Table 1.

| Infections | Pre-Pandemic | Pandemic |
|------------|-------------|----------|
| CDI        |             | 15%      |
| MRSA BSI   |             | 5%       |
| VRE BSI    |             | 3%       |

* Standardized infection ratio

Use in patients to compare incidence rates.

Methods: We conducted a retrospective cohort study to identify the prevalence, microbiology, and outcomes of secondary pneumonia and bloodstream infections (BSIs) in patients hospitalized with COVID-19. Patients aged ≥18 years with a positive SARS-CoV-2 real-time polymerase chain reaction assay admitted to 4 academic hospitals in Atlanta, Georgia, between February 15 and May 16, 2020, were included. We extracted electronic medical record data through June 16, 2020. Microbiology tests were performed according to standard protocols. Possible ventilator-associated pneumonia (VAP) was defined according to Centers for Disease Control and Prevention (CDC) criteria. We assessed in-hospital mortality, comparing patients with and without infections using the \( \chi^2 \) test. SAS University Edition software was used for data analyses. Results: In total, 774 patients were included (median age, 62 years; 49.7% female; 66.6% black). In total, 335 patients (43.3%) required intensive care unit (ICU) admission, 238 (30.7%) required mechanical ventilation, and 120 (15.5%) died. Among 238 intubated patients, 65 (27.3%) had a positive respiratory culture, including 15 with multiple potential pathogens, for a total of 84 potential pathogens. The most common organisms were Staphylococcus aureus (29 of 84; 34.5%), Pseudomonas aeruginosa (16 of 84; 19.0%), and Klebsiella spp (14 of 84; 16.7%). Mortality did not differ between intubated patients with and without a positive respiratory culture (41.5% vs 35.3%; \( P = .37 \)). Also, 5 patients (2.1%) had a CDC-defined VAP (1.7% VAPs per 1,000 ventilator days); none of them died. Among 536 (69.3%) nonintubated patients, 2 (0.4%) had a positive Legionella urine antigen and 1 had a positive respiratory culture (for S. aureus). Of 774 patients, 36 (4.7%) had BSI, including 5 with polymicrobial BSI (42 isolates total). Most BSIs (24 of 36; 66.7%) had ICU onset. The most common organisms were S. aureus (7 of 42; 16.7%), Candida spp (7 of 42; 16.7%), and coagulase-negative staphylococci (5 of 42; 11.9%); 12 (28.6%) were gram-negative. The most common source was central-line–associated BSI (17 of 36; 47.2%), followed by skin (6 of 36; 16.7%), lungs (5 of 36; 13.9%), and urine (4 of 36; 11.1%). Mortality was 50% in patients with BSI versus 13.8% without (\( p < .0001 \)). Conclusions: In a large cohort of patients hospitalized with COVID-19, secondary infections were rare: 2% bacterial pneumonia and 5% BSI. The risk factors for these infections (intubation and central lines, respectively) and causative pathogens reflect healthcare delivery and not a COVID-19–specific effect. Clinicians should adhere to standard best practices for preventing and empirically treating secondary infections in patients hospitalized with COVID-19.

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COVID-19 Contact Tracing in a Pediatric Hospital: Maximizing Effectiveness Through Specialized Team and Automated Tools

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Background: In their interim infection prevention and control recommendations for the coronavirus disease 2019 (COVID-19) pandemic, the Centers for Disease Control and Prevention (CDC) recommend that healthcare facilities have a plan to identify, investigate, and trace potential COVID-19 exposures. In an academic hospital, the scale of such tracing is substantial, given that medically complex patients can have dozens of staff contacts across multiple locations during an encounter. Furthermore, the family-centered care model employed by pediatric institutions precludes visitor exclusion, further complicating tracing efforts. Despite this complexity, tracing accuracy and timeliness is of paramount importance for exposure management. To address these challenges, our institution developed a contact-tracing system that balanced expert participation with automated tracing tools. Methods: Our institution’s contact-tracing initiative includes positive patients, parents and/or visitors, and staff for the enterprise’s inpatient, procedural, and ambulatory locations at the main campus and 4 satellites. The team consists of 11 staff and is overseen by an infection preventionist. For positive patients and parents and/or visitors, potentially exposed staff are automatically identified via a report that extracts staff details for all encounters occurring during the patient’s infectious period. For positive staff, trained contact tracers call the staff member to determine whether mask and distancing practices could result in others meeting CDC exposure criteria. Any potentially exposed healthcare workers (HCWs) receive an e-mail that details exposure criteria and provides follow-up instructions. These HCWs are also entered into a secure, centralized tracking database that (1) allows infection prevention and occupational

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