Disclosures. All Authors: No reported disclosures

360. Evaluation of Cycle Threshold Values in Patients with Symptomatic COVID-19 Infection

Danielle Dixon, DO1; Julieta Madrid-Morales, MD2; Jose Cadena-Zuluaga, MD3; Christopher R. Frei, PharmD, FCCP, BCPS1; 1University of Texas Health, San Antonio, San Antonio, Texas; 2University of Texas Health Science Center at San Antonio, Texas, USA; San Antonio, Texas; 3University of Texas Health and science Center San Antonio, Audie L. Murphy VA Medical Center, San Antonio, Texas, San Antonio, Texas

Session: P-15. COVID-19 Diagnostics

Background. One of the tests used to identify COVID-19 infections is the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) reverse transcriptase quantitative polymerase chain reaction (RT-qPCR) test. There is a measure known as the cycle threshold (Ct) value, which provides an indirect measure of viral load. It has been proposed that the Ct value could help with clinical decisions regarding duration of isolation. We hypothesize that Ct values will correlate with symptom duration in a population of veterans with COVID-19 infection.

Methods. We reviewed the records of patients presenting to the emergency department (ED) or admitted to Audie L. Murphy VA Medical Center in San Antonio, Texas with positive SARS-CoV-2 PCR tests. We looked at patients who received multiple SARS-CoV-2 RT-qPCR tests. We compared date of onset of symptoms and cycle threshold values from their initial test to another test ordered after 7, 10, and 20 days from symptom onset. We recorded the Ct value for the N2 and E genes. Patients were classified into mild, severe and critical based on Center for Disease Control and Prevention (CDC) criteria. A Ct value of >30 as threshold for transmissible disease was used based on previously published studies.

Results. We identified 49 patients with more than two SARS-CoV-2 RT-qPCR tests. Patients with mild disease with tests less than or equal to ten days from symptom onset (n=10) had a mean Ct value 23.2 (±6.6) and 26.0 (±5.8) for the E and N2 genes. Patients with mild disease with tests greater than ten days from symptom onset (n=4) had mean Ct values of 26.0 (±6.5) and 27.8 (±6.8). When we stratified the patient population by disease severity, patients with severe and critical disease with tests less than ten days from symptom onset (n=24) had mean Ct values of 20.1 (±7.3) and 23.4 (±5.4). Patients with severe and critical disease greater than twenty days (n=8) had Ct values of 29.0 (±5.1) and 31.1 (±5.4).

Conclusion. We found that Ct values increased with longer symptom duration. We currently use the CDC criteria to discontinue isolation at ten days for mild disease and twenty days for severe and critical disease. The findings of this study suggest that our current practice for duration of isolation correlates with increasing Ct values near or above the threshold for transmissible disease.

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361. Aseptic Meningitis Associated to SARS Cov2 Infection and MIS-C: Pediatric Presentation of Covid-19

Mónica J. Olguín Quintana, MD1; SERGIO RENÉ BONILLA PELLEGRINI, MD2; RODOLFO N. JIMÉNEZ JUÁREZ, PhD3; María Citlalli Casillas, Casillas, Casillas3; 1Hospital Infantil de México Federico Gómez, Ciudad de México, Mexico City, Mexico; 2Hospital Infantil de México, Ciudad de México, Distrito Federal, Mexico; 3Hospital Español, Miguel Hidalgo, Distrito Federal, Mexico

Session: P-15. COVID-19 Diagnostics

Background. Novel SARS CoV2 may target the central nervous system and several neurological symptoms have been reported in patients with Coronavirus disease (COVID-19). Mucocutaneous and inflammatory symptoms are important in pediatric population associated to immune dysregulation. There are few reports of clinical manifestations in children and less frequently the isolation and affection of Central Nervous System.

Methods. A previously healthy four months female infant with familiar contact to SARS-CoV2 four weeks ago. Start with fever of 104°F, vomiting, maculopapular rash on the anterior thorax and upper extremities involving the palms and soles associated with edema. On physical examination, irritable, bulging anterior fontanelle, non-purulent bilateral conjunctival injection, cheilitis and rash was confirmed.

Results. Laboratory findings: thrombocytopenia, elevated D-Dimer, fibrinogen, PCT, CRP, ferritin and ESR with hypoalbuminemia. MIS-C is integrated with cutaneous, gastrointestinal and neurological affections. Empirically ceftriaxone, vancomycin and acyclovir are started due to suspicion of meningococcalpneumonia. RT-PCR...
for SARS-CoV-2 positive. CSS: transparent appearance, slightly xanthochromic color, coagulation and negative film. Proteins 105 mg/dl, glucose 45 mg/dl, leukocytes 121 mm3, erythrocytes 66 mm3, PMN 8% and MNN 92%. Negative culture, PCR Herpes Virus negative, Viral load for SARS-CoV2 in CSS 3,400 cpm/ml and plasma 118,900 cpm/ml. Asptic meningitis is confirmed by SARS-CoV-2. Antiviral and anti-biotics are discontinued and Gamma globulin and methylprednisolone are administered. Evolving favorably and egress at 6th day to complete oral steroid treatment for 3 more days.

Conclusion. The mechanism by which SARS-CoV2 affects the CNS is still unknown. This findings suggests direct infection can be possible. Although it is also described vascular affection has been found that the Spike protein of the virus binds to ACE-2 receptor present in the cerebral vascular endothelium. Neurological manifestations have been described even without respiratory symptoms. A novel pediatric case with viral load for SARS-CoV-2 in CSS is demonstrated. Importance of detecting SARS-CoV-2 in children with encephalitis, which can progress satisfactorily.

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362. Saliva as a Reliable Sample Type for Mass SARS-CoV-2 Testing Strategies
Anne Wyllie, PhD1; Chantal B. Vogels, PhD2; Orchard M. Allicock, PhD3; Anne Watkins, MPH4; Mary Petrone, Masters of Philosophy5; Deryn Yolda-Carr, B.S. Microbiology and Molecular Genetics6; Christina Harden, MPH7; Doug Brackney, PhD8; Chaney C. Kalinich, MPH9; Mallery I. Breban, B.S. Biology10; Isabel M. Ott, B.S. Biology11; Robby Sikka, MD12; Lelahon Kadiri, MD, PhD13; Nathan D. Grubbaugh, PhD14; Yale School of Medicine, New Haven, Connecticut; 2Yale School of Public Health, New Haven, Connecticut; 3Minnesota Timberwolves, Minneapolis, Minnesota; 4Yale University, New Haven, Connecticut; the Yale IMPACT Research Team

Session: P-15. COVID-19 Diagnostics

Background. Quickly detecting and isolating individuals positive for SARS-CoV-2 is essential for limiting virus spread. Policy makers rely on the number of active cases to make decisions, and individuals use this information to evaluate risk should they return to public spaces. Robust testing strategies have been plagued with limited authorized diagnostic assays and high test prices, with large-scale implementation hampered by worldwide supply chain issues.

Methods. Having identified its potential early in the pandemic, we simplified saliva based-COVID-19 diagnostic testing by (1) not requiring collection tubes with preservatives, (2) replacing nucleic acid extraction with a simple enzymatic and heating step, and (3) testing specimens for SARS-CoV-2 in duplex RT-qPCR. Moreover, we validated this approach ("SalivaDirect") with reagents and instruments from multiple vendors to circumvent supply chain disruptions.

Results. SalivaDirect's simplified protocol does not compromise on sensitivity. In our hospital cohort, we found a high positive agreement (94%) between saliva tested with SalivaDirect and nasopharyngeal swabs tested with a commercial RT-qPCR kit. With the National Basketball Association we tested 3,779 saliva specimens from healthy individuals and detected low rates of invalid (0.3%) and false-positive (< 0.05%) results. Using comparative assays and sample types, we also demonstrated SalivaDirect to efficiently detect SARS-CoV-2 in asymptomatic individuals.

SalivaDirect is a simplified method for SARS-CoV-2 detection

(a) Schematic overview of SalivaDirect workflow depicting the main steps of mixing saliva with proteinase K, heat inactivation, and duplex qRT-PCR testing. Figure created with BioRender.com. (B) SARS-CoV-2 is stable in saliva for at least 7 days at 4°C, room temperature (RT), and 30°C without addition of stabilizing buffers. Spiked-in saliva samples of low virus concentrations (12, 25, and 50 SARS-CoV-2 copies/mL) were kept at the indicated temperature for 7 days and then tested with SalivaDirect. N1 cycle threshold (Ct) values were lower when kept for 7 days at 30°C as compared to fresh specimens (Kruskal-Wallis; p = 0.03). Horizontal bars indicate the median. (C) Comparing Ct values for saliva treated with proteinase K and heat as compared to nucleic extraction yields higher N1 Ct values without extraction (Wilcoxon; p < 0.01). (D) Testing extracted nucleic acid from saliva with the N1 primer-probe set (singleplex) as compared to a multiplex assay showed stronger N1 detection in multiplex (Wilcoxon; p < 0.01). The dotted line in (B)–(D) indicates the limit of detection.

Conclusion. Saliva is a valid alternative to swabs for SARS-CoV-2 screening. Importantly, SalivaDirect enables labs to utilize existing infrastructure, improving test implementation time and requiring limited investment to scale-up to meet mass testing needs. With the safe and reliable self-collection of saliva, our vision is to help provide accessible and equitable testing solutions, especially in low-resource and remote settings.

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363. Characteristics of Envelope and Nuclear Gene Expression Patterns in 353. Individualized Prognostics in COVID-19 Facilitated by Computer Aided Recognition of Blood Leukocyte Subsets
Claudia R. Libertin, MD1; Prakash Kempaiaih, n/a2; Ravindra Durvasula, M.D.2; Ariel Rivas, DVM, PhD, PhD3; Mayo Clinic, Jacksonville, Jacksonville, FL; Mayo Clinic, Jacksonville, Florida; University of New Mexico, Albuquerque, New Mexico

Session: P-15. COVID-19 Diagnostics

Background. Reverse transcription-polymerase chain reaction (RT-PCR) is used for the diagnosis of COVID-19, caused by SARS-CoV-2. RT-PCR is a method that detects the virus by amplifying two regions of the target viral genome, namely the nuclear (N) and surface (S) encoding sequences. However, no reports have shown a relationship between the symptoms and the gene expression patterns, especially in asymptomatic patients. Herein, we validated the characteristics of E and N gene expression patterns using RT-PCR on samples obtained from asymptomatic COVID-19 positive patients.

Methods. In this retrospective cohort study, conducted at Juntendo University Nerima Hospital, Tokyo, Japan, SARS-CoV-2 RT-PCR positive patients whose specimens had been obtained and analyzed by our laboratory technicians from September 1, 2020 to December 31, 2020 were enrolled. For RT-PCR, the LightMix Modular SARS-CoV-2 reagent (TIB MOLBIOL company) was used. After excluding patients who had symptoms, background, demographic, laboratory, and gene expression pattern data were collected from RT-PCR-positive asymptomatic patients. We also investigated patients who met the release criteria of the Center for Disease Control and prevention. Continuous and categorical variables were analyzed, with p < 0.05 set as statistical significance using the student-t test, chi-square test, or Fisher’s exact test, respectively.

Results. Of 92 RT-PCR-positive asymptomatic patients, 57 comprised the expression E only group (Group E) and 35 comprised the E+N group (Group E+N). Significantly more patients in Group E met the release criteria compared to those in Group E+N [41 (71%) vs 10 (28%), p < 0.001]. Among patients who met the release criteria, those in Group E+N had significantly more immunosuppression [7 (70%) vs 8 (30%), p=0.004]. Moreover, among the patients who underwent RT-PCR screening, no patients in Group E developed symptoms [0 vs 6 (42%), p=0.02].

Conclusion. The results of this study suggest that RT-PCR-positive asymptomatic patients can be divided into three patterns: pre-symptomatic, E-positive patients; post-symptomatic covid-19-recovered patients, regardless of gene E and N expression patterns; and false positive, gene E-positive patients.

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364. Individualized Prognostics in COVID-19 Facilitated by Computer Aided Recognition of Blood Leukocyte Subsets
Claudia R. Libertin, MD1; Prakash Kempaiaih, n/a2; Ravindra Durvasula, M.D.2; Ariel Rivas, DVM, PhD, PhD3; Mayo Clinic, Jacksonville, Jacksonville, FL; Mayo Clinic, Jacksonville, Florida; University of New Mexico, Albuquerque, New Mexico

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Background. To determine whether CBC differentials of COVID+ inpatients can predict, at admission, both maximum oxygen requirements (MOR) and 30-day mortality.

Methods. Based on an approved IRB protocol, CBC differentials from the first 3 days of hospitalization of 12 SARS-CoV-2 infected patients were retrospectively extracted from hospital records and analyzed with a privately owned Pattern Recognition Software (PRS, US Patent 10,429,389 B2) previously validated in sepsis, HIV, and hantavirus infections. PRS partitions the data into subsets immunologically dissimilar from one another, although internally similar.

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Abstracts