

assessment of genomic diversity. Here, we evaluate the reliability of SCCmec typing, *spa* typing, and CC assignment using WGS data compared to traditional methods to ensure that backwards compatibility is maintained. **Methods:** *S. aureus* isolates were obtained from a convenience sample of iSA cases reported through the EIP surveillance system. Overall, 78 iSA isolates with diverse *spa* repeat patterns, CCs, SCCmec types, and antimicrobial susceptibility profiles were sequenced (MiSeq, Illumina). Real-time PCR and Sanger sequencing were used as the SCCmec and *spa* typing reference methods, respectively. *spa*-MLST mapping (Ridom SpaServer) served as the reference method for CC assignment. WGS assembly and multilocus sequence typing (MLST) were performed using the CDC QuAISAR-H pipeline. WGS-based MLST CCs were assigned using eBURST and SCCmec types using SCCmecFinder. *spa* types were assigned from WGS assemblies using BioNumerics. For isolate subtyping, previously published and validated canonical single-nucleotide polymorphisms (canSNPs) as well as the presence of the Panton-Valentine leukocidin (PVL) toxin and arginine catabolic mobile element (ACME) virulence factor were assessed for all genome assemblies. **Results:** All isolates were assigned WGS-based *spa* types, which were 100% concordant (78 of 78) with Sanger-based *spa* typing. SCCmecFinder assigned 91% of isolates (71 of 78) SCCmec types, which were 100% concordant with reference method results. Also, 7 isolates had multiple cassettes predicted or an incomplete SCCmec region assembly. Using WGS data, 96% (75 of 78) of isolates were assigned CCs; 3 isolates had unknown sequence types that were single-locus variants of established sequence types. Overall, 70 isolates had CCs assigned by the reference method; 100% (70 of 70) concordance was observed with WGS-based CCs. Analysis of canSNPs placed 42% (33 of 78) of isolates into CC8, with 17 (52%) of these isolates classified as USA300. PVL and ACME were not accurate markers for inferring the USA300 subtype as 24% (4 of 17) of isolates did not contain these markers. **Conclusions:** *S. aureus* CCs, SCCmec, and *spa* types can be reliably determined using WGS. Incorporation of canSNP analysis represents a more efficient method for CC8 assignment than the use of genomic markers alone. WGS allows for the replacement of multiple typing methods for increased laboratory efficiency, while maintaining backward compatibility with historical typing nomenclature.

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Presentation Type:

Top Rated Posters

National Surveillance of Methicillin-Resistant *Staphylococcus aureus* Bloodstream Infections in Canadian Acute-Care Hospitals

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Dalhousie University; Bonita Lee, Stollery Children's Hospital, Edmonton; Jerome Leis, University of Toronto; Allison McGeer, Mount Sinai Hospital; Jennifer Parsonage, Alberta Health Services; Donna Penney, Eastern Health, St. John's, IPAC Canada, Winnipeg; Anada Silva, Public Health Agency of Canada; Jocelyn Srigley, BC Children's & Women's Hospitals; Paula Stagg, Western Memorial Regional Hospital; Jen Tomlinson, Winnipeg Health Sciences Centre; Joseph Vayalunkal, Alberta Childrens Hospital; Connie Gittens-Webber, Hamilton Health Sciences Centre; Stephanie Smith, University of Alberta; CNISP PHAC, Public Health Agency of Canada

Background: Bloodstream infections (BSIs) due to methicillin-resistant *Staphylococcus aureus* (MRSA) are important causes of morbidity and mortality in hospitalized patients. Long-term national MRSA BSI surveillance establishes rates for internal and external comparison and provide insight into epidemiologic, molecular, and resistance trends. Here, we present and discuss National MRSA BSI incidence rates and trends over time in Canadian acute-care hospitals from 2008 to 2018. **Methods:** The Canadian Nosocomial Infection Surveillance Programme (CNISP) is a collaborative effort of the Association of Medical Microbiology and Infectious Disease Canada and the Public Health Agency of Canada. Since 1995, the CNISP has conducted hospital-based sentinel surveillance of MRSA BSIs. Data were collected using standardized definitions and forms from hospitals that participate in the CNISP (48 hospitals in 2008 to 62 hospitals in 2018). For each MRSA BSI identified, the medical record was reviewed for clinical and demographic information and when possible, 1 blood-culture isolate per patient was submitted to a central laboratory for further molecular characterization and susceptibility testing. **Results:** From 2008 to 2013, MRSA BSI rates per 10,000 patient days were relatively stable (0.60–0.56). Since 2014, MRSA BSI rates have gradually increased from 0.66 to 1.05 in 2018. Although healthcare-associated (HA) MRSA BSI has shown a minimal increase (0.40 in 2014 to 0.51 in 2018), community-acquired (CA) MRSA BSI has increased by 150%, from 0.20 in 2014 to 0.50 in 2018 (Fig. 1). Laboratory characterization revealed that the proportion of isolates identified as CMRSA 2 (USA 100) decreased each year, from 39% in 2015 to 28% in 2018, while CMRSA 10 (USA 300) has increased from 41% to 47%. Susceptibility testing shows a decrease in clindamycin resistance from 82% in 2013 to 41% in 2018. **Conclusions:** Over the last decade, ongoing prospective MRSA BSI surveillance has shown relatively stable HA-MRSA rates, while CA-MRSA BSI rates have risen substantially. The proportion of isolates most commonly associated with HA-MRSA BSI (CMRSA2/USA 100) are decreasing and, given that resistance trends are tied to the prevalence of specific epidemic types, a large decrease in clindamycin resistance has been observed. MRSA BSI surveillance has shown a changing pattern in the epidemiology and laboratory characterization of MRSA BSI. The addition of hospitals in later years that may have had higher rates of CA-MRSA BSI could be a confounding factor. Continued comprehensive national surveillance will provide valuable information to address the challenges of infection prevention and control of MRSA BSI in hospitals.

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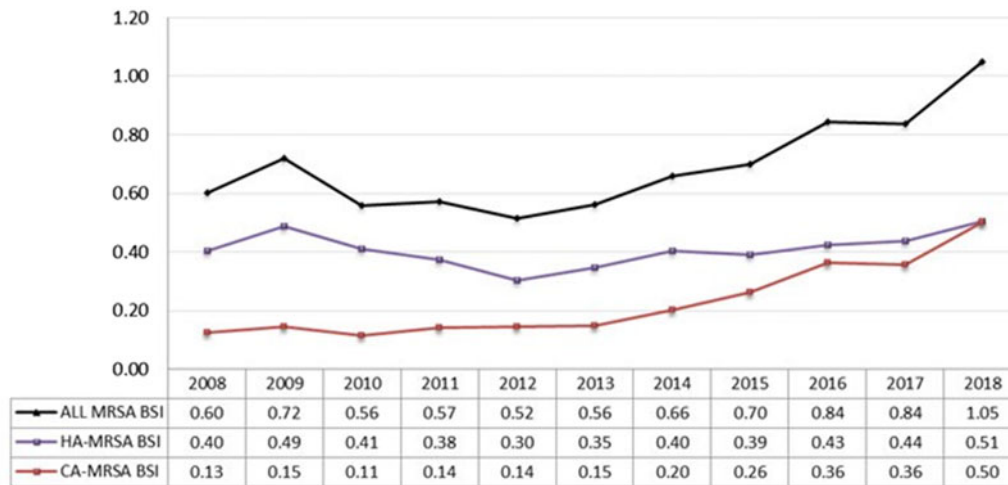


Figure 1. MRSA BSI rates per 10,000 patient days, 2008 – 2018

Fig. 1.

Presentation Type:

Top Rated Posters

No Device, No Problem? Healthcare-Associated Bloodstream and Urinary Tract Infections in a Children's Hospital

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Background: Central-line-associated bloodstream infection (CLABSI) and catheter-associated urinary tract infection (CAUTI) definitions continue to be refined to ensure accuracy. As facilities decrease CLABSI and CAUTI, and as midline catheters become more widely utilized, we sought to understand our non-central-line bloodstream infections (NCLBSI) and non-catheter-associated urinary tract infections (NCAUTI). Total healthcare-associated bloodstream infections (HABSI) and urinary tract infections (HAUTI) may provide more objective measures. **Methods:** The CHOC Children's Hospital is a 334-bed quaternary-care hospital in Orange, California, with 146 intensive care unit (ICU) beds. We retrospectively reviewed all HABSI (CLABSI + NCLBSI) and HAUTI (CAUTI + NCAUTI) from July 1, 2016, to June 30, 2019, for demographic and microbiologic data. Both HABSI and HAUTI were defined as healthcare-associated infection when the date of event occurs on or after the third calendar day of admission. CLABSI and CAUTI were both defined

using CDC-NHSN criteria. Mucosal barrier injury laboratory-confirmed bloodstream infections were excluded. **Results:** In a 3-year period, there were 100 HABSI, of which 26 (26%) were NCLBSI. The mean age for HABSI was 81 months. Enteric gram-negative infections (42%) and *Staphylococcus aureus* (35%) were the most common etiology for NCLBSI. The most common etiologies for CLABSI were coagulase-negative staphylococci (23%), *Staphylococcus aureus* (22%), and enteric gram-negatives (22%). *Pseudomonas aeruginosa* accounted for 16% of CLABSI, but no NCLBSI (Fig. 1). There was 1 midline catheter NCLBSI. There were 49 HAUTI, of which 39 (80%) were NCAUTI. One asymptomatic bacteremic urinary tract infection was included with the CAUTIs. The mean age for HAUTI was 55 months. The most common etiology of CAUTI was *Pseudomonas aeruginosa* (50%), whereas for NCAUTI the most common etiology was enteric gram-negative organisms (69%) (Fig. 2). In total, 11 HAUTI (22%) resulted in secondary sepsis. Most HABSI and HAUTI occurred in the ICU setting. There were 6 deaths (6%) among HABSI patients and 3 deaths (8%) among HAUTI patients within 2 weeks of infection (Fig. 3). **Conclusions:** A preponderance of HABSI were CLABSI, but most HAUTI were NCAUTI. Although patient demographic and microbiologic differences exist in CLABSI and NCLBSI as well as CAUTI and NCAUTI, *S. aureus* and *P. aeruginosa* are important pathogens, particularly in device-associated infections. Trending total numbers of

Figure 1. CLABSI and NCLBSI Pathogens
July 1, 2016 - June 30, 2019

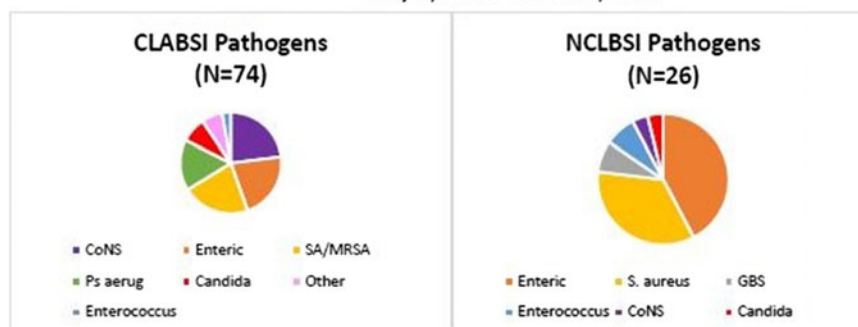


Fig. 1.