Results. US300-LV exhibited a larger number of differentially expressed genes when exposed to Hg (n = 114) compared with Cu treatment (n = 16). The most common functional groups of genes upregulated after Hg exposure included those involved in amino acid metabolism (n = 18). In contrast, 45 genes were downregulated after Hg exposure, mostly associated to host immune system defense (n = 11). qRT-PCR confirmed that the most upregulated genes were those involved in murein hydrolase activity, Hg resistance and the transcriptional regulator Cro/Orf 9 genes that were downregulated, functional groups included ype VII secretion system, immune modulators and leucocidins. Copper treatment resulted in only 12 genes that were upregulated including those in the COMER element (n = 6), amidoncid metabolism (n = 3), ROS response (n = 1), host immune system defense (n = 1) and unknown function (n = 1). Downregulated genes were those associated to host immune system defense (n = 2), energy generation (n = 1) and unknown function (n = 1).

Conclusion. Differential adaptive responses after exposure to HM in USA300-LV suggest a role in the evolution of antimicrobial resistance and successful spread in the region. Metabolic adaptations involving amino acid metabolism seem to play a role in the evolution of HM resistance in MRSA.

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558. Evaluating Length of Stay Data for Use in Targeting Prevention of Methicillin-Resistant Staphylococcus aureus (MRSA) Bloodstream Infections
Katyrina Gosin, MPH; Kelly M. Hatfield, MSPH; Sarah H. Yi, PhD, MS; Sujan Reddy, MD, MSc; Hannah Wolford, MSPH; Qunna Li, MSPH, MMS; Jonathan R. Edwards, MStat; Rachael Slayton, PhD, MPH; James Rags, PhD and Justin O’Hagan, ScD; Centers for Disease Control and Prevention (CDC), Atlanta, Georgia

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Background. Evidence suggests that interventions such as MRSA decolonization are useful in the prevention of MRSA bloodstream infections (BSI) both during hospitalization and post-discharge. However, decolonization may be costly and have diminishing effectiveness when used on all inpatients. Hospital length of stay (LOS) is a known risk factor for MRSA BSI. To determine whether LOS could be useful in prioritizing patients for intervention, we aimed to evaluate (i) distribution of time from admission to hospital-onset (HO) MRSA BSI, and (ii) frequency and LOS of hospitalizations that preceded community-onset (CO) MRSA BSI.

Methods. MRSA-positive blood cultures among adults admitted to New York hospitals from 2013 to 2016 were identified in the Centers for Disease Control and Prevention’s (CDC’s) National Healthcare Safety Network (NHSN). We linked these data to admissions in New York’s hospital discharge dataset, the Statewide Planning and Research Cooperative System (SPARCS), where the NHSN blood culture collection date was between a patient’s SPARCS admission and discharge dates and there was an exact match for birth date, gender and facility. Time to MRSA BSI was defined as the number of days from admission (day 1) to collection of a blood culture positive for MRSA. We defined positive blood cultures collected on days 1–3 as CO, and those collected on days 4 or later as HO.

Results. We linked 10,425 (79%) MRSA BSIs from NHSN to SPARCS. 78% (8,147) of MRSA BSIs were CO and 22% (2,278) were HO. The median time to HO MRSA BSI was 10 days (IQR 6–21) (Figure 1), in contrast to the median LOS for all hospitalizations of 4 days (IQR 3–7). By definition, 35% of all hospitalizations were never at risk of HO MRSA BSI because their LOS was <4 days. Among CO MRSA BSI, 48% were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1). The most LOS were discharged from a hospital in the 90 days preceding their BSI (Figure 1).

Conclusion. Over half of HO MRSA BSI occur on or after day 10 of hospitalization and a large fraction of CO MRSA BSI had a lengthy hospitalization shortly before their BSI diagnosis. Our results suggest that patients likely to have a long LOS could be evaluated as potential targets for prevention strategies (e.g., decolonization) to reduce both HO and CO MRSA BSI.

Figure 1. Cumulative percent of hospital-onset Methicillin-resistant Staphylococcus aureus bloodstream infections (BSI) from day 0 through admission, percent of hospitalizations with a length of stay (LOS) at least 4 days, and percent of patient-days contributed by hospitalizations with a LOS of at least 4 days in New York, USA (2009–2016).

559. Two Different Beasts: Comparing Epidemiology of Healthcare-Associated vs. Community-Acquired Methicillin-Resistant Staphylococcus aureus Bacteremia
Luke McLaughlin, MD1; and Stephanie Smith, MD1; 1University of Alberta, Edmonton, AB, Canada

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Background. Methicillin-resistant staphylococcus aureus (MRSA) bloodstream infection (BSI) is associated with significant morbidity and mortality. Healthcare-Associated (HCA) MRSA infections continue to be associated with higher hospitalization costs and hospital mortality. Community-onset (CO) MRSA infections are more common among patients with prior healthcare exposure and in those with prior healthcare exposure has traditionally been associated with severe invasive disease, while community-associated (CA) MRSA infection occurring within 48 hours of hospitalization and without prior healthcare exposure has been observed in otherwise healthy individuals. We characterized the epidemiology, resistance patterns, and clinical outcomes associated with MRSA BSI over a 5 year period comparing patients with community-onset bacteremia to those with hospital onset bacteremia.

Methods. We performed a retrospective chart review of 151 MRSA bloodstream infections from 2013–2018 at the University of Alberta Hospital (Edmonton, Canada). We assessed each BSI by: classification (CA vs. HCA), presence of MRSA risk factors, source of infection, MRSA resistance, rate of ICU admission, and 30-day mortality.

Results. The median age of all patients with MRSA BSI was 53 years (range 23–94). MRSA BSI occurred more commonly in males for both CA and HCA infection (53% and 62%). HCA-MRSA infections had a higher rate of previous MRSA colonization (64.8%) compared with CA-MRSA patients (41.7%). Injection drug use was more common in otherwise healthy individuals. We characterized the epidemiology, resistance patterns, and clinical outcomes associated with MRSA BSI over a 5 year period comparing patients with community-onset bacteremia to those with hospital onset bacteremia.

Conclusion. Invasive MRSA infection continues to be associated with significant morbidity and mortality. We found that healthcare-associated MRSA BSI was associated with a high rate of prior MRSA colonization as well as a higher rate of ICU admission and 30-day mortality. There are significant differences in the demographics of patients with CA BSI compared with HCA BSI. Interventions to prevent these infections need to be targeted to the geographic location of acquisition.

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560. Relating Whole-Genome Sequencing of Methicillin-Resistant Staphylococcus aureus Isolates to Transmission Dynamics and Efficacy of Control Interventions
Seth Blumberg, MD PhD1; Travis Porco, PhD2; Bo Shoopin, MD, PhD3 and Michael Phillips, MD4; 1NYU, New York City, New York; 2University of California, San Francisco, San Francisco, California; 3NYU Langone Health, New York, New York; 4New York University, New York, New York

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Background. Methicillin-resistant staphylococcus aureus (MRSA) colonization of hospitalized patients is associated with higher readmission rates and increased morbidity. Depending on the mechanisms of transmission, numerous potential control interventions exist to reduce the burden of disease. However, given the preponderance of asymptomatic
561. Genomic Epidemiology of Methicillin-Resistant Staphylococcus aureus in Two Cohorts of High-Risk Military Trainees

Robyn S. Lee, PhD; Eugene V. Millar, PhD; Anna Callenderullo, BA; Caroline E. English, BA; Alexander E. Krasniewski, BA; Jason W. Bennett, MD MSPH; and William P. Hanage, PhD.

School of Public Health, Boston, Massachusetts; Uniformed Services University of the Health Sciences, Bethesda, Maryland

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Background. Methicillin-resistant Staphylococcus aureus (MRSA) skin and soft-tissue infections (SSTIs) are common among military recruits. Identifying which anatomical sites other than the nares (36% oropharyngeal, 26% perianal, 14% inguinal).

Methods. A cohort study of US Army Infantry trainees at Fort Benning, GA (June and September 2015). Participants from two training Courses were screened for colonization on multiple anatomic sites throughout the 14-week cycle as well as the time of clinical infection. MRSA+ samples were sequenced with Illumina HiSeq. Multi-locus sequence type (MLST) and virulence genes were identified in silico. Single nucleotide polymorphism (SNP) distances between soldiers' bacteria were compared with assessing for potential transmission.

Results. Of 383 soldiers enrolled, 84 (22%) were colonized with MRSA during the study. Forty-two of 84 had a single positive colonization sample, of which 76% were from anatomical sites other than the nares (36% oropharyngeal, 26% perianal, 14% inguinal). Twelve trainees had MRSA SSTI during training (50% had colonization detected prior to infection). All were PFGE-type US300 (ST8) and were lukS/lukF-positive. SNP-based mechanisms and assess control efficacy. By identifying clusters of transmission, whole-genome sequencing (WGS) provides an opportunity to overcome these challenges.

Methods. We sought to apply cluster analysis techniques to WGS data for MRSA, in order to assess MRSA prevalence, transmissibility, the degree of transmission heterogeneity and the potential effectiveness of control. Our model builds upon previous work that showed a direct relationship between the size distribution of infection clusters, the effective reproduction number \(R\) and the dispersion parameter \(k\). To demonstrate its functionality, our model was applied to existing WGS data for MRSA isolates collected during a 12 month period in the East of England (DOI: 10.1126/scitranslmed.a9745).

Results. The effective reproduction number for the East of England data is 0.29 (95% CI: 0.24–0.36). The dispersion parameter is 0.09 (0.03–0.33) reflecting a high degree of transmission heterogeneity. This implies all transmission is caused by just 12% of the cases of MRSA.

Conclusion. High degree of transmission heterogeneity seen in MRSA transmission suggests that the risk for infection is variable. This observation motivates the need for more detailed mechanistic modeling of hospital-based MRSA transmission which integrates patients-specific factors, movement data and genome sequencing. Such models could be used to forecast which patients are at greatest risk for either acquiring or transmitting MRSA, thereby improving targeted control.

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562. Reducing MRSA Bacteremia in Adult Patients through MRSA Decolonization Bundle

Erin Goldman, DO; Jennifer LeRose, MPH; Abdul Ramos-Mercado, MD; Justin Oring, DO; and Teena Chopra, MD, MPH.

Wayne State University, Oak Park, Michigan; Detroit Medical Center, Detroit, Michigan; Detroit Medical Center, Detroit, Michigan; Wayne State University, Detroit, Michigan

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Background. Patients colonized with methicillin-resistant Staphylococcus aureus (MRSA) are at an increased risk of developing a subsequent MRSA infection. Moreover, these individuals may serve as an endogenous reservoir to spread the bacteria to other patients. In an attempt to reduce MRSA bacteremia rates, a decolonization protocol was developed and implemented at a tertiary teaching hospital in Detroit, Michigan. In this study, we evaluate the intervention's impact on community-onset (CO) and hospital onset (HO) MRSA bacteremia rates.

Methods. Infection Control developed an MRSA decolonization bundle for adults that consisted of daily Chlorhexidine gluconate (CHG) bathing and twice-daily nasal swabs with 10% Povidone-iodine (PI) or Nozin for individuals with iodine allergies. Patients with known risk factors for developing an MRSA infection, such as patients residing in an intensive care unit and/or undergoing specified procedures, were prescribed the bundle for their length of stay (Figure 1). Contraindications for nasal decolonization included inhalation injuries, CSF leaks, ENT surgeries, and transperidural surgeries. A retrospective chart review of high-risk patients was conducted to determine compliance with the elements of the MRSA decolonization bundle. Rates of CO and HO MRSA bacteremia per 1,000 patient-days were graphed against compliance with bundle elements (2 nasal swabs and 1 CHG bath per day). To quantify the correlation, a linear regression model and the Pearson coefficient was used.

Results. Approximately 2,000 and 1,000 opportunities for nasal decolonization and CHG bathing, respectively, were identified between September 2018 and March 2019. The data suggest a strong correlation between compliance with MRSA decolonization elements and rate of HO MRSA bacteremia \(R^2 = 0.785\) and a moderate association between nasal decolonization and rate of CO bacteremia \(R^2 = 0.322\) (Figures 2 and 3).

Conclusion. The MRSA decolonization bundle of CHG bathing and nasal swabs appears to be an effective strategy to decrease HO MRSA bacteremia rates with higher bundle compliance being associated with lower rates of infection.

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