Conclusion. A novel drain cover in an open layout NICU was 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 baumannii, and S. maltophilia. The most common organisms isolated from sinks were, in order, P. aeruginosa, Acinetobacter baumannii and S. maltophilia. An unusual species, Acinetobacter ursingii skin commensal with sinks and endotracheal tube. 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 positive ETT cultures. Post drain cover implementation, 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 cover.

Conclusions. 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.

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

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Background. Increasing prevalence of mupirocin-resistant Staphylococcus aureus has been reported, and chlorhexidine resistance has become an issue. This study aimed to determine 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 centre, were collected prospectively from August 2017 to July 2018. The isolated underwent multilocus sequence typing and were screened for genes causing chlorhexidine resistance (qac A/B), quaternary ammonium resistance (smr), mupirocin resistance (ileS mutation, Map A, MupB), and Pantone Valentine Leucocidin (pvl) toxin.

Results. During the study period, a total of 49 non duplicate isolates were 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 = 4), and pneumonia 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 (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 IV, 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 strains may be a major source of MRSA eradication in healthcare 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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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 assis-
tants (CNA) in acute care settings. In 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. RNs and CNAs spent a median 21.8 minutes per RN/CNA room entry and exit. 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 (P = 0.76). The reoccurrence of RN/CNA entries in time spent in the room for contact, contact-droplet, and no isolation (P = 0.92).

Conclusion. Data derived from infrared signal AHMS badges can provide in-sight 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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Background. Healthcare-associated infections (HAI) remain the leading cause of morbidity and mortality among hospitalized children. Within community hospitals, HAI prevention initiatives have only been inconsistently implemented. Our study uses data from a large network that 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 blood stream 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.

Results. Thirty hospitals reported 150 HAI among 141 infants over the 6-year 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, 3]) (P = 0.031). CLABSIs represented 35% of HAI, HAP/VAE were 23% and CAUTI were 12%. There were no isolated primary organisms 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 CLABSIs (17%) and HAP/VAE (33%). Nine centers with ≥ 24 NICU and Central line (CU) use data reported a median (IQR) rate of 1.2 (0.2, 2.4) CLABSIs/1,000 central line days. There was no change in median CLABSI rate over time (P = 0.47), Figure 1.

Conclusion. CLABSIs, most commonly caused by S. aureus, represented the majority of HAIs reported in a heterogeneous set of community hospitals participating in an infection control network. Further research into device utilization practices may inform future interventions to reduce HAI.
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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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 due to urinary tract (41% vs. 67%, P < 0.01). Order of AmpC Ent groups B2/D, and 50% co-harbored a single MBL gene, 68% were blaoct, and 25% blsaA. Predominant organisms were Enterobacter cloacae (59%) and Escherichia coli (32%); 27% of AmpC. E. cloacae belonged to ST114 and 62% co-harbored a blaOXA-24 gene, predominately blaOXA-24 (94%). Most AmpC. E. coli strains were unrelated; 71% carried blaKPC, 64% belonged to phylogroups B2/D, and 50% co-harbored blaKPC. 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 urinary 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 during 2016–18 (OR 2.6, CI 1.1–6.3).

Conclusion. AmpC. Ent infections often had healthcare onset, were more likely to be respiratory infections, and were more common in black, non-Hispanic children. AmpC. Ent commonly co-harbored blaKPC 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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596. Distinct, Segregated Daptomycin-Susceptible and Daptomycin-Non-susceptible Staphylococcus aureus Populations Associated with Tricuspid-Valve Infective Endocarditis
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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-non-susceptible 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 daptomycin gradient plate 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-resistant.