Results. MSSA BSI decreased from 0.37 per 1,000 hospital days (n = 15) to 0.00 (n = 0), P = 0.0092. All MSSA infections decreased from 0.62 (n = 25) to 0.11 (n = 2), P = 0.0078. Of 694 eligible neonates, 98.8% were screened at least once for MSSA colonization, which was detected in 92 (13.4%) infants. Median weekly prevalence of colonization was 6.7%. Median length of stay of neonates after initial detection of colonization was 30 days. Of colonized neonates, 92% received mupirocin treatment, with a median of 1 course of mupirocin treatment per patient (range, 1–7 courses). Of 54 isolates tested, all were mupirocin-susceptible. In contrast, there was no significant change in the rates of either MRSA (P = 0.71) or Gram-negative (P = 0.45) BSIs. In the comparison NICU, there was no significant change in rate of MSSA BSIs (P = 0.34).

Conclusion. Despite a substantial burden of MSSA-colonized neonates, the intervention was associated with elimination of MSSA BSI and an 82% reduction in rate of MSSA infections. A potential confounding factor was the occurrence of a cluster of mupirocin-resistant MRSA during the intervention period with the associated intensified infection prevention measures.

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2305. *Staphylococcus aureus* Screening and Decolonization for Pediatric Patients Undergoing Cardiovascular Surgery at Texas Children's Hospital (TCH): A Trainee Quality Improvement Initiative

Catherine Foster, MD; Daniel Ruderfer, MD; Gabriella Lamb, MD; Juri Boguniewicz, MD; Ryan Rochat, MD PhD GEMS; Lucila Marquez, MD, MPH; Debra Palazzi, MD and Claire E. Bocchini, MD; Baylor College of Medicine and Texas Children's Hospital, Houston, Texas

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Background. Colonization with *Staphylococcus aureus* increases the risk of developing healthcare-associated infections (HAIs) in adults, but its role in pediatrics remains unclear. We hypothesized that use of a *S. aureus* screening and decolonization protocol for pediatric patients undergoing cardiovascular (CV) surgery would result in a reduction of invasive *S. aureus* infections.

Methods. A *S. aureus* screening and decolonization protocol (Table 1) was implemented for patients undergoing CV surgery at TCH on January 1, 2018. We retrospectively identified and reviewed charts of pediatric patients with *S. aureus* infections following CV surgery pre-protocol (2017) and post-protocol (January 1, 2018–March 31, 2018). We defined invasive *S. aureus* infections as: bacteremia, mediastinitis, superficial and deep surgical site infections (SSIs) and ventilator-associated pneumonias (VAPs). A subset of charts were reviewed pre- and post-protocol for methicillin-resistant *S. aureus* (MRSA) polymerase chain reaction (PCR) result, use of mupirocin and chlorhexidine gluconate (CHG), and choice of intraoperative antibiotic. Data were analyzed with Fisher's exact.

Results. Of 694 pediatric CV surgery patients in 2017, we identified 13 patients with 15 invasive *S. aureus* infections: bacteremia (5), VAP (4), and SSI (6). Twelve of these infections were caused by methicillin-susceptible *S. aureus* (MSSA) and 3 were MRSA. The median time to infection was 19 days. In the first 3 month post-protocol period, there were 175 pediatric CV surgery patients with 0 invasive *S. aureus* infections. Seventy-five charts each were reviewed pre- and post-protocol to assess protocol adherence (Figure 1). Post-protocol MRSA screening peaked at 64%, which increased further to 70% when excluding infants <30 days. Of 40 patients screened with a MRSA PCR, only 1 (2.5%) was positive. Cefazolin use remained high pre- and post-protocol (72/75 vs. 73/75 respectively).

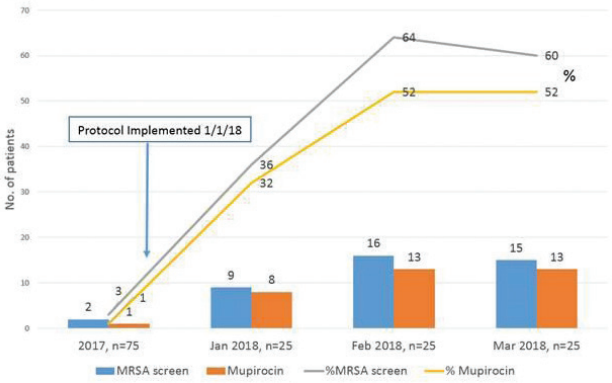
Conclusion. Most pediatric invasive *S. aureus* infections are caused by MSSA. Following protocol implementation, we observed a decrease in invasive *S. aureus* infections in CV surgery patients at TCH (P = 0.05), though continued monitoring for protocol compliance and development of *S. aureus* and other bacterial infections are needed.

Table 1. *Staphylococcus aureus* Infection Prevention Protocol for Pediatric Patients Undergoing Cardiovascular Surgery at Texas Children's Hospital

Recommendation	Description
Universal Decolonization	• Population: All patients undergoing CV Surgery • Action: Apply topical mupirocin to anterior nares BID for 5 days AND use 2% chlorhexidine gluconate antiseptic wipes as directed according to patient weight daily for 5 days[a] • Timing: Start 5 days prior to surgical procedure date
MRSA Screening	• Population: All patients undergoing CV Surgery • Action: Using a single swab, swab the nares, axilla, and groin of the patient for MRSA PCR testing • Timing: Perform at least 3-4 hours prior to surgical procedure
Screening-Directed Preoperative Antibiotic	• Population: All patients undergoing CV Surgery • Action: Administer cefazolin[b] • Timing: 0-60 minutes prior to incision; re-dose every 4 hours • Population: MRSA-positive patients undergoing CV surgery should receive cefazolin in addition to the following: • Action: Administer vancomycin • Timing: 0-120 minutes prior to incision; no re-dosing

[a]At preoperative visit, patients are given packets containing: chlorhexidine wipes, an instruction sheet, and a prescription for mupirocin.
[b]Cefazolin was the first-line agent for intraoperative prophylaxis at our institution pre protocol. In patients with a documented β-lactam allergy, may refer to A&I for penicillin allergy testing. If β-lactam allergy confirmed, administer clindamycin and re-dose every 6 hours or a one-time dose of vancomycin for gram-positive coverage.

Figure 1. *Staphylococcus aureus* Infection Prevention Protocol Use



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

2306. Molecular Epidemiology of and Risk Factors for *Staphyloccus aureus* (SA) Colonization in a Chinese Neonatal Intensive Care Unit (NICU)

Wenjing Geng, MD, PhD[1,2]; Thomas McConville, MD[2]; Alexandra Hill-Ricciuti, MPH[3]; Yujie Qi, MD[1]; Lisa Saiman, MD, MPH[3,4] and Anne-Catrin Uhlemann, MD, PhD[2]; [1]Beijing Children's Hospital, Beijing, China, [2]Columbia University Medical Center, New York, New York, [3]Pediatrics, Columbia University Medical Center, New York, New York, [4]New York Presbyterian Hospital, New York, New York

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Background. SA infections place a significant burden on NICUs worldwide. However, little is known about the burden of SA in Chinese NICUs. In this study, we describe the molecular epidemiology of SA in the tertiary care 50-bed NICU of Beijing Children's Hospital and examine risk factors (RFs) for SA colonization in neonates.

Methods. From May 2015 to March 2016, we prospectively collected nasal swabs from 536 neonates <28 days of age admitted from the community, perinatal services, or other hospitals. SA isolates were characterized by multilocus sequence type (MLST), staphylococcal chromosomal cassette *mec* (*SCCmec*) type, *agr*, spa-type, cytotoxicity and superantigen (*SAg*) genes. The characteristics of MRSA vs. MSSA and infecting vs. colonizing isolates were compared using Mann–Whitney U and Fisher's tests. Logistic regression was used to compare characteristics of infants colonized vs. uncolonized with SA.

Results. We identified 96 (18%) and 23 (4%) neonates with SA colonization and/or infection on admission. Among the 96 colonized infants, 28 had MRSA and 68 had MSSA. ST59-SCCmecIVa-t437-agr-1 (20/28, 71%) and ST188-t189-agr-1 (11/68, 16%) were the common colonizing MRSA and MSSA clones, respectively. Among 23 isolates associated with infection, 17 were MRSA and ST59-SCCmecIVa-t437-agr-1 (6/17, 35%) was also the most common clone. Of the 119 SA isolates, 108 (91%) contained at least one *SAg* gene; however, none carried *sasX*. Cytotoxicity was significantly different among the main clones (P = 0.04). While MRSA and MSSA had similar cytotoxicity (83.7% vs. 85.9%, P = 0.45), infecting isolates had higher cytotoxicity than colonizing isolates (87.6% vs. 84.5%, P < 0.01). Female sex (OR_{ADJ} = 2.05, P < 0.01), age >7 days (OR_{ADJ} = 7.14, P < 0.01), and vaginal delivery (OR_{ADJ} = 2.16, P < 0.01) were RFs for SA colonization, while antibiotic use was protective (OR_{ADJ} = 0.25, P < 0.01).

Conclusion. SA colonization was common in infants admitted to our NICU and 2 clones predominated. MRSA and MSSA did not differ in cytotoxicity, although infecting isolates had higher cytotoxicity. Several non-modifiable risk factors for SA colonization were identified. Our results suggest that screening infants for SA is useful and interventions to target cytotoxic clones should be explored.

Disclosures. **A. C. Uhlemann**, Merck: Investigator, Grant recipient.

2307. Use of Whole-Genome Sequencing to Determine Adhesin and Biofilm-Associated Gene Profiles Among Pediatric *Staphylococcus aureus* Device-Related Infection Isolates Compared With Skin and Soft-Tissue Infection Isolates

Catherine Foster, MD[1]; Melissa Kok, BS[1]; Anthony Flores, MD, MPH, PhD[2]; Ruth Ann Luna, PhD[1]; Sheldon L. Kaplan, MD, FIDSA[1] and Kristina G. Hulten, PhD[1]; [1]Baylor College of Medicine and Texas Children's Hospital, Houston, Texas, [2]University of Texas Health Science Center, Houston, Texas

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Background. Adhesins or microbial surface component recognizing adhesive matrix molecules (MSCRAMMs) and the *ica* locus help mediate *S. aureus* adherence to host tissue and biofilm formation and are thought to play important roles in the

pathogenesis of device related infections (DRIs). We hypothesized that *S. aureus* isolates from pediatric DRIs differ in MSCRAMM and biofilm-associated gene profiles and display greater strain diversity compared with skin and soft-tissue infection (SSTI) isolates.

Methods. Patients and isolates were identified from a prospective *S. aureus* surveillance study at Texas Children's Hospital, 2008–2016. Clinical data were collected retrospectively. Age and date of infection matched SSTI control isolates were selected 4:1. Isolates were genotyped by pulsed-field gel electrophoresis. Whole genome sequencing was performed (Illumina MiSeq). Data were analyzed with CLC Genomics Workbench for the presence of MSCRAMMS (*clf*A, *clf*B, *ebh*, *fbp*, *fnbp*A, *fnbp*B, *isd*A, *isd*B, *sdr*C, *sdr*D, *sdr*E), biofilm-associated genes (*icaA,D,B,C)*, accessory gene regulator group, and by multilocus-sequence typing (MLST) with eBurst analysis (www.phyloviz.net). Conditional logistic regression and Fisher's exact were used for analysis (STATA11).

Results. Forty-five patients with 47 DRIs were identified (Table 1). Isolates from 47 DRIs and 188 SSTIs were analyzed for the presence of MSCRAMM and biofilm-associated genes. *clf*A, *clf*B, *fbp*, *isd*A, *isd*B, and *icaA,D,B,C* were present among DRIs and SSTIs more than 98% of the time. Isolates from DRIs or SSTIs did not differ significantly in carriage of MSCRAMMs or the *ica* locus. DRIs were MSSA (34, 72%), non-USA300 (39, 83%), and belonged to 19 sequence types (STs). SSTIs were MSSA (79, 42%), nonUSA300 (57, 30%), and belonged to 39 STs (Table 2). Among DRI isolates, STs 5 and 8 were most common (23% each, Figure 1). SSTI isolates were predominately ST8 (68%).

Conclusion. *S. aureus* isolates from DRIs were significantly more likely to be MSSA and nonUSA300 ($P < 0.0001$ for both) compared with SSTIs. The majority of *S. aureus* isolates harbored all MSCRAMM and biofilm-associated genes analyzed. Evaluating genetic polymorphisms and gene expression profiles may clarify the role of adhesion genes in the pathogenesis of DRIs vs. SSTIs.

Table 1. Clinical Characteristics and Outcomes of patients with *S. aureus* DRIs

Clinical characteristic	DRIs[a] n= 47 (%)	Outcome	DRIs[a] n= 47 (%)
Gender, n (%)		**Hospitalization** (days)	
Male	25 (53)	median, range	10, 1-45
Age (years)		**Surgical procedure**, n (%)	
median, range	12, 1-20	Incision and drainage	47 (100)
		More than 1 procedure	12 (26)
		Device removal	22 (47%)
Time to infection, n (%)		**Definitive antibiotic agent**, n (%)	
0-30 days	12 (26)	Cefazolin	16 (34)
31-90 days	18 (38)	Cephalexin	6 (13)
91-365 days	14 (30)	Clindamycin	9 (19)
>365 days	3 (6)	Nafcillin	6 (13)
		TMP-SMX	1 (2)
		Vancomycin	6 (13)
		Combination	3 (6)
Type of device, n (%)		**Definitive antibiotic route**, n (%)	
Orthopedic spinal rod	22 (47)	Intravenous in hospital	11 (23)
Other orthopedic hardware[b]	19 (40)	Intravenous home health	25 (53)
Vagal nerve stimulator	3 (6)	Oral	11 (23)
Baclofen pump	2 (4)		
Cochlear implant	1 (2)		
Perioperative antibiotic, n (%)		**Antibiotic duration** (weeks)	
Cefazolin	33 (92)	median, range	4, 1-18
Clindamycin	1 (3)		
Piperacillin-tazobactam	1 (3)		
Vancomycin	1 (3)		
Prior history, n (%)		**Transition to oral suppressive therapy**, n (%)	23 (49)
Device infection	15 (32)		
S. aureus infection	11 (23)		

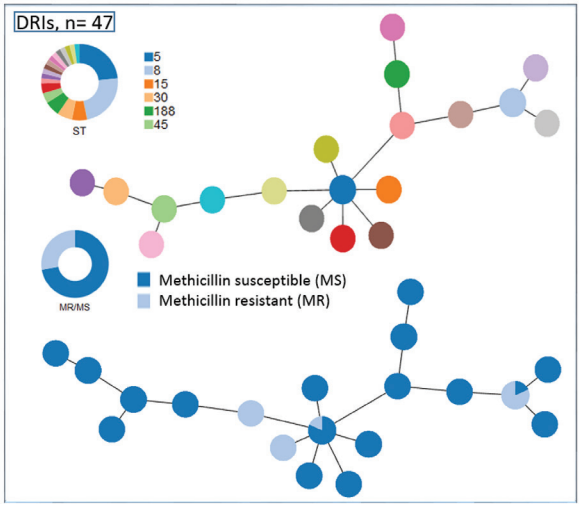
[a]Two patients had 2 DRIs, [b]Includes bars, plates, and screws

Table 2. Molecular characteristics of *S. aureus* isolates from DRIs and SSTIs

Molecular Characteristic	All isolates n=235 (%)	DRI isolates n=47 (%)	SSTI isolates n=188 (%)	P value
MRSA	122 (52)	13 (28)	109 (58)	<0.0001
MSSA	113 (48)	34 (72)	79 (42)	
USA300[a]	139 (59)	8 (17)	131 (70)	<0.0001
agr group[b]	n=233 (%)	n=47 (%)	n=186 (%)	
I	173 (74)	21 (45)	152 (82)	<0.0001
II	34 (15)	19 (40)	15 (8)	<0.0001
III	17 (7)	6 (13)	11 (6)	0.12
IV	8 (3)	0	8 (4)	0.36
Nontypeable	1 (0)	1 (2)	0	
MLST	n=233 (%)	n=47 (%)	n=186 (%)	
8	137 (59)	11 (23)	126 (68)	<0.0001
5	19 (8)	11 (23)	8 (4)	<0.0001
72	6 (3)	1 (2)	5 (3)	1.0
30	6 (3)	3 (6)	3 (2)	0.1
121	5 (2)	0	5 (3)	0.59
45	5 (2)	2 (4)	3 (2)	0.27
Other (46 STs)	55 (24)	19 (40)	36 (19)	

[a]PFGE result was not available for 1 isolate, [b]PCR was performed when *agr* group was inconclusive by whole genome sequencing (n=17)

Figure 1. Distribution of sequence types (ST) among *S. aureus* DRI isolates by eBurst



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2308. The Prevalence of Antiseptic Tolerance Genes Among Gram-Positive Bloodstream Pathogens in Children

Lauren Sommer, MS[1]; Jennifer Krauss, PhD[2]; Kristina G. Hulten, PhD[3]; James Dunn, PhD, D(ABMM)[4]; Sheldon L. Kaplan, MD, FIDSA[3] and J. Chase McNeil, MD[5]; [1]Baylor College of Medicine, Houston, Texas, [2]Pathology, Baylor College of Medicine, Houston, Texas, [3]Baylor College of Medicine and Texas Children's Hospital, Houston, Texas, [4]Pathology, Texas Children's Hospital, Houston, Texas, [5]Pediatrics, Section of Infectious Disease, Baylor College of Medicine, Houston, Texas

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Background. The presence of the *smr* and *qacA/B* genes in *Staphylococcus aureus* have been correlated with reduced susceptibility to antiseptics. Recently, *S. aureus* bearing these genes have been reported to be associated with nosocomial acquisition of infection and underlying medical conditions. Antiseptic tolerance (AT) genes have also been reported in coagulase negative staphylococci (CoNS) and enterococci; however, little data are available regarding their prevalence. We sought to describe the frequency of *smr* and *qacA/B* among bloodstream isolates of *S. aureus*, CoNS and enterococci obtained at Texas Children's Hospital (TCH).

Methods. Banked CoNS, *S. aureus* and enterococci isolated from blood cultures collected from October 1, 2016 to October 1, 2017 were obtained from the TCH clinical microbiology laboratory. All isolates underwent PCR for the *qacA/B* and *smr* genes. CoNS and enterococci were identified to the species level with MALDI-TOF mass spectrometry. Medical records were reviewed for all cases; CoNS were considered true pathogens if >1 blood culture was positive.

Results. 268 CoNS, 19 *Enterococcus* spp. and 116 *S. aureus* isolates were identified and included (Figure 1). 83.2% of CoNS possessed at least one AT gene compared with 36.2% of *S. aureus* and 31.5% of enterococci ($P < 0.001$, Figure 2). Neither antiseptic gene was detected in *E. faecium* isolates ($n = 4$) compared with 43.8% of *E. faecalis* ($P = 0.2$). Among CoNS, methicillin-resistance was found more commonly among *qacA/B*-positive (77.2% vs. 40%, $P = 0.04$) and *smr*-positive isolates (93.8% vs. 60.5%, $P = 0.02$). 38.4% of CoNS bloodstream isolates were considered true infections; among these, the presence of either AT gene was strongly associated with nosocomial infection ($P < 0.001$). AT genes in *S. aureus* were associated with nosocomial infection ($P = 0.007$) as well as the diagnosis of CLA-BSI ($P = 0.001$). There was no correlation with genotypic AT in enterococci and any examined clinical variable.

Conclusion. AT is common among bloodstream staphylococci and *E. faecalis* isolates at TCH. Among CoNS, the presence of AT genes is strongly correlated with nosocomial acquisition of infection consistent with previous studies in *S. aureus*. These data suggest that the healthcare environment contributes to AT among staphylococci.