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 decrement CO-HA MRSA infections.

**Funding:** from CDC Broad Agency Announcement: Genomic Epidemiology of Community-Onset 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**

Davina Campbell, Centers for Disease Control and Prevention; Gillian McAllister, Centers for Disease Control and Prevention; Adrian Lawsin; Nicholas Vlachos; Kelly Jackson, Centers for Disease Control and Prevention; Isaac See, Centers for Disease Control and Prevention; Alison Halpin, US Centers for Disease Control and Prevention; Maria Karlsson; Joseph Lutgring, Centers for Disease Control and Prevention; Runa Gokhale; Erin Epson, California Department of Public Health, Healthcare-Associated Infections Program; Susan Petit, Connecticut Department of Public Health; Ruth Lynfield; Susan Ray, Emory University School of Medicine and Grady Health System; Lee Harrison; William Schaffner, Vanderbilt University School of Medicine; Gihwai Dumyati, University of Rochester; Thomas Ewing, ORISE; Michelle Adamczyk, Goldbelt C6, LLC; Amy Gargis, Centers for Disease Control and Prevention

**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

---

**Figure 1. Onset types**

*HO*: infection >72 hours into hospitalization. CO-HA: infection in an outpatient or within 72 hours of hospitalization among patients with prior healthcare exposures (hospitalization, surgery, dialysis, long term care in past year; MRSA infection or colonization in prior 6 months). CO: infection as an outpatient or within 72 hours of hospitalization among patients without healthcare exposures in prior year. A) Height of bars indicate percent infection type by onset-type. In both A and B, the proportion of bars indicates proportion of STs in those with the epidemiological factors of interest. B) Height of bars indicate percent epidemiological factor by onset type. All factors were significantly different by a three-way Chi square test (p < 0.0001: Jail Ever, Diabetes, MRSA colonization or infection in past 6 months, Hospitalization in past year; p = 0.002: HIV; p < 0.05: Current Drug Use).
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.

**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**

Linda Pelude, Public Health Agency of Canada; Jennifer Campbell, Public Health Agency of Canada; National Microbiology Laboratory; George Golding; Suzanne Bakai-Anderson, Hamilton Health Sciences Centre; Pat Bedard, Children’s Hospital of Eastern Ontario Infection Prevention and Control Program; Jeannette Comeau, Dalhousie University; Joan Durand, Alberta Health Services; John Embil, University of Manitoba; Joanne Embree, Health Sciences Centre, Winnipeg, MB; Gerald Evans, Kingston Health Sciences Centre; Charles Frenette, McGill University Health Center; Allana Ivany, IWK Health Centre; Kevin Katz, North York General Hospital; Pamela Kibsey, Royal Jubilee Hospital; Joanne Langley, 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 Vayalamkal, 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.

**Funding:** None

**Disclosures:** None

**Doi:** 10.1017/ice.2020.561