The MRSA Chilean-Cordobes (ChC) clone belongs to the clonal complex 5 (CC5) and typically carries SCC mec I. The ChC clone predominated widely throughout several countries of Latin America (LA), but during the mid-2000s a CA-MRSA CC8 LA variant (USA300-LV) quickly replaced the ChC in Colombia and Ecuador. Most notably, this replacement was not observed in Peru or Chile. Here, we aimed to understand the phylogenomic relatedness of the CC5 ChC clone obtained from different countries of LA.

Methods. We sequenced and analyzed the genomes of 115 MRSA isolates obtained between 2011–2014 from bloodstream infections in 6 LA countries (Argentina, Brazil, Colombia, Chile, Peru, and Venezuela). All isolates were confirmed as ChC clone by pulsed-field gel electrophoresis (PFGE). We used core genome-based phylogenomic reconstructions and molecular clock analysis to infer the relationships and time of divergence between clades.

Results. Whole-genome-based multilocus sequence typing determined that 110/115 isolates belonged to ST5 and carried SCC mec I. The phylogenomic reconstruction showed ChC isolates clustered into 4 major clades distinctly segregated by country of origin (Figure 1). Interestingly, isolates recovered from Chile divided into 2 different clades that segregate according to the city of origin (Santiago [SCL] or Concepción [CON]), suggesting these clades evolved independently. Molecular clock analyses suggested all clades share a common ancestor with the divergence of the Chilean clades occurring earlier (Figure 2). Of note, analysis of heavy metal genes suggested the divergence between Chilean isolates was characterized by the loss of a mercury resistance gene cluster, which is present in an 88% of CON isolates, but only in 28% of SCL (Figure 2).

Conclusion. MRSA isolates belonging to the ChC clone from 6 LA countries clustered in 4 clades according to the geographical region of isolation. This segregation suggests divergent adaptations that may respond to different selective pressures. Heavy metal resistance could play a role in the ability of the MRSA ChC to disseminate in specific geographical locations.
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 murine hyaluronidase activity, Hg resistance and the transcriptional regulator Cro/Crl. Of 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), amino acid 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 US300-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
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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 after day 3 were considered 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 2). The median LOS of these prior hospitalizations was 8 days (IQR 5–14), and 87% were at least 4 days in length.

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 MRSA bloodstream infections by day since 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. New York, 2013–2016

Figure 2. Number of weeks from most recent hospital discharge to community-onset (CO) MRSA bloodstream infection (BSI), stratified by previous hospital length of stay (LOS): long LOS 48 days vs. short LOS ≤16 days in New York hospitals, 2013–2016

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559. Two Different Beasts: Comparing Epidemiology of Healthcare-Associated vs. Community-Acquired Methicillin-Resistant Staphylococcus aureus Bacteria
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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 (occurring >48 hours after hospitalization or 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 bacteria 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%, respectively). HCA-MRSA infections had a higher rate of previous MRSA colonization (64.8%) compared with CA-MRSA patients (41.7%). Injection drug use was higher in CA-MRSA infections (47% vs. 11%). The most common source of CA-BSI transmission (30%) while line-associated infections were the most common in HCA-BSI. C glandaminic resistance was common (46–53% susceptible) while resistance to tetracyclines (91–97% susceptible) and trimethoprim/sulfamethoxazole (98–100% susceptible) was uncommon. HCA-MRSA BSI was associated with a higher rate of ICU admission (44% vs. 33%) and 30-day mortality (18.7% vs. 11.7%).

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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