

1. Altman, D. R. et al. Genome Plasticity of agr-defective *Staphylococcus aureus* during clinical infection. *Infect. Immun.*(2018).

**Disclosures.** All authors: No reported disclosures.

### 553. Outbreak of Methicillin-Resistant *Staphylococcus aureus* Associated with Hepatic Artery Infusion Pumps

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**Session:** 61. HAI: MRSA Epidemiology

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**Background.** Device-related infections account for a fourth of all HAIs. Hepatic artery infusion pump (HAIP) devices are used to deliver chemotherapy directly into the hepatic artery. This device is used primarily in patients with colorectal cancer for the management of unresectable hepatic metastases. We describe the infection rates and outbreak management of MRSA-related infections in newly placed HAIPs.

**Methods.** In December 2018, a cluster of 3 MRSA cases was identified within 15–26 days of HAIP insertion. From January 1, 2017 to December 31, 2018, patients with culture proven SSIs within 30 days of HAIP placement were identified through the infection control database to establish baseline rates. Procedural denominator data were found by querying CPT procedure codes. EMR was reviewed to extract clinical characteristics. In response to the cluster, healthcare personnel (HCP) were screened for MRSA by PCR and environmental cultures performed. PFGE and whole-genome sequencing (WGS) was performed to compare isolates recovered in culture and SNP analysis performed using the BioNumerics software v7.6.

**Results.** In December 2018, 3/15 patients with HAIP procedures developed MRSA infections within 30 days of the procedures (post-op days: 15,16,26). The baseline 30 day SSI rate for HAIP in 2017 was 1.3% (2/160). No infections, prior to the cluster, in 2017–18 were MRSA related. All patients were male, with a median age of 49 years (range: 45–54). Sixty HCP who provided direct care during the peri and early post-operative period for the 3 cases were screened for MRSA carriage; 2/60 (3.3%) were positive. All 56 environmental cultures were negative for MRSA. WGS of the 3 patient samples showed 2/3 samples were identical (1 SNP difference); confirming common source transmission. Only one HCP isolate was available for WGS and shown to be unrelated to the two patient isolates. Both employees underwent decolonization. Review of HAIP handling did not reveal obvious lapses, but mask use and strict hand hygiene were enforced with HCPs. No further infections have been identified in the 76 procedures since the cluster.

**Conclusion.** WGS confirmed common source transmission between two newly placed HAIP although the definitive source could not be identified. Surveillance and prevention efforts should extend to all types of vascular access devices.

**Disclosures.** All authors: No reported disclosures.

### 554. The Changing Epidemiology of Methicillin-Resistant *Staphylococcus aureus* Causing Bacteremia in Hiroshima, Japan During 2008–2017

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**Background.** Recently, the Japanese intrinsic community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) clone (CA-MRSA/J), classified as sequence type (ST) 8 carrying staphylococcal cassette chromosome *mec* (SCC*mec*) type IV1 (ST8-IV1), has been identified that causes invasive infections similar to those of USA300 clone. However, epidemiological information regarding epidemic CA-MRSA clones is limited in Japan. This study was performed to investigate the changing epidemiology of MRSA causing bacteremia in Japan.

**Methods.** We performed whole-genome sequencing of MRSA isolates causing bacteremia at Hiroshima University Hospital between January 2008 and December 2017. MRSA isolates were subjected to multilocus sequence typing, SCC*mec* typing and were analyzed for virulence factors. Clinical data of patients with MRSA bacteremia were analyzed.

**Results.** A total of 193 MRSA strains causing bacteremia were identified during the study period. Among these, most belonged to ST764-IIa (30%; 59 of 193) and ST5-IIa (26.9%; 52 of 193). The proportion of ST5-IIa MRSA decreased from 39.6% (42 of 106) in 2008–2012 to 11.5% (10 of 87) in 2013–2017, and that of ST764-IIa MRSA increased from 23.6% (25 of 106) to 39.1% (34 of 87) in the same time period. The proportion of CA-MRSA (MRSA carrying SCC*mec* type IV or V) increased from 28.3% (30 of 106) in 2008–2012 to 42.5% (37 of 87) in 2013–2017. In CA-MRSA strains, clonal complex (CC) 8-IV MRSA was predominant (76.1%; 51 of 67). Those belonging to CC8-IV MRSA isolates were ST380-IVc (18 of 51), ST8-IV1 (CA-MRSA/J; 15 of

51), ST8-IVj (15 of 51), ST8-IVa (2 of 51), and ST4803-IV1 (1 of 51). The rate of hospital-onset infections of ST380-IVc, ST8-IV1, and ST8-IVj were 83.3%, 46.7%, and 60%, respectively. In CA-MRSA/J strains, including their variants (e.g., ST4803-IV1), 14 of 16 strains (87.5%) carried genes for toxic shock syndrome toxin (*tst-I*), enterotoxin C (*sec*), and enterotoxin L (*sel*), while none of the ST380-IVc and ST8-IVj MRSA strains carried these genes.

**Conclusion.** During the study period of 10 years, predominant ST5-IIa MRSA causing hospital-onset infections was replaced by ST764-IIa MRSA. In CA-MRSA clone, ST380-IVc, ST8-IV1 (CA-MRSA/J), and ST8-IVj were dominant and have already spread to the healthcare environment.

**Disclosures.** All authors: No reported disclosures.

### 555. The Burden of Invasive *Staphylococcus Aureus* Disease Among Native Americans on the Navajo Nation

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**Background.** Native Americans in the southwestern United States (US) may be at higher risk for invasive infections due to *Staphylococcus aureus*. The objective of this study was to determine the burden of invasive *S. aureus* among Native Americans on the Navajo Nation.

**Methods.** Prospective population and laboratory-based surveillance for invasive *S. aureus* infections was conducted from May 2016 through April 2018. A case was defined as a Native American individual living on or around the Navajo Nation with *S. aureus* isolated from a normally sterile body site. Incidence rates were calculated using the Indian Health Service User Population from 2016 and 2017 as the denominators for Years 1 and 2, respectively. Age-standardized incidence rates were calculated using US Census data from 2015 as the reference group.

**Results.** 363 cases were identified (Year 1: 159; Year 2: 204). Most cases were adults (96.9%; median age: 56.0 years) and had ≥1 underlying medical condition (94.5%), of which the most common were diabetes (63.2%), hypertension (39.1%), and obesity (37.2%). 38.0% of cases were categorized as community acquired and 28.7% of infections were methicillin-resistant (MRSA). 83.2% of cases were hospitalized, 10.7% required amputation, and 6.5% died within 30 days of the initial culture. The overall incidence of invasive *S. aureus* was 74.4 per 100,000 persons (95% confidence interval [CI]: 67.1, 82.4) with a significantly higher incidence in the second year (Year 1: 64.9; Year 2: 84.0; incidence rate ratio: 1.29; 95% CI: 1.05, 1.59). The overall incidence of invasive MRSA was 21.3 per 100,000 persons (95% CI: 17.6, 25.8) with no significant difference by year (Year 1: 21.2; Year 2: 21.4; incidence rate ratio: 1.01; 95% CI: 0.69, 1.48). The incidence of invasive *S. aureus* and MRSA increased with age and was highest among individuals ≥65 years of age. The overall age-standardized incidence of invasive MRSA was 25.9 per 100,000 persons (Year 1: 26.0; Year 2: 25.7; for comparison US 2015 general population: 18.8 per 100,000 persons).

**Conclusion.** The Navajo Nation has a higher burden of invasive MRSA than the general US population. Further research is needed to evaluate trends over time and identify prevention strategies and opportunities for intervention.

**Disclosures.** All authors: No reported disclosures.

### 556. Phylogenomic Epidemiology of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Chilean-Cordobes Clone in Latin America

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