Background. Controlling methicillin-resistant *Staphylococcus aureus* (MRSA) colonization is a common strategy to prevent transmission and recurrent infection. Standard decolonization regimens include nasal application of mupirocin ointment; however, increasing rates of mupirocin-resistance (Mup-R) have been noted globally. At our institution there has been an increase in community-acquired MRSA (CA-MRSA) infections among children living in Brooklyn, New York. A genotypic geographic cluster of an outbreak clone of the CA-MRSA strain USA 300 with a high rate (>85%) of mupirocin resistance, mediated by the plasmid borne *mupA* gene, was identified prompting investigation into an alternative decolonizing agent. We sought to investigate retapamulin, a topical pleuromutilin antibiotic, which has been shown to be effective against *S. aureus* with *in vitro* and *in vivo* activity against MRSA and a low propensity to develop resistance.

Methods. Broth microdilution was used to determine the minimum inhibitory concentrations (MIC) of retapamulin against 53 Mup-R MRSA isolates collected from pediatric patients (aged 9 months–17 years) presenting to our institution over an 18 month period with clinical MRSA infection. Susceptibility defined as ≤0.5 mg/L susceptible (EUCAST). Whole genome sequence data were analyzed for the presence of *rplC* and *cfr* gene mutations known to confer resistance to retapamulin.

Results. All 53 isolates were susceptible to retapamulin. 49/53 (92%) strains were inhibited at MIC 0.25 mg/L, 2/53 (4%) at MIC 0.125 mg/L, and 2/53 (4%) at MIC 0.5 mg/L. DNA sequence analysis showed that one isolate had a first-step mutation in the *rplC* gene, but it was not associated with reduced phenotypic susceptibility to retapamulin, as the MIC of that isolate was 0.25 mg/L.

Conclusion. Retapamulin demonstrated excellent *in vitro* activity against a genotypic cluster of Mup-R isolates from pediatric patients presenting to our institution with MRSA infection. These data suggest that retapamulin may be a promising alternative decolonization therapy for MRSA and a viable option to prevent the spread of mupirocin-resistant MRSA clones. Further research includes an ongoing randomized, placebo-controlled trial testing the *in vivo* efficacy of retapamulin as a nasal and perirectal decolonizing agent in children.

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1219. Increasing Methicillin Resistance of *Staphylococcus lugdunensis* in a Tertiary Care Community Hospital in Japan

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Background. *Staphylococcus lugdunensis*, a coagulase-negative staphylococcus, has virulence and pathogenicity similar to that of *Staphylococcus aureus*. Methicillin resistance and presence of *mecA* gene are not common in *S. lugdunensis* in many parts of the world. Recently, higher prevalence of methicillin-resistant S. *lugdunensis* is reported from Taiwan and Japan. We describe the change in methicillin resistance of *S. lugdunensis* in a tertiary care community hospital in Sapporo, Japan.

Methods. We performed a retrospective study of *S. lugdunensis*, isolated from inpatients and outpatients at our hospital from 2008 to 2017. Rate of methicillin resistance of the first 5 years from 2008 to 2012, and that of the second 5 years from 2013 to 2017 were compared. Risk factors of methicillin resistance were also evaluated. Phenotypic detection of methicillin resistance was identified using broth microdilution by VITEK two system (bioMérieux).

Results. A total of 369 cases of *S. lugdunensis* were detected during the study period. Of all cases, 228 (61.8%) were men, and 177 (48.0%) were hospitalized. Twenty-one isolates (5.7%) were positive in blood culture, 216 (58.5%) were positive in cultures of skin and soft tissue. Methicillin-resistant strains were found in 43 (31.6%) of 136 isolates from 2008 to 2012, and in 108 (46.4%) of 233 from 2013 to 2017 (OR 1.87; 95% CI 1.20–2.91; $P = 0.006$). Of patients with methicillin-resistant *S. lugdunensis*, 105 cases (69.5%) were hospitalized ($P < 0.001$).

Conclusion. In our hospital, methicillin-resistant *S. lugdunensis* is increasing over the 10 years. Further research is needed to assess trend of methicillin resistance of *S. lugdunensis* in other healthcare facilities and countries.

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1220. Impact of Mandatory Infectious Diseases Consultation on the Use of Core Measures and Mortality in *Staphylococcus aureus* Bacteremia (SAB) at an Academic Medical Center

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Background. Multiple studies have shown that Infectious Diseases (ID) consultation significantly improves adherence to guidelines for patients with SAB and decreases mortality. Data from a prior retrospective study done at Hahnemann University Hospital showed that ID consultation improved the use of guideline-based core measures for SAB management. Based on these data, a mandatory ID consultation was established at our institution in November 2016.

Methods. A retrospective, observational study was conducted to evaluate patient characteristics, adherence to core measures for SAB, and in-hospital mortality. All patients with at least one documented blood culture positive for *S. aureus* were stratified into two groups: pre-mandatory consult (January 1, 2014–November 1, 2016) and post mandatory consult (November 2, 2016–February 1, 2018).

Results. Three hundred seventy-three discrete episodes of SAB were included in the final analysis, 238 episodes before mandatory consult, and 135 episodes after the mandatory consult policy was enacted. Mandatory consultation significantly improved the use of the following core measures for SAB: surveillance blood cultures (87.7% pre vs. 99.2% post, $P < 0.001$), echocardiography (81.9% vs. 96.9%, $P < 0.001$), early targeted antimicrobial therapy with nafcillin or cefazolin in MSSA (71.7% vs. 88.6%, $P < 0.001$), and appropriateness of final antibiotic choice (80.2% vs. 95.2%, $P < 0.001$). In addition, in-hospital mortality (15.4% vs. 6.2%, $P = 0.011$), and infection-related mortality (14.3% vs. 5.6%, $P = 0.011$) were found to be statistically significantly lower in the post mandatory consultation patients.

Conclusion. Implementation of a mandatory ID consultation for patients with SAB at our institution was associated with increased adherence to guideline-based core measures for management of SAB, and decreased in-hospital and infection-related mortality. Our results suggest that mandatory ID consultation for SAB should be considered at all institutions.

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

1221. Genetic Characteristics of Healthcare-Associated Methicillin-Resistant *Staphylococcus aureus* (HA-MRSA) Belonging to Clonal Complex 5 (CC5) in Latin-America

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Background. MRSA are responsible for a high proportion of healthcare-associated infections. HA-MRSA is multidrug resistant, and infections occur most frequently among inpatients, for example, those who have undergone invasive medical procedures or those aged 50 to 60 years and older. Dominance of multidrug-resistant CC5 (Chilean and New York/Japan clones) was prevalent in infections in Latin America with the notable exception of Colombia and Ecuador where USA300-LV isolates dominate. We performed genetic characterization of HA-MRSA-CC5 isolates recovered from infections in nine countries (12 hospitals).

Methods. Species identification of *S. aureus* and presence of *mecA* were performed by PCR. We determined MICs to common anti-MRSA antibiotics and performed screening for VISA phenotype. Molecular characterization included detection of lukSF-PV and SCC*mec* typing. PFGE and MLST were performed in selected MRSA isolates with susceptibility patterns typical of the Chilean (ST5-MRSA-I) and USA300-LV (ST8-MRSA-IV) lineages.

Results. A total of 665 *S. aureus* isolates were prospectively recovered from 592 patients. A high frequency of methicillin resistance (>40%) was observed in all countries (62%, 55%, 44%, and 40% in BRA, PER, CHI and ARG, respectively). Decreased susceptibility to VAN was not observed and VAN MIC90 was 1 μg/mL. In PER and CHI, the overwhelming majority of isolates (89%) belonged to the Chilean/Cordobes clone (CC5) with susceptibility patterns typical of this lineage (Resistance to β-lactams, MLSB-type, quinolones, and aminoglycosides). The New York/Japan clone (ST5-MRSA-II) was predominant in Brazil, replacing the prevalent hospital-associated Brazilian (ST239-MRSA-III) lineage. Most Argentinian MRSA isolates exhibiting a CA (ST5-IV) pattern, previously described in this country.

Conclusion. A variety of MRSA genetic lineages are circulating in Latin America with geographic clustering and clonal replacement. Dissemination of the CA-USA300-LV has not occurred beyond the northern region of the subcontinent.

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1222. Risk Factors and Outcomes for Daptomycin Nonsusceptible Methicillin-Resistant *Staphylococcus aureus* Bloodstream Infections

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