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)		

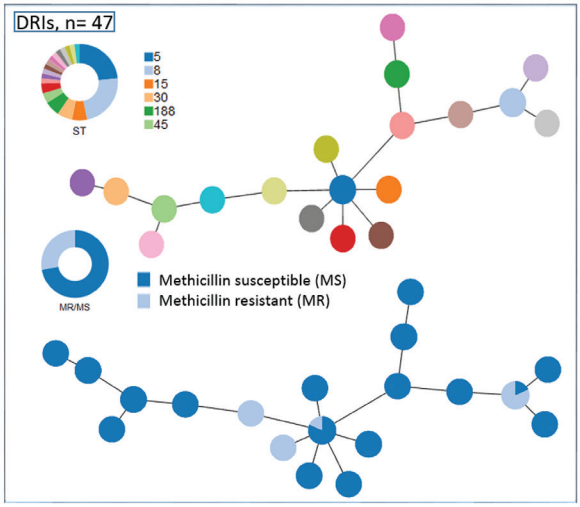
[a]Two patients had 2 DRIs, [b]Includes bars, plates, and screws

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



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

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

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Session: 246. Pediatric Healthcare Associated Infections

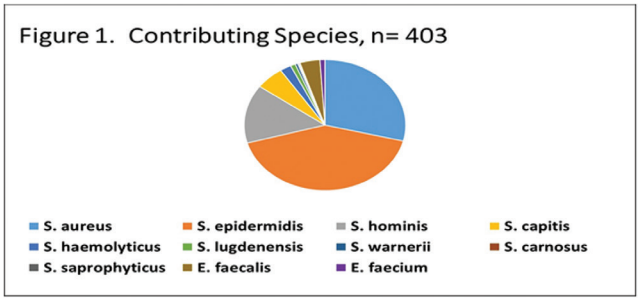
Saturday, October 6, 2018: 12:30 PM

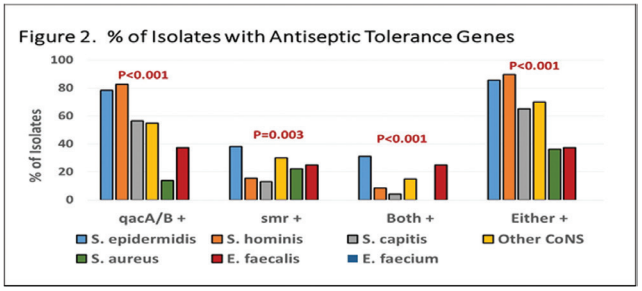
Background. The presence of the *smr* and *qacA/B* genes in *Staphylococcus aureus* have been correlated with reduced susceptibility to antiseptics. Recently, *S. aureus* bearing these genes have been reported to be associated with nosocomial acquisition of infection and underlying medical conditions. 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.





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

2309. Promoting Healthcare Worker (HCW) Use of Personal Protective Equipment in Pediatric Ambulatory Settings

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Saturday, October 6, 2018: 12:30 PM

Background. Existing Centers for Disease Control (CDC) and American Academy of Pediatrics (AAP) guidelines promote HCW personal protective equipment (PPE) use to prevent respiratory virus transmission in pediatric clinics; however, adherence to recommendations is inconsistent. We evaluated the effectiveness of two strategies designed to cue HCW use of PPE in a pediatric primary care clinic.

Methods. We implemented two HCW-focused interventions: (1) prompt for front desk respiratory symptom screen with placement of droplet signs on examination room door for symptomatic patients and (2) universal masking of healthcare workers during all patient encounters. Each intervention was implemented over a 2-week period and preceded by a washout period. We obtained caregiver report of HCW hand hygiene and mask use during patient encounters and measured differences in the proportion of behavior observed compared with washout periods.

Results. We obtained 217 caregiver reports of clinician handwashing and mask use before, during and after the patient encounter. There was no difference in nurse pre- or post-encounter hand hygiene behavior before and after each intervention (Baseline 65.9%; Droplet: 73.3%, $P = 0.34$; Universal masking: 77.5%, $P = 0.16$ and Baseline 53.3%; Droplet: 66.6%, $P = 0.14$; Universal masking: 55%, $P = 0.85$, respectively). There was also no difference in pre- or post-encounter MD hand hygiene behavior before and after each intervention: (Baseline 86.9%; Droplet: 77.8, $P = 0.17$; Universal masking: 87.5%; $P = 0.92$ and Baseline 75%; Droplet: 71.1%, $P = 0.62$; Universal masking: 80.0%; $P = 0.53$, respectively). However, there was a significant difference in observed mask use during encounters among both RNs and MDs before and after each intervention: (Baseline: 17.4%; Droplet: 44.4%, $P < 0.05$; Universal masking: 42.5%, $P < 0.05$ and Baseline: 20.6%; Droplet: 51.1%, $P < 0.05$; Universal masking: 62.5%, $P < 0.05$, respectively).

Conclusion. Respiratory symptom screening with visual prompts to use PPE and universal masking may not significantly impact hand hygiene behavior in a setting with high hand hygiene use but may increase mask use. Such interventions could provide a useful and low cost tool to help prevent the spread of respiratory viruses in primary care settings.

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2310. Reasons Pediatric Providers Obtain Endotracheal Aspirate Cultures and How Results Inform Patient Management

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Session: 246. Pediatric Healthcare Associated Infections
Saturday, October 6, 2018: 12:30 PM

Background. Endotracheal aspirate cultures (EACs) are commonly obtained in many PICUs. However, EACs cannot distinguish between bacterial colonization and infection, and may promote antibiotic overuse if collected in patients without clinical signs and symptoms of ventilator-associated infections (VAIs). We examined clinician's reasons to obtain EACs and whether the results informed clinical management.

Methods. We conducted a structured survey of nurse practitioners and physicians caring for ventilated children to inform a quality improvement initiative to optimize the use of EACs in the PICU at a tertiary care children's hospital. We assessed EACs obtained from patients mechanically ventilated for at least 24 hours from November 2017 to February 2018. This was a 2-part survey: part 1 conducted within 1–2 days after obtaining an EAC, part 2 conducted after EACs results were reported.

Results. 25 surveys were completed. Nearly half (44%) of EACs were obtained for isolated clinical signs of fever, hypotension, laboratory abnormalities, or ventilator increases, while the remainder were obtained for a combination of reasons. Most EACs (60%) were collected as a "pan culture" with urine and blood cultures, and 92% of EACs had a previous EAC. At the time of ordering, providers thought the EAC would help with diagnosis of VAI (68%), antibiotic selection (80%), and believed it was very important for the patient's management (60%). After results were available, 40% of patients were given a diagnosis of VAI. Antibiotic therapy was discontinued in 12% and modified in 16% based on the EAC results. Antibiotics were changed based on a different test in 52%, or unchanged in 20%. Of the patients with a prior EAC, 72% of EACs resulted the same or fewer bacteria. On follow-up, 56% of the providers reported the EAC provided little to no value for the patient's management.

Conclusion. A large proportion of EACs were obtained due to isolated changes in a patient's clinical status and most EACs were obtained from patients who had prior EACs. Results were often similar to prior EAC results, infrequently led to changes in antibiotic selection and many providers did not find the results helpful. These findings suggest there is opportunity to standardize and reduce the use of EACs in the PICU.

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2311. Atypical Cat Scratch Disease Presentations

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Session: 247. Pediatric Bacterial Infections
Saturday, October 6, 2018: 12:30 PM

Background. Cat scratch disease (CSD) is caused by *B henselae*, a Gram-negative intracellular bacilli which is transmitted to humans via cat bite/scratch. Typical CSD presents as regional lymphadenopathy and fever. However, there are multiple atypical presentations of cat scratch disease that have been reported including prolonged fever, absence of lymphadenopathy and systemic complications such hepatosplenic disease, osteomyelitis, Parinaud oculoglandular syndrome, neuroretinitis, encephalitis, and bacillary angiomatosis among other rare presentations. The aim of this study was to review the frequency, presentation, and treatment outcomes of aytpical CSD presentations at Nationwide Children's Hospital (Columbus OH).

Methods. This was a retrospective study performed at Nationwide Children's Hospital, Columbus, OH. EMR of patients were reviewed between January 2010 and March 2017 using ICD9 or ICD 10 codes for CSD. Patients were identified on the basis of compatible clinical presentation and confirmatory serological test or PCR results for *B. henselae*. Clinical, radiological, and histopathological findings were collected

Results. A total of 204 patients were serologically diagnosed as having cat scratch disease between January 2010 and July 2017. Of the 204 cases, 166 (81%) had typical CSD and 38 (18.6%) had atypical CSD. Of the atypical manifestations, 20 (52%) patients had no lymphadenopathy, 12 (31%) had osteomyelitis, 12 (31%) patients had hepatic and/or splenic microabscesses, 4 (10.5%) had osteomyelitis and hepatic/splenic involvement, 3 (1.5%) had encephalitis, 2 (5.2%) had neuroretinitis, and there was one case each (2.6%) of Parinaud oculoglandular syndrome, uveitis, pulmonary cavitary lesion, myocarditis, and endocarditis. Fever of unknown origin was present in 28 (75.6%) of the atypical CSD cases. The median duration of antibiotic treatment was 25 days (IQR 31) and median duration of illness in patients with atypical CSD was 51 days (IQR 56). The majority of patients were treated with dual antibiotic therapy that included rifampin.

Conclusion. In children with fever of unknown origin, serologic testing for CSD should be performed even in the absence of lymphadenopathy and a search for underlying systemic complications is recommended for prompt diagnosis and appropriate treatment.

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2312. *Bordetella holmesii* Bacteremia in Pediatric Patients: A Single-Center Experience

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Session: 247. Pediatric Bacterial Infections
Saturday, October 6, 2018: 12:30 PM

Background. *Bordetella holmesii* is a respiratory pathogen, known to cause bacteremia predominantly among patients with functional or anatomical asplenia. Currently, there is no consensus on optimal treatment for *B. holmesii* infection nor are there established interpretative criteria. This study aims to describe treatment of pediatric patients diagnosed with *B. holmesii* bacteremia, and treatment outcomes, in order to help establish an optimal therapeutic strategy.

Methods. We conducted a retrospective chart review of pediatric patients with microbiologically confirmed *B. holmesii* bacteremia at Children's Healthcare of Atlanta, 2011–2018. We extracted demographic and clinical information of the identified patients from the medical record, and evaluated antimicrobial choice, hospital days, and treatment outcomes.