590. Reduction of Endotracheal Colonization by Gram-Negative Bacilli in a Neonatal Intensive Care Unit Through Use of a Novel Drain Cover Melissa Buck, MD¹; Michael Antunes, MD²; Brewster Kingham³; Shawn W. Polson, PhD³ and Stephen C. Eppes, MD²; ¹Sidney Kimmel Medical College at Thomas Jefferson University, Wilmington, Delaware; ²Christiana Care Health System, Newark, Delaware; ³University of Delaware, Newark, Delaware

Session: 64. HAI: Pediatric

Thursday, October 3, 2019: 12:15 PM

Background. Splash and aerosolization from sink drains are a source of contamination, particularly by Gram-negative bacilli (GNB), in healthcare facilities. Neonatal Intensive Care Unit (NICU) outbreaks of infection due to GNB have been attributed to NICU sinks. Recent studies found that a dome-shaped drain cover placed in sinks in an adult ICU prevented dispersal of sink drain bacteria to the environment and hands of healthcare providers. Our NICU routinely performs weekly surveillance cultures of all endotracheal tubes (ETT) and has previously reported a correlation of ETT colonizing organisms with bacteria isolated from blood in late onset sepsis. Our objective was to determine whether the use of a drain cover in every sink in a level III 72 bed NICU could lead to a decrease in the isolation of GNB in the ETTs of hospitalized infants.

Methods. All 34 sink drains and basins in an open layout NICU were cultured. Drain covers were then installed and replaced on a routine basis. Weekly endotracheal tube cultures were performed for all intubated infants.

Results. Prior to implementation of drain covers, the most common GNBs cultured from ETTs were, in order, E. cloacae, Klebsiella spp., Acinetobacter spp., and S. maltophilia. The most common organisms isolated from sinks were, in order, P. aeruginosa, Acinetobacter spp. and S. maltophilia. An unusual species, Acinetobacter ursingii, was common in both sinks and endotracheal tubes. Before and after the implementation of drain covers, the median time to first isolation of a GNB was 14 and 17 days, respectively. Prior to draining cover implementation, there were 31 new GNB isolates during 700 ventilator days (rate of 44.3/1000 ventilator days) among infants with any positive ETT cultures. Post drain cover there were 26 new GNB isolates during 900 ventilator days (rate of 28.9/1000 ventilator days). There was a shift in microbial species isolated from ETTs with Klebsiella spp. and S. marcescens predominating after implementation of drain covers.

Conclusion. The use of a novel drain cover in the sinks in a NICU can reduce the frequency of GNB colonizing the ETTs of patients and can lengthen the time to first positivity. Mitigating sinks as a reservoir for GNB may reduce the likelihood of these bacteria infecting a vulnerable population. Disclosures. All authors: No reported disclosures.

591. Mupirocin and Chlorhexidine Resistance in Staphylococcus aureus Isolated from Children in South Korea

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Session: 64. HAI: Pediatric

Thursday, October 3, 2019: 12:15 PM

Increasing prevalence of mupirocin-resistant Staphylococcus Background. aureus have been reported, and chlorhexidine resistance has become an issue. This study aimed to investigate the prevalence of mupirocin and chlorhexidine resistance in both colonized and infection causing Staphylococcus aureus in children, and find factors associated with increased virulence.

Methods. Staphylococcus aureus, isolated from children <18 years old admitted at a single center, were collected prospectively from August 2017 to July 2018. The isolates underwent multilocus sequence typing and were screened for genes causing chlorhexidine resistance (qac A/B), quaternary ammonium resistance (smr), mupirocin resistance (ileS mutation, Mup A, MupB), and Pantone Valentine Leucocidin (pvl) toxin.

During the study period, a total of 49 non-duplicate isolates were Results. included, of which 69.4% (n = 34) were Methicillin-resistant Staphylococcus aureus (MRSA). Of the colonizers (n = 25), the most common sequence type was ST 72 (68.0%), whereas among pathogens (n = 24), ST 72 (29.2%) and ST 89 (29.2%) were most prevalent. Pathogens in this study caused abscess formation (n = 3), sepsis (n = 3)= 4), and skin infections such as cellulitis and omphalitis (n = 17). Mupirocin resistance was found in 16.0% among colonizers vs. 45.8% among pathogens (P = 0.023). High-level mupirocin resistance was more common (n = 3/25, 12.0%) than low-level mupirocin resistance (n = 1/25, 4.0%) in colonizers, whereas, pathogens had similar rates of low-level (25.0%) and high-level (n = 20.8%) mupirocin resistance. PVL toxin gene was more frequently found in colonizers than pathogens (64.0% vs. 33.3%, P = 0.032), and all isolates had quaternary ammonium resistance genes. Chlorhexidine resistance gene was found in only 3 MRSA isolates colonized in the nares of preterm infants. All were SCCmec type 4, however, two were ST 72, spa type t1054, which had high -level mupirocin resistance and PVL toxin gene.

Conclusion. A PVL toxin gene-positive MRSA which had genes causing mupirocin and chlorhexidine resistance were found in the nasal carriages of preterm infants. These stains may cause failure of MRSA eradication in hospital settings, using conventional methods of nasal mupirocin application and chlorhexidine bathing.

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592. Assessment of Time Spent in the Room by Nurses and Nursing Assistants on a Pediatric Ward by Patient Isolation Status and Demographics

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Session: 64. HAI: Pediatric

Thursday, October 3, 2019: 12:15 PM

Background. Published reports have raised concern that RNs spend less time in hospital rooms of patients requiring isolation precautions. Other patient-related factors including race/ethnicity, primary language, and socio-economic factors reportedly influence the mean time spent in the room by RNs and certified nursing assistants (CNAs). At a children's hospital the automated hand hygiene monitoring system (AHHMS) has motion sensors that detect patient room entry and exit and sensors that detect hand hygiene events. Time spent in patient rooms by RNs and CNAs was examined using AHHMS data captured for patients on a 24-bed pediatric hospital ward for multiple patient characteristics to evaluate factors influencing the duration of visits.

Methods. RNs and CNAs routinely wore badges with infrared signal technology to monitor hand hygiene compliance, generating time-stamped data for room entries and exits, identified by user job category. Over a 30 day period, April 2016, RN and CNA time in the room was compared by patient characteristics including: length of stay, white yes/no, Hispanic yes/no, interpreter needed yes/no, and isolation status of contact-droplet, contact, or none. Mean minutes spent in the room for RNs and CNAs were evaluated with a random-effects linear model and gamma distribution.

Results Admissions for 220 patients occurred in the 24 rooms during the evaluation period; 88 RNs and 28 CNAs completed 18,641 time-stamped room entries and exits. The natural log of patient length of stay (hours) was significantly associated with increased RN and CNA minutes spent in the room (P < 0.001). Interpreter required was not associated with time in the room (P = 0.72), nor was race (P = 0.60), nor was Hispanic ethnicity (P = 0.81). There were no significant differences in time spent in the room for contact, contact-droplet, and no isolation (P = 0.92).

Conclusion. Data derived from infrared signal AHHMS badges can provide insight into RN and CNA care patterns. Isolation status and patient demographics were unrelated to mean RN and CNA time in the room. Patient length of stay was the only predictor of increased nursing time spent providing direct patient care. These results contrast with previous reports demonstrating fewer nursing interactions based on patient demographics or isolation.

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593. Burden of Healthcare-Associated Infections among Hospitalized Infants within Community Hospitals

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Session: 64. HAI: Pediatric

Thursday, October 3, 2019: 12:15 PM

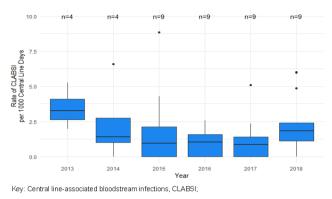
Background. Healthcare-associated infections (HAI) remain the leading cause of morbidity and mortality among hospitalized children. Within community hospitals with targeted infection prevention efforts, participation in an infection control network has led to significant decreases in device or procedure-related infections among adult patients. The impact of these interventions has not been assessed in pediatric patients admitted to community hospitals.

Methods. We conducted a retrospective cohort study to describe the burden of HAI among hospitalized infants (< 1 year old) within 53 community hospitals participating in the Duke Infection Control Outreach Network (DICON) from 2013-2018. We determined the frequency of device-related HAI, central line-associated bloodstream infections (CLABSI), catheter-associated urinary tract infections (CAUTI) and hospital-associated pneumonia or ventilator-associated events (HAP/VAE) using National Healthcare Safety Network (NHSN) definitions; and the burden of HAIs among neonatal intensive care units (NICU) and non-NICU centers. The trend of HAI was analyzed with Spearman's correlation.

Thirty hospitals reported 150 HAI among 141 infants over the 6-year Results. period. Median (IQR) time to infection was 10 (4, 20) days after admission. Hospitals with a NICU (15) reported more HAI (median 5, (IQR: 3, 12)) than hospitals without a NICU (median 2 (IQR: 1, 2)) (P = 0.031). CLABSI represented 35% of HAI, HAP/VAE were 23% and CAUTI were 12%. The most frequently isolated primary organism for all HAI was Escherichia coli (22 HAI, 15%) which was also isolated in 39% of CAUTI. Methicillin-resistant and methicillin-susceptible Staphylococcus aureus (S. aureus) were the most commonly isolated organisms among CLABSI (17%) and HAP/VAE (33%). Nine centers with ≥4 years of NICU and Central line (CL) use data reported a median (IQR) rate of 1.2 (0, 2.4) CLABSIs/1,000 central line days. There was no change in median CLABSI rate over time (P = 0.47), Figure 1.

CLABSI, most commonly caused by S. aureus, represented the Conclusion. majority of HAI reported from hospitalized infants within community hospitals participating in an infection control network. Further research into device utilization practices may inform future interventions to reduce HAI.

Figure 1: Boxplots of CLABSI rate, by year, in each hospital reporting central line days shows no change in rate of CLABSI over the study period.



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594. A Multi-Centered Study of the Clinical and Molecular Epidemiology of AmpC Cephalosporinase-Producing (AmpC) *Enterobacteriaceae (Ent)* Infections in Children

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Session: 64. HAI: Pediatric

Thursday, October 3, 2019: 12:15 PM

Background. AmpC producing *Ent* are an important cause of multidrug-resistant (MDR) infections in pediatrics. Since most AmpC *Ent* studies have been conducted in adults, we characterized the molecular epidemiology of AmpC *Ent* strains with transmissible resistance and identified factors associated with AmpC *Ent* infections in children.

Methods. A case-control study of children (0-18 years) at 4 Chicago hospitals during 2011-18 was performed. Cases were 44 children with infections due to *Ent* harboring an AmpC as detected by DNA microarray (Check-Points*). PCR, DNA sequencing, MLST, and phylogenetic analyses were performed. Controls (ctrls) were 132 children with expanded-spectrum cephalosporin-susceptible *Ent* infections matched by age and hospital. Demographics; residence; comorbidities; device, anti-biotic, and healthcare exposures were evaluated. Predictors of AmpC *Ent* infection were assessed by logistic regression.

Results. The median age of AmpC *Ent* patients was 3.0 years; 50% were male. Of bla_{AmpC} genes, 68% were $bla_{ACT/MIR-MPP}$ and 25% bla_{CMYMPP} . Predominant organisms were *Enterobacter cloacae* (59%) and *Escherichia coli* (32%); 27% of AmpC *E. cloacae* belonged to ST114 and 62% co-harbored a *blaESBL* gene, predominately bla_{SHV} (94%). Most AmpC *E. coli* strains were unrelated; 71% carried bla_{CMYP} 64% belonged to phylogroups B2/D, and 50% co-harbored bla_{CTX-M} . On bivariate analysis vs. ctrls, AmpC *Ent* infections were more likely to be respiratory (39% vs. 18%, P < 0.01) and less likely to be unitary tract (41% vs. 67%, P < 0.01) or community-acquired (14% vs. 33%, P < 0.02). By multivariable analysis, children with AmpC *Ent* infections were more likely to be nonwhite, non-black, non-Hispanic (OR 4.7, CI 1.4–16.1) and have infections due to *Enterobacter* (OR 7.7, CI 3.5–17). Differences in gender, healthcare location, residential neighborhood, antibiotic exposures, comorbidities, devices or outcomes

Conclusion. AmpC *Ent* infections often had healthcare onset, were due to *Enterobacter*, and occurred in nonwhite, non-black, non-Hispanic children. AmpC *Ent* commonly co-harbored *bla*_{SHV} and *blaCTX-M* ESBL genes which affects therapeutic options and suggests the need for contact precautions. Control of AmpC *Ent* infections in children will require validating sources and risk factors.

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595. Intranasal Mupirocin with Chlorhexidine Bathing has Limited Effectiveness for MRSA Decolonization among Neonates

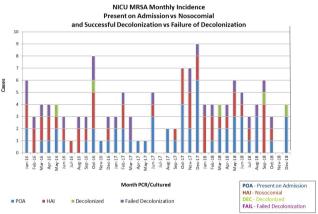
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Session: 64. HAI: Pediatric Thursday, October 3, 2019: 12:15 PM **Background.** MRSA colonization is a common neonatal problem and is associated with invasive infection. Good hand-washing and contact precautions reduce transmission. However, long-term contact isolation, sometimes for months, causes dissatisfaction among neonatal intensive care unit (NICU) care providers and parents. We examined the effectiveness of MRSA decolonization among neonates over 3 years.

Methods. Our NICU patients are routinely screened for MRSA colonization by PCR testing of nasal and rectal swabs upon admission and every 2 weeks. Patients with a history of MRSA infection or colonization became eligible for MRSA eradication upon reaching 2000g. Our protocol included intranasal muporocin 2% ointment applied to both nares twice daily for 5 days and 2% chlorhexidine wipe bath daily for 7 days. Wipes were used for bathing from the neck down for at least 20 sec per wipe. Two wipes were used for patient's < 10 kg with the first wipe being used on the neck, chest, arms, and back, and the second wipe being used on the legs, buttocks, and perineum. Patients were excluded from chlorhexidine bathing if they had a known allergy, were < 27 weeks gestation, < 1 week chronological age, receiving phototherapy, or had severe skin disease, open wounds, or burns. Contact isolation was discontinued if 2 sets of nares and rectal PCR swabs 5 days apart were negative and the patient had not been on antibiotics during the screening period. Surveillance MRSA PCR testing continued. Contact isolation was to be re-initiated if subsequent MRSA screening was positive. Patients were not decolonized a second time.

Results. Among infants admitted to the NICU during from 2016 to 2018 MRSA colonization was identified in 102 patients. Fifty-six were noted to have colonization present on admission and 46 were acquired on or after hospital day 3. The decolonization protocol with follow-up screening was completed in 33 infants. Successful decolonization was achieved for only 5 (15%) of infants. There were no adverse reactions noted among neonates and no MRSA decolonized patients reverted to positive by PCR screening while in hospital.

Conclusion. 85% of neonates with MRSA failed decolonization. Using mupirocin intranasally and chlorhexidine bathing to decolonize neonates with MRSA was welcomed by staff and families, but was poorly effective.



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596. Distinct, Segregated Daptomycin-Susceptible and Daptomycin-Nonsusceptible *Staphylococcus aureus* Populations Associated with Tricuspid-Valve Infective Endocarditis

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Session: 65. Mechanisms of Antimicrobial Resistance

Thursday, October 3, 2019: 12:15 PM

Background. Loss of daptomycin susceptibility in *Staphylococcus aureus* is often associated with sequestered foci of infection, driven by selection pressure from both administered antibiotics and host defense peptides. Susceptibility testing of the organism cultured from blood is assumed to parallel that of the infectious foci, such as heart valves. We studied a case of tricuspid valve endocarditis where one leaflet yielded exclusively daptomycin-nonsusceptible *S. aureus* and another leaflet yielded purely daptomycin-susceptible *S. aureus*. We examined the responses of the two populations to different anti-staphylococcal therapies to identify regimens effective against both isolates.

Methods. Both isolates were whole-genome-sequenced using Illumina technologies. The presence of heterogeneous daptomycin-resistant subpopulations was assessed by dilution plating and population analysis profiling. One compartment pharmacokinetic/pharmacodynamic modeling was used to simulate different potential antistaphylococcal pharmacotherapies against each isolate. Hemolysin activity was evaluated as a surrogate for accessory gene regulator function.

Results. The daptomycin-susceptible isolate did not demonstrate heteroresistance while the daptomycin-resistant population was uniformly daptomycin