Investigator)**Leonard-Meron** (Grant/Research Support, Scientific Research Study Investigator)**Lilly** (Grant/Research Support, Scientific Research Study Investigator)

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

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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 nasopharyngeal swabs. Cycle threshold (Ct) values less than 35 were considered positive, and whole genome sequencing was performed by reverse transcription, multiplex PCR, and Nanopore sequencing. Phylogenetic analysis was conducted on sequenced isolates and compared with publicly available global sequences. Sequence characteristics and viral loads were correlated with each clade.

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 were ordered by relative abundance as Clades 1 (n=122, 68.9%), 2 (n=34, 19.2%), and 3 (n=8, 4.5%). Over this time, Clade 1 viruses have been increasing in incidence across the USA and globally while Clade 2 viruses were uniquely predominant in Illinois with limited global distribution. Ct values were compared across clades [Figure 2]. Significantly lower average Ct values (higher viral loads) were observed in Clade 1 relative to both Clade 2 (p=0.0002) and Clade 3 (p=0.0011). These findings were independent of time from symptom onset to specimen collection.

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

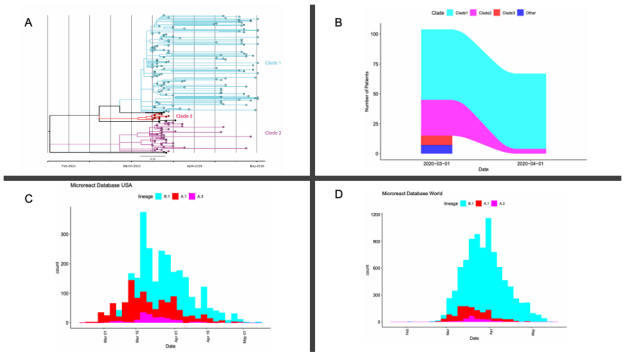

Figure 1. (A) Phylogenetic analysis of SARS-CoV-2 Isolates in Chicago. (B) Number of patients per clade in Chicago from March 14, 2020 through May 1, 2020. (C) Clade distribution throughout the US. (D) Clade distribution throughout the world.

Associations Between Viral Clade and Ct Value

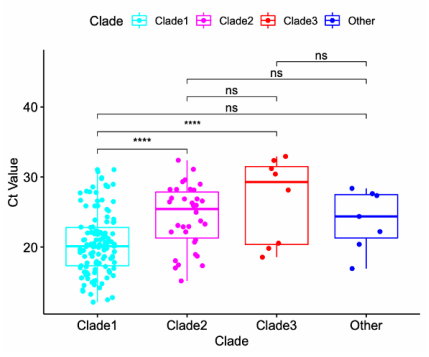

Figure 2. Associations between Viral Clade and Ct Value. PCR Cycle threshold (Ct) values of patient samples grouped by major Clade assignment. Horizontal lines in each box represent the median value and the lower and upper error bars are the interquartile ranges. Significance is indicated for the comparisons performed within each fitted model (** = q-value<0·05; **** = q-value <0·01).

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. Ison, 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

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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 respiratory 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 were Y=-2.09 + 0.618X (r=0.821), Y=-0.783 + 0.213X (r=0.510), and 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 were Y=-0.820 + 0.0344X (r=0.935), Y=-2.70 + 0.0205X (r=0.774), and Y=-1.92 + 0.0491X (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.

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

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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 mechanical 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.