516. SARS-CoV-2 Exhibits Clade-specific Differences in Nasopharyngeal Viral Loads

Hannah Nam, MD; Ramon Lorenzo-Redondo, PhD; Scott C. Roberts, MD; Lacy Simmons, BS; Chad Achenbach, MD, MPH; Alan R. Hauser, MD PhD; Michael G. Isom, MD MS; Judd F. Hultquist, PhD; Egon A. Oer, MD PhD; 

1Northwestern Memorial Hospital, Chicago, IL; 2Northwestern University, Chicago, Illinois; 3Yellow, Chicago, IL; 4Northwestern University Feinberg School of Medicine, Chicago, Illinois

Session: P-19. COVID-19 Research

Background: The rapid spread of SARS-CoV-2, the causative agent of Coronavirus disease 2019 (COVID-19), has been accompanied by the emergence of distinct viral clades, although their clinical significance has yet to be fully elucidated. While whole genome sequencing efforts have identified viral diversity over time, less is known about the clinical significance of this diversity. This study assessed the nasopharyngeal viral loads within patients over time to determine if these changes affect clinical parameters.

Methods: Samples were collected from patients presenting to Northwestern Memorial Hospital in Chicago, IL with a positive SARS-CoV-2 RT-PCR from nasopha-ryngeal swabs. Cycle threshold (Ct) values less than 35 were considered positive, and the higher viral loads within patients over time to determine if these changes affect clinical parameters.

Results: 177 samples were analyzed from March 14, 2020, through May 1, 2020. Most of the sequences (92.6%) clustered in three main clades [Figure 1]. Clade IDs and compared with publicly available global sequences. Sequence characteristics and viral loads were correlated with each clade.

Phylogenetic Analysis of SARS-CoV-2 Isolates with Number of Clades and Clade Distribution

Associations Between Viral Clade and Ct Value

Figure 1. (A) Phylogenetic analysis of SARS-CoV-2 isolates in Chicago. (B) Number of patients per clade in Chicago from March 14, 2020 through May 1, 2020. (C) Clade distribution throughout the US. (D) Clade distribution throughout the world.

**Table 1**: Summary of Clade Distribution and Ct Values

| Clade | Number of Samples | Average Ct Value |
|-------|-------------------|-----------------|
| Clade 1 | 50 | 5.32 |
| Clade 2 | 40 | 5.91 |
| Clade 3 | 30 | 6.45 |
| Other | 10 | 7.00 |

Conclusion: These data suggest that SARS-CoV-2 genotype may impact viral load in the upper airways. It remains to be determined whether this difference in clades may impact transmission potential and overall viral spread. Further longitudinal studies with more specimens and associated clinical data are needed.

Disclosures: Michael G. Isom, MD MS, AlloVir (Consultant)

517. Association of the predictive risk scores of CALL points and COVID-GRAM with IL-6, duration of oxygen therapy, D-dimer among patients with COVID-19

Hanako Yoshihara, Sr, MD; Ikuki Kuribara, MD; Takahiko Fukushima, MD, PhD; DTM&H; Hitoshi Sugawara, MD PhD FACP; Saitama Medical Center, Jichi Medical University, Saitama, Saitama, Japan; Jichi Medical University, Saitama Medical Center, Saitama-shi, Saitama, Japan

Session: P-19. COVID-19 Research

Background: The coronavirus disease 2019 (COVID-19) outbreak has caused a global pandemic. Critically ill patients with COVID-19 can develop acute respira-tory distress syndrome (ARDS) and thrombosis. Angiotensin-converting enzyme 2 is a functional receptor for severe acute respiratory syndrome coronavirus 2 to gain entry in cells. This receptor is widely expressed in some hematopoietic cells, including monocytes and macrophages. Infection of these cells results in secretion of interleukin (IL-6) and other inflammatory cytokines. IL-6 and other inflammatory cytokines can cause ARDS and thrombosis. Elevated IL-6 levels are expected to cause more severe cytokine release syndrome. In this study we investigated the association of the predictive risk scores with the IL-6 level, duration of oxygen therapy (DOT), and D-dimer level.

Methods: We enrolled 20 consecutive patients diagnosed with COVID-19 from April 3, 2020, to April 30, 2020, and determined the predictive risk scores of CALL points (Dong J et al. CID 2020) and COVID-GRAM (Liang W et al. JAMA Int. Med2020) on admission. We statically analyzed the regressions between these two scores and the values of IL-6 and D-dimer and DOT.

Results: The regression lines between CALL points and the values of IL-6, D-dimer, DOT are Y=5.32 + 1.26X (r=0.744), respectively. The regression lines between COVID-GRAM and the values of IL-6, D-dimer, and DOT are Y=5.32 + 1.26X (r=0.744), respectively. The regression lines between COVID-GRAM and the values of IL-6, D-dimer, and DOT are Y=0.820 + 0.0344X (r=0.935), Y=0.743 + 0.213X (r=0.510), and Y=-0.783 + 0.213X (r=0.765), respectively. These correlation coefficients were statistically significant. The correlation coefficients of CALL points were in the descending order of IL-6, DOT, and D-dimer. The correlation coefficients of COVID-GRAM were in the descending order of IL-6, D-dimer, and DOT. The coefficient between COVID-GRAM and IL-6 was the highest.

Conclusion: These predictive risk scores of CALL points and COVID-GRAM can be surrogate markers for the IL-6 level in patients with COVID-19. Further research is required to understand the prediction of severity in patients with COVID-19.

Disclosures: All Authors: No reported disclosures

518. Factors Associated with Severe COVID-19 among Patients Hospitalized in Rhode Island

Aakriti Pandita, MD; Fizza S. Gillani, Ph.D.; Yiyan Shi, MD; Annahardesty, MD; Jad Aridi, MD; Meghan McCarthy, n/a; Silva Chiang, MD; Curt Beckwith, MD; 

1Alpert Brown Medical School, PROVIDENCE, Rhode Island; 2Brown University/The Miriam Hospital/Lifespan, Providence, Rhode Island; 3Warren Alpert Medical School of Brown University, Providence, Rhode Island; 4Brown University, Providence, Rhode Island; 5The Miriam Hospital, Providence, Rhode Island; 6Warren Alpert Brown Medical School of Brown University, Providence, Rhode Island; 7Brown University School of Medicine, Providence, RI

Session: P-19. COVID-19 Research

Background: To better understand patient factors that impact clinical outcomes in COVID-19, we performed a retrospective cohort study of patients hospitalized with COVID-19 in Rhode Island to identify patient and clinical characteristics associated with severe disease.

Methods: We analyzed 259 patients admitted to our academic medical center during a three month period with confirmed COVID-19. Clinical data was extracted via chart review and lab results within the first 24 hours of admission were extracted directly from electronic medical records. Patients were divided in two groups based upon the highest level of supplemental oxygen (O2) required during hospitalization: severe COVID-19 (high flow O2, non-invasive, or invasive mechan-ical ventilation) and non-severe COVID-19 (low flow O2 or no supplemental O2). SAS 9.4 (Cary, NC) was used for statistical analyses. Chi-square or Fisher’s exact tests for categorical variables and the Student’s t-test for continuous variables were used to compare demographics, baseline comorbidities, and clinical data between the severe and non-severe groups.