692. Secondary Infections and Coinfections in Coronavirus Disease 2019 (COVID-19)

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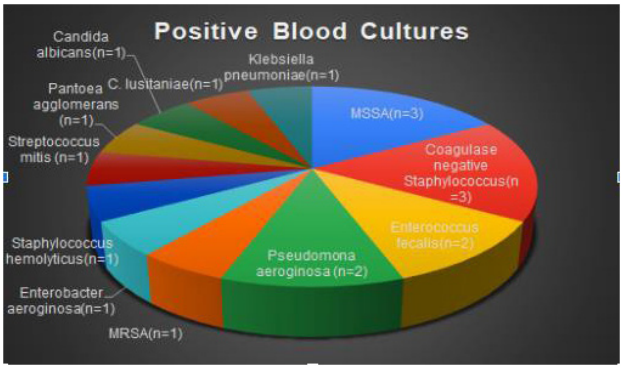
Session: P-27. Diagnostics: Virology

Background: While a common phenomenon in other viral illnesses, data regarding coinfection/superinfections in Coronavirus Disease 2019 (COVID-19) is limited and emerging. Superinfections may contribute to the overall high mortality in those suffering from severe COVID19. We aimed to study the rate of coinfections and secondary bacterial/fungal infections among SARS-CoV-2 positive cases in a community hospital.

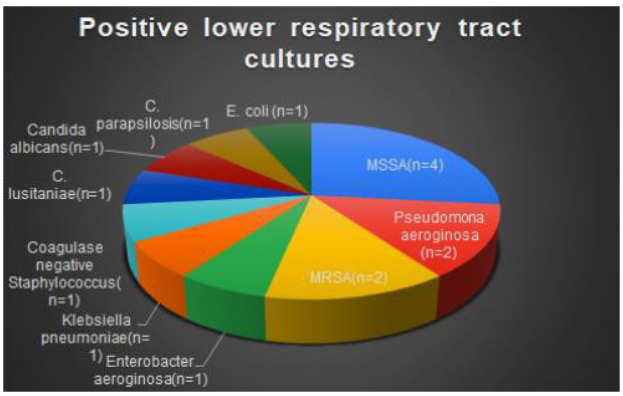
Methods: This is a single-centre IRB approved, retrospective observational study. Adult patients with laboratory-confirmed SARS-CoV-2 by Real-Time Reverse Transcriptase–Polymerase Chain Reaction assay of nasopharyngeal swabs admitted from March 1st to April 20th 2020 were included. Relevant clinical and laboratory data were manually collected from electronic medical records.

Results: A total of 129 patients were included in the study. 91 patients had a respiratory pathogen panel PCR on admission. This panel includes testing for influenza, parainfluenza virus, respiratory syncytial virus, coronavirus, adenovirus, rhinovirus, *Bordetella pertussis, Bordetella parapertussis, Chlamydophila pneumoniae,* and *Mycoplasma pneumoniae*. Only one patient was positive for coinfection with the parainfluenza virus. None of them was found to be positive for bacterial coinfection at admission. Thirteen patients (10.1%) had secondary bacterial or fungal infections that developed during their respective hospital stays, 12 of them were critically ill. The mean duration from admission to the onset of secondary infection was 13 days.

Positive Blood Cultures



Positive Lower Respiratory Tract Cultures



Conclusion: Our data revealed that the rate of viral coinfection was 1.1 % and bacterial coinfection was 0% at admission. Study timing can play a role as upper respiratory virus infection rate is low in the population during March and April. Secondary infections were found to be common in patients admitted to the ICU. Potential explanations for this include compromised immunity in severely ill patients, extended ICU stay, central venous catheters and endotracheal intubation. It is evident that with severe COVID-19 illness, an extended hospital course often ensues, leading to increased risk of secondary infections and contributing to the overall high mortality of these patients.

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693. Shaking Things Up: Direct-to-PCR Viral Detection off Swabs Using Shaker-Mill Homogenization

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Session: P-27. Diagnostics: Virology

Background: As the number of viral diseases are on the rise, it is critical to continue to innovate and advance diagnostic, treatment, and surveillance methods surrounding viral infections. Currently, one of the most reliable methods for viral infection detection are polymerase chain reaction (PCR) based assays. These assays often involve procedures of swabbing a patient, processing the sample to lyse the virus, extract, and purify it's nucleotides, and then run the purified genetic material via PCR for detection of a gene product needed to confirm the patient's suspected diagnosis. This process requires time to complete and is dependent on the availability of the reagents and plastics required to complete the lysis, extraction, purification, and amplification procedures. Herein, we have developed a method to detect virus off a swab using solely shaker-mill based mechanical lysis and the transfer of the viral lysate directly to a PCR based assay, bypassing the reagent heavy and time consuming extraction and purification steps.

Methods: Using Human Coronavirus 229E (HCoV-229E) as a model system, we spiked swabs with clinically relevant levels of the virus for proof-of-concept testing. Swabs were spiked in serial dilutions from 1.2e7 copies/mL to 1.2e1 copies/mL. The swabs were then placed in 2mL tubes with viral transport media (VTM) to mimic the specimen collection procedures in the clinic prior to processing via shaker-mill homogenization. After homogenization, 1 uL of viral lysate was run in RT-qPCR for amplification of the nucleocapsid (N) gene, qualifying viral detection from the sample.

Results: HCoV-229E spiked swabs were run through the two-step process of homogenization direct to RT-qPCR for viral detection. After running 54 swabs, we confidently determined our limit of detection to be 1.2e3 viral copies/mL with 96.30% sensitivity in vitro.

Conclusion: We have successfully proven that shaker-mill homogenization provides sufficient viral lysis off swabs, where the resulting lysate can be used directly in PCR based assays for the detection of virus. This finding allows for decreased run time in traditional PCR based diagnostics and reduces the reagents and plastics required for each sample, ultimately reducing the cost and time of each viral test when compared to traditional PCR based methods.

Disclosures: Zachary P. Morehouse, MS, OMS-III, Omni International Inc (Consultant) Caleb Proctor, BS, Omni International Inc (Employee) Gabriella Ryan, BS, Omni International Inc (Employee) Rodney J. Nash, PhD, Omni International Inc (Employee)

694. Unexpected Diversity of Rotavirus Genotypes in Pediatric Population

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Session: P-27. Diagnostics: Virology

Background: Rotavirus (RV) is the leading cause of viral gastroenteritis in children. Although RV genotypes differ geographically and temporally, five are the predominant genotypes circulating worldwide. Aim of our study was to monitor possible changes in distribution of Rotavirus genotypes circulating in Greek pediatric population during the post vaccine era.

Methods: Demographic data and fecal samples were collected from children ≤15 years old with symptoms of acute gastroenteritis who visited emergency units of Pediatric Hospitals in Greece from September 2016 to August 2019. Samples were tested for RV Group A antigen with rapid immunochromatographic assay. Positive samples were further G and P typed employing RT-PCR, semi-nested multiplex PCR and Sanger sequencing of the VP7 and VP4 genes.

Results: A total of 660 children participated in the study with median age 31±29 months. Males outnumbered females (59%). Most of them lived in urban cities (85%). RV genotyping distribution was G4P[8] (41%), G1P[8] (22%), G2P[4] (14%), G9P[8] (8%), G9P[4] (5,5%), G12P[8] (2%) and G3P[8] (1,8%). Unusual and mixed genotypes were identified in 3,2% and 2,5% of the samples respectively. During 2016-2017 and 2017-2018, G4P[8] was the predominant genotype in 67% and 51% of the annual samples. However, in 2018-2019 the most common genotypes were G9P[8] and G9P[4] (33% in total) followed by G2P[4] (27%). Interestingly, the genotype G9P[4] was not detected at all in the first two years of the study.

Conclusion: This study indicates diversity of the predominant RV genotypes in Greek children during 2016-2019. The emergence of G9 as the most common genotype as well as the significant detection of uncommon ones highlight the importance of continuous surveillance of RV genotyping during the post vaccine period.

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695. Infective endocarditis in people who inject drugs (PWID) at UK Medical Center

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