

Methods. With institutional review board approval, we recruited ER nurses who were assigned to COVID-19 isolation zone with more than 6 months' ER work experience. After their demographic information were collected through a questionnaire, their nursing practices and practice time during their 1 shift (day or evening) were recorded by one researcher using a stopwatch and an observation form. For each observation shift, unit-related information was collected, including the numbers of hospitalized patients, admission, discharge, and transfer of patients. For each nursing practice, frequency and total time spent were analyzed using descriptive statistics with SPSS 26.0 program.

Results. From January 4 to February 22, 2021, a total 18 nurses (27.4 years old on average with 25.2 months of ER experience) were observed from 20 different shifts. During the observation period, the average number of nurses' working hours was 8.27 ± 0.39 hours. A total of 6,567 tasks were monitored with 337,703 seconds (93.81 hours) of the total time spent. Infection control practices were most frequent (33.88%) followed by nursing management (27.80%), assessment and observation (11.07%), medication (10.35%), pre and post examination care (4.86%), education (4.37%), communication (4.10%), safety care (1.10%), and others (0.03; Table 1). Nursing management (e.g., nursing recording) was most time-consuming (49.29%) followed by assessment and observation (15.03%), medication (12.94%), patient education (6.10%), infection control (5.30%), and safety care (1.64%).

Conclusion. This study showed that infection control practices were most frequent while time spent was relatively insignificant among ER nurses in charge of COVID-19 isolation zones. Further studies for more observations or with different study designs at other ER settings are necessary to understand nurse's burdens with COVID-19 emergency care.

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415. A Whole Genome Sequencing Analysis of a Multi-unit Long-term Care Facility COVID-19 Outbreak

Ling Yuan Kong, MD, FRCPC, DTM&H¹; Leighanne Parkes, MD, FRCPC¹; Yves Longtin, MD²; Christina Greenaway, MD, MSc³; Jerry Zaharatos, MD, FRCPC⁴; Vivian Loo, MD, M.Sc.⁴; Noémie Savard, MD, FRCPC⁵; Réjean Dion, MD⁶; Fournier Éric, n/a⁶; Michel Roger, MD, PhD⁶; Sandrine Moreira, MSc, PhD⁶; ¹SMBD Jewish General Hospital, Montreal, Quebec, Canada; ²Jewish General Hospital, Montreal, Montreal, QC, Canada; ³Jewish General Hospital, McGill University, Montreal, Montreal, QC, Canada; ⁴McGill University, Montreal, Quebec, Canada; ⁵Direction de la santé publique de Montréal, Montreal, Quebec, Canada; ⁶Institut national de la santé publique du Québec, Sainte-Anne-de-Bellevue, Quebec, Canada

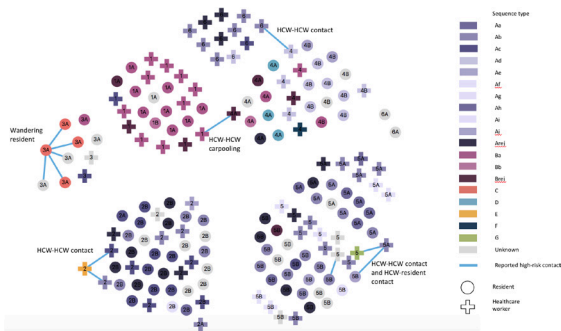
Coronavirus Sequencing in Québec (CoVSeq) Consortium

Session: P-19. COVID-19 Infection Prevention

Background. The coronavirus disease (COVID-19) pandemic has affected residents in long-term care facilities (LTCF) significantly. Understanding transmission dynamics in this setting is crucial to control the spread of COVID-19 in this population. Using whole genome sequencing (WGS) of SARS-CoV-2, we aimed to delineate the points of introduction and transmission pathways in a large LTCF in Quebec, Canada.

Methods. Between 2020-10-28 and 2021-01-09, COVID-19 cases occurred in 102 residents and 111 HCW at a 387-bed LTCF; cases were distributed in 11 units on 6 floors. As part of outbreak analysis, SARS-CoV-2 isolates underwent WGS using the Oxford Nanopore Minion and the Artic V3 protocol. Lineage attribution and sequence types (ST, within 3 mutations) were assigned based on Pangolin classification and variant analysis. Epidemiologic data including date of positive PCR test, resident room number and HCW work location were collected. Self-reported high-risk exposures were collected by HCW questionnaire via phone interview after consent. Cases and their ST, geo-temporal relations and HCW-reported exposures were examined via network plots and geography-based epidemic curves to infer points of introduction and paths of transmission.

Results. Of 170 isolates available from 100/102 residents and 70/111 HCW, 130 (76.4%) were successfully sequenced. Phylogenetic analysis revealed 7 separate introductions to the LTCF. Grouping of ST by units was observed, with temporal appearance of ST supporting HCW introduction in 7/11 units. Proportion of phone interview completion was low at 35% (26/70). Few HCW recalled specific high-risk exposures. Recalled exposures supported by genetic linkage revealed potential between-unit introductions from HCW-to-HCW transmission at work and outside the workplace (e.g. carpooling). On one unit, a wandering resident was identified as a likely source of transmission to other residents (Figure 1).



Network plot of cases clustered by geographic unit, colour-coded by sequence type. Circles represent residents; addition signs represent healthcare workers. Blue lines represent identified high-risk exposures. Node labels represent floor and unit identifiers; 2 units per floor.

Conclusion. We demonstrate the complex genomic epidemiology of a multi-unit LTCF outbreak, putting into evidence the importance of a multi-faceted approach to limit transmission. This analysis highlights the utility of using WGS to uncover unsuspected transmission routes, such as HCW contact outside work, which can prompt new infection control measures.

Disclosures. All Authors: No reported disclosures

416. Diagnostic Yield of Serial COVID-19 Testing in Hospitalized Patients

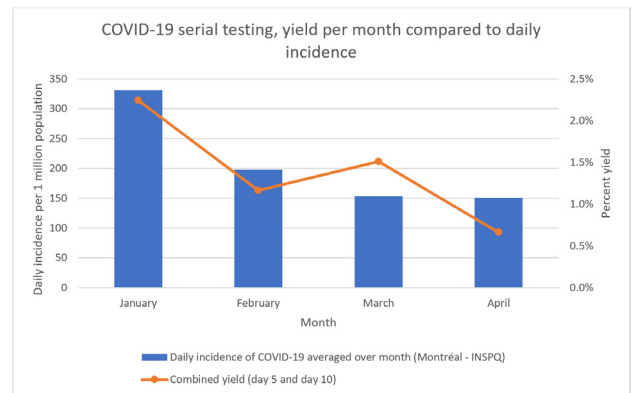
Jeremy Li, MD¹; Charles Frenette, MD, FRCPC²; Vivian Loo, MD, M.Sc.¹; ¹McGill University, Montreal, Quebec, Canada; ²McGill University Health Centre, Montreal, Quebec, Canada

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Background. Accurate and rapid diagnosis of SARS-CoV-2 infection is essential to prevent nosocomial transmission. Patients with negative COVID-19 tests at admission may still be in the incubation phase during hospitalisation. False negative results can occur when patients are tested too early. The incidence of COVID-19 infections in Montréal, Canada started to increase in December 2020. Because of this rise, on January 4th, 2021, the Infection Control Service of the McGill University Health Centre (MUHC) recommended serial COVID-19 testing for all admitted patients on days 5 and 10 after admission. The aim of this study is to examine the diagnostic yield of serial COVID-19 testing.

Methods. We retrospectively analyzed SARS-CoV-2 test results for patients admitted to the MUHC between January 4, 2021, and April 30, 2021. Nasopharyngeal swabs were collected from patients for SARS-CoV-2 PCR testing. Multiple testing platforms were used (Roche Cobas 6800, Thermo ScientificTM King Fisher and Cepheid GeneXpert) because of the high volume of samples. Tests were classified as admission, day 5, and day 10 tests if they were done on days 0 to 2, 3 to 7, and 8 to 12 respectively. Patients positive for SARS-CoV-2 on admission were excluded from the analyses. The diagnostic yield of serial testing for patients admitted during each month was calculated by dividing the number of patients testing positive on day 5 or day 10 by the total number of patients who underwent serial testing during that month.

Results. There were 2945 admissions of 5 days or more and 1777 admissions of 10 days or more. Of these, 1509 patients and 841 patients respectively were serially tested for SARS-CoV-2 as recommended for a compliance rate of 51% at day 5 and 47% at day 10. Ten (0.7%) and 12 (1.4%) patients tested positive on days 5 and 10 respectively. The diagnostic yield of serial testing was highest for patients admitted in January 2021 at 2.2%, when the average daily incidence of COVID-19 was highest in Montréal (see Figure).



The diagnostic yield of serial testing for each month, compared to the average daily COVID-19 incidence rate in Montréal, Québec, Canada.

Conclusion. The diagnostic yield of serial SARS-CoV-2 testing in hospitalized patients is low when the overall community incidence is low. However, diagnostic yield of serial testing increases when community incidence of COVID-19 is higher and should be considered in this situation.

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417. COVID-19 Aerostudy: Evaluation of SARS-CoV-2 Virus in the Air of Patients Hospitalized with COVID-19

Hamed Hamza, MD, MPH¹; Margaret Seitsema, PHD²; Lorraine Conroy, PHD²; Alfredo J. Mena Lora, MD³; Eric Wenzler, PharmD BCPS BCIDP AAHIVP²; Scott Borgetti, MD³; Benjamin Ladner, MD²; Tracy Cable, MD²; Ashley Dahlquist, n/a³; Nahed Ismail, PHD MD²; Steven Fisher, MD⁴; Taha Ali, MD²; Dagmar Sweeney, n/a⁴; Susan C. Bleasdale, MD²; ¹UTC School of Public Health, Chicago, Illinois; ²University of Illinois at Chicago, Chicago, Illinois; ³University of Illinois Hospital, Chicago, Illinois; ⁴University of Illinois at Chicago, Chicago, Illinois