.1.526, P.1

**Figure 6.** The distribution of Pangolin lineages among asymptomatic LSUHSC Summer 2020 samples (n=47) and symptomatic UMC Summer 2021 samples (n=47) are shown. Lineages were assigned to samples with coverage >84% (left) and >63% (right) using Illumina DRAGEN COVID Lineage App. Samples with >90% coverage were uploaded to international database GISAID.

## Example of California Variant Mutation

```
LSUsample001-01112021 SARS-CoV-2 GCAAACGGAAAGATTGCTGATTATAAATATAAATACCAGATGATTTTACAGGCTGCGT 22860
GCAAACGGAAAGATTGCTGATTATAAATATAAATACCAGATGATTTTACAGGCTGCGT 22860
LSUsample001-01112021 SARS-CoV-2 TATAGCTTGAATCTTAACAATCTTGATTCTAAGGTTGGTGAATTTATAATACCGTA 22920
TATAGCTTGAATCTTAACAATCTTGATTCTAAGGTTGGTGAATTTATAATACCGTA 22920
```

**Figure 7.** This alignment between an LSUHSC sample and the original SARS-CoV-2 Wuhan consensus sequences reveals a T22917G substitution, which results in the L452R mutation in the spike protein of SARS-CoV-2. The L452R mutation is the defining mutation for the B.429 California (Epsilon) variant.

## Conclusions

The compelling findings of this study and 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 changing field of COVID-19 research can help institutions like LSUHSC learn from past disease control measures and more efficiently minimize similar outbreaks in the future.