



Fig. 1.

were the most common strain type, our findings highlight the need for WGS to discern relationships between individuals to understand the intermixing of healthcare and community networks for CO-HA infections. Higher resolution genomic analysis may help guide whether interventions need to be at hospital discharge or in the community to have the most impact on decreasing CO-HA MRSA infections.

Funding: Funding: from CDC Broad Agency Announcement: *Genomic Epidemiology of Community-Onset Invasive USA300 MRSA Infections*; Contract ID: 75D30118C02923

Disclosures: None

Doi:10.1017/ice.2020.559

Presentation Type:

Top Rated Posters

Molecular Typing of Invasive *Staphylococcus aureus* from the Emerging Infections Program (EIP) Using Whole-Genome Sequencing

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Background: The CDC has performed surveillance for invasive *Staphylococcus aureus* (iSA) infections through the Emerging Infections Program (EIP) since 2004. SCCmec and spa typing for clonal complex (CC) assignment and genomic markers have been used to characterize isolates. In 2019, whole-genome sequencing (WGS) of isolates began, allowing for high-resolution

assessment of genomic diversity. Here, we evaluate the reliability of SCC*mec* 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, SCC*mec* types, and antimicrobial susceptibility profiles were sequenced (MiSeq, Illumina). Real-time PCR and Sanger sequencing were used as the SCC*mec* 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 SCC*mec* types using SCC*mec*Finder. *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 Pantone-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. SCC*mec*Finder assigned 91% of isolates (71 of 78) SCC*mec* types, which were 100% concordant with reference method results. Also, 7 isolates had multiple cassettes predicted or an incomplete SCC*mec* 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, SCC*mec*, 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.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.560

Presentation Type:

Top Rated Posters

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

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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.

Funding: None

Disclosures: None

Doi:10.1017/ice.2020.561