TGIF!

Today I am reviewing 4 articles. The first is a very nice genomic surveillance analysis from Houston. The next two highlights the impact of HAIs during COVID. The last article reminds us the overuse of antibiotics in COVID patients and how PCT may be helpful.

I hope everyone has a wonderful weekend.

Ed

Sequence Analysis of 20,453 SARS-CoV-2 Genomes from the Houston Metropolitan Area Identifies the Emergence and Widespread Distribution of Multiple Isolates of All Major Variants of Concern
medRxivpublished online February 26, 2021 article provided by Cesar Arias
doi.org/10.1101/2021.02.26.21252227
The investigators used extensive genome sequencing program involving 20,453 virus specimens from COVID-19 patients dating from March 2020, we report identification of all important SARS-CoV-2 variants among Houston Methodist Hospital patients residing in the greater metropolitan area. Specimens obtained from symptomatic patients with a high degree of suspicion for COVID-19 disease were tested in the Molecular Diagnostics Laboratory at Houston Methodist Hospital. Libraries for whole virus genome sequencing were prepared according to version 3 of the ARTIC nCoV-2019 sequencing protocol. Long reads were generated with the LSK-109 sequencing kit, 24 native barcodes (NBD104 and NBD114 kits), and a GridION instrument (Oxford Nanopore). Short sequence reads were generated with either a NextSeq 550 or NovaSeq 6000 instrument (Illumina).

In genome sequencing conducted in January and February 2021, we discovered our first variants of concern. These included 23 UK variants (B.1.1.7), two South African variants (B.1.351), and four Brazilian variants (P.1). We also identified 162 patients infected with the California variants (B.1.429, N = 143; B.1.427, N = 19) and 39 patients infected with Brazil P.2 variants 2020. None of the affected patients were from a common household or reported recent international travel, suggesting that every infection was independently acquired locally or during domestic travel.

Comment: Although these variants are currently at relatively low frequency in this population, they are geographically widespread throughout Houston. Houston is the first city in the United States to have all variants documented by genome sequencing [aren't we lucky!]. As vaccination accelerates worldwide, increased genomic surveillance of SARS-CoV-2 is essential to understanding the presence and frequency of variants and their patterns of spread and impact on transmission.

COVID-19 Pandemic, CLABSI, and CAUTI: The Urgent Need to Refocus on Hardwiring Prevention Efforts
Infect Control Hosp Epidemiol published online February 2021
DOI: 10.1017/ice.2021.70
This study was a retrospective evaluation of CLABSI and CAUTI outcomes in 78 hospitals from a single healthcare system over two periods: pre-COVID-19 (March 2019-February 2020; 12 months), and during the COVID-19 pandemic (March-August 2020; 6 months). They evaluated whether there was an association with increased CLABSI or CAUTI events with COVID-19 pandemic, and if the microbiology of the associated organisms changed.

There were 795,022 central line-days and 817,267 urinary catheter-days over the two study periods.

Compared to pre-COVID-19 period, CLABSI rates increased during the pandemic period from 0.56 to 0.85 (51.0%) per 1,000 line-days (p<0.001) and from 1.00 to 1.64 (62.9%) per 10,000 patient-days (p<0.001). Hospitals with monthly COVID-19 patients representing >10% of admissions had an NHSN device standardized infection ratio for CLABSI that was 2.38 times higher compared to those with <5% prevalence during the pandemic period (p=0.004). Coagulase-negative staphylococcus CLABSI increased by 130% from 0.07 to 0.17 events per 1,000 line-days (p<0.001), and *Candida sp.* by 56.9% from 0.14 to 0.21 per 1,000 line-days (p=0.01). In contrast, no significant changes were identified for CAUTI (0.86 vs. 0.77 per 1,000 catheter-days; p=0.19)

Comment: The pandemic has had a disruptive effect on the US healthcare system resulting in an abrupt drop in admissions for most common conditions and leading to a selective increase in severity of illness among hospitalized patients especially during surges. Infection prevention has been pulled in multiple directions making it difficult to focus on basic practices. Preliminary results from other organizations have confirmed increased BSI especially during surges. See below.

COVID-19 Increased the Risk of ICU-Acquired Bloodstream Infections: A Case–Cohort Study from the Multicentric OUTCOMEREA Network
Intensive Care Med 2021; 47:180–187
doi.org/10.1007/s00134-021-06346-w
The investigators conducted a matched case-cohort study, based on prospectively collected data from a large ICU cohort. Critically ill COVID-19 patients were matched with similar non-COVID-19 patients. ICU-BSI was defined by an infection onset occurring > 48 h after ICU admission. They estimated the effect of COVID-19 on the probability to develop an ICU-BSI using proportional sub distribution hazards models.

They identified 321 COVID-19 patients and 1029 eligible controls in 6 ICUs. Finally, 235 COVID-19 patients were matched with 235 non-COVID-19 patients. They observed 43 ICU-BSIs, 35 (14.9%) in the COVID-19 group and 8 (3.4%) in the non-COVID-19 group ($p \leq 0.0001$), respectively. ICU-BSIs of COVID-19 patients were more frequently of unknown source (47.4%). COVID-19 patients had an increased probability to develop ICU-BSI, especially after 7 days of ICU admission. Using proportional sub distribution hazards models, COVID-19 increased the daily risk to develop ICU-BSI (sHR 4.50, 95% CI 1.82–11.16, $p=0.0012$). Among COVID-19 patients ($n=235$), a significantly increased risk for ICU-BSI was detected in patients who received tocilizumab or anakinra (sHR 3.20, 95% CI 1.31–7.81, $p=0.011$) but not corticosteroids.

Comment: Using high-quality prospectively collected data from several ICUs, they showed that the daily hazard rate of ICU BSI in critically ill COVID-19 patients was increased, especially from seven days after ICU admission compared to non-COVID ICU patients. Matched COVID-19 patients had slightly increased SOFA score compared to non-matched COVID-19 patients. The investigators focused only on ICU-BSIs. It would be of interest to look at other HAIs especially VAPs.

Limited Utility of Procalcitonin in Identifying Community-Associated Bacterial Infections in Patients Presenting with Coronavirus Disease 2019
Antimicrob Agents Chemother published online January 25, 2021
doi:10.1128/AAC.02167-20
Investigators conducted a retrospective cohort study of 2443 patients who underwent PCT measurements within 72 hours of presenting with COVID-19 at two hospital emergency departments. Concurrent bacterial infections were categorized into bacteremia, pneumonia, and bacteriuria, yielding

148 patients with 159 infections for a rate of 6.1% for community-associated bacterial infection (CAI). The most common bacterial causes of pneumonia were *Staphylococcus aureus* and *Pseudomonas*. Patients with CAI had higher mean PCT serum concentrations than those without CAI (13.16 vs. 2.00 ng/mL, *P*=0.009), with the highest PCT concentrations among bacteremic patients. A PCT cutoff of 0.5 ng/mL had sensitivity 0.50, specificity 0.71, positive predictive value 0.017, and negative predictive value (NPV) 0.993 for identifying bacterial pneumonia. PCT cutoffs of 0.25 or 0.5 ng/mL had NPV >0.967 for all infections tested.

Comment: This study confirms other reports that bacterial coinfection at presentation is uncommon (6% here but <5% in other studies). The study suggests a PCT <0.5 supports not prescribing antibiotics; however, with more severe COVID-19 one can have higher PCT which makes it difficult to discriminate between bacterial coinfection. In that case such patients may receive a short course of antibiotics until cultures and clinical judgment can help distinguish these overlapping groups. Median PCT in 5700 COVID-19 cases admitted in NYC = 0.2 (IQR 0.1-0.6). [JAMA 2020;323:2052-2059] There has been widespread overuse of antibiotics in COVID patients which has led to increased AR. [Infect Control Hosp Epidemiol. 2021;42:84-88]. Like infection prevention, antimicrobial stewardship programs have been distracted by the changing treatment guidelines for patients infected with SARS-CoV-2.