minutes weekly, but 450 minutes would have been required to observe all 15 sites. Yearly, the required hours to observe these active construction sites once weekly would be 390 hours. In addition to the observational hours, 124 hours were spent in design meetings alone, not considering the preparation time and follow-up required for these meetings. **Conclusions:** In a large academic medical center, IPs had time available to visit only a quarter of active projects on an ongoing basis. Increasing dedicated IP time in construction projects is essential to mitigating infection control risks in large hospitals. **Funding:** None

Disclosures: None

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## **Presentation Type:**

Top Rated Posters

## Legal Requirements for Infection Prevention and Control Training Among Healthcare Personnel

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Background: When healthcare providers lack infection prevention and control (IPC) knowledge and skills, patient safety and quality of care can suffer. For this reason, state laws sometimes dictate IPC training; these requirements can be expressed as applying to various categories of healthcare personnel (HCP). We performed a preliminary assessment of the laws requiring IPC training across the United States. Methods: During February-July 2018, we searched WestlawNext, a legal database, for IPC training laws in 51 jurisdictions (50 states and Washington, DC). We used standard legal epidemiology methods, including an iterative search strategy to minimize results that were outside the scope of the coding criteria by reviewing results and refining search terms. A law was defined as a regulation or statute. Laws that include IPC training for healthcare personnel were collected for coding. Laws were coded to reflect applicable HCP categories and specific IPC training content areas. Results: A total of 278 laws requiring IPC training for HCP were identified (range, 1-19 per jurisdiction); 157 (56%) did not specify IPC training content areas. Among the 121 (44%) laws that did specify IPC content, 39 (32%) included training requirements that focused solely on worker protections (eg, sharps injury prevention and bloodborne pathogen protections for the healthcare provider). Among the 51 jurisdictions, dental professionals were the predominant targets: dental hygienists (n = 22; 43%), dentists (n = 20; 39%), and dental assistants (n = 18; 35%). The number of jurisdictions with laws requiring training for other HCP categories included the following: nursing assistants (n = 25; 49%), massage therapists (n = 11; 22%), registered nurses (n = 10; 20%), licensed practical nurses (n = 10; 20%), emergency medical technicians and paramedics (n = 9; 18%), dialysis technicians (n = 8; 18%), home health aides (n = 8;16%), nurse midwives (n = 7;14%), pharmacy technicians (n = 1,14%)= 7; 14%), pharmacists (n = 6; 12%), physician assistants (n = 4; 8%), podiatrists (n = 3; 6%), and physicians (n = 2; 4%). Conclusions: Although all jurisdictions had at least 1 healthcare personnel IPC training requirement, many of the laws lack specificity and some focus only on worker protections, rather than patient safety or quality of care. In addition, the categories of healthcare

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personnel regulated among jurisdictions varied widely, with dental professionals having the most training requirements. Additional IPC training requirements exist at the facility level, but this information was not analyzed as a part of this project. Further analysis is needed to inform our assessment and identify opportunities for improving IPC training requirements, such as requiring IPC training that more fully addresses patient protections. **Funding:** None

Disclosures: None

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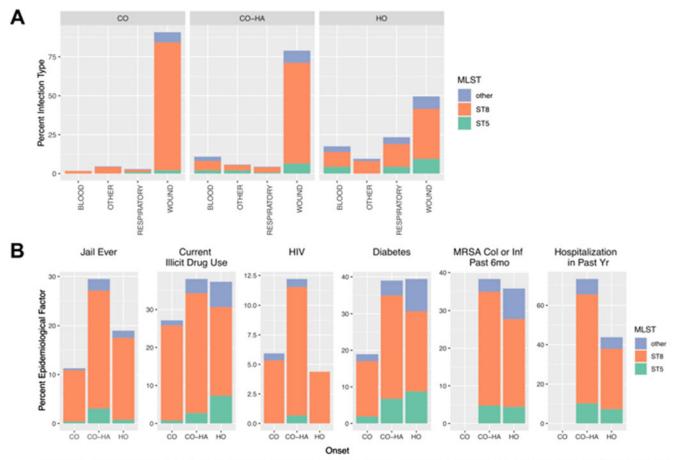
## **Presentation Type:**

Top Rated Posters

Molecular Epidemiology of Community-Onset (CO), Community-Onset Healthcare-Associated (CO-HA) and Hospital-Onset (HO) Methicillin-Resistant *Staphylococcus aureus* (MRSA)

Stephanie Thiede, University of Michigan; Darjai Payne, Rush University Medical Center; Alla Aroutcheva, Rush University Medical Center/Cook County Health; Michael Schoeny, Rush University Medical Center; Robert Weinstein, Rush University Medical Center; Evan Snitkin, University of Michigan; Kyle Popovich, Rush University Medical Center

Background: Previous work suggests an intermingling of community and hospital transmission networks driving the MRSA epidemic, but how those with CO-HA infections fit into the network remains unclear. We integrated epidemiologic data and wholegenome sequencing (WGS) from existing MRSA clinical isolates to determine whether there were distinguishable features of CO-HA MRSA infections that could guide interventions. Methods: We examined 955 existing clinical MRSA isolates from 2011 to 2013 from patients at Cook County Health, the major public healthcare network in Chicago, Illinois. We performed electronic and manual chart review to ascertain community (eg, illicit drug use, incarceration history) and healthcare exposures and comorbidities. WGS was performed on all sequences, and sequences were typed with multilocus sequence typing (MLST). We assessed the distribution of epidemiological factors and sequence type (ST) across onset type. Results: Infections were more frequent in males (70%); 61% of individuals with infection were African American and 21% were Hispanic. Overall, wound infections were the most common (81%) followed by blood (7%) and respiratory (6%). 82% of infections were ST8 (most USA300), 8% were ST5 (USA100) and 10% were other STs (Fig. 1a). Using standard epidemiologic definitions, we identified 523 CO, 295 CO-HA, and 137 HO infections. USA300 infections were common across CO, CO-HA, and HO categories, whereas USA100 was more frequently observed among CO-HA and HO. Current illicit drug use and history of incarceration-factors typically associated with CO-MRSA-were observed among both CO-HA and HO infections. 38% of CO-HA and 36% of HO had a history of MRSA infection or nasal colonization in the prior 6 months. As expected, 73% of CO-HA had a history of recent hospitalization, but this was also true for 44% of HO cases; points for intervention for both groups, especially CO-HA patients, include outpatient, inpatient, and ER care. Diabetes was common across categories, and HIV was more commonly observed among CO-HA cases (Fig. 1b). Conclusions: We characterized the genomic and epidemiologic features of CO-HA MRSA infections relative to CO and HO. By MLST and epidemiological analysis, CO-HA infections share similarities to both CO and HO. Although USA300 infections



**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 people 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 bar 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).

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.

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## **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. SCC*mec* 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