that generated it must be compliant with CLIA. CLIA validation of WGS methods is critical to ensuring safety with regard to patient clinical care.

Methods. As a way to help facilitate WGS implementation, we sought to identify the challenges for the establishment and use of CLIA-compliant WGS workflows in SPHLs. An environmental scan was performed in which we assessed materials produced at CDC, by the Association of Public Health Laboratories (APHL), by a Next-generation Sequencing Tri-agency workgroup, as well as published papers and guidance. We also engaged stakeholders through conversations with SPHL partners, APHL, and several groups within CDC.

Results. Our analysis revealed relevant resources and key WGS validation materials were dispersed and difficult to locate. To address this, we developed a CDC Next-generation Sequencing Resource Roadmap, to house key materials. After we reviewed, selected, and collated the resources, our web developer created a visual roadmap webpage to guide the user through the resources. This roadmap was then reviewed and tested for initial use internally at CDC.

Conclusion. This communication tool has the potential to provide critical resources needed to develop functional WGS validation strategies.

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2299. Oral Microbiome of High-Risk Children: A Cohort Study

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Background. Vulnerable pediatric populations are at high risk of bloodstream infection (BSI) and sepsis, such as patients of the pediatric intensive care unit (PICU) and bone marrow transplant (BMT) wards. Previous research demonstrates that commensal gut anaerobes provide host resistance against colonization and infection with pathogens but data on other body sites is lacking. Characterization of overlap or differences in commensal microbes of the mouth can provide insight on factors that may put these populations at risk for invasive disease.

Methods. A cohort study of patients (0–18 years) at a large pediatric quaternary care center from 2017 to 2018 was conducted. Cohort group 1 children were admitted to the PICU; cohort group 2 patients were admitted to the BMT unit. Matching was by age range. Metagenomic sequencing of oral swabs and statistical analysis was performed. A retrospective review of causes of BSI in both groups from 2016 to 2018 was also conducted.

Results. Eighteen patients in the PICU group and 21 patients in the BMT group were identified. Common causes of BSI from 2016 to 2018 vary in each cohort (Figure 1). Unlike *Enterobacteraciae*, which were more common in the BMT cohort, *Pseudomonas aeruginosa* was a more common cause of BSI among PICU patients. When evaluating the oral microbiomes, the number of reads for *Pseudomonas aeruginosa* was significantly higher in the PICU group compared with the BMT group ($P = 0.0019$, Figure 2).

Conclusion. Children in the PICU have a statistically significant difference in the frequency of oral colonization with *Pseudomonas aeruginosa* when compared with BMT patients. Unique characteristics of these populations may impact oral microbiomes of patients and their subsequent epidemiology of BSIs. Future studies should focus on preventive measures to decrease the risk of colonization with pathogenic bacteria.

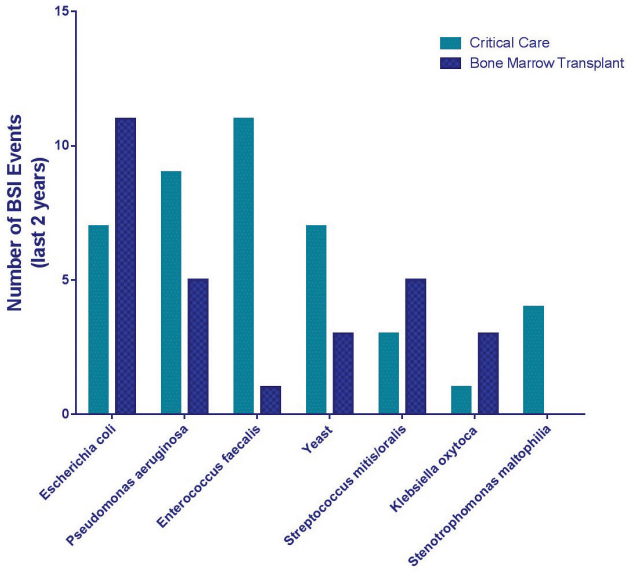

Figure 1. Causes of bloodstream infection in critical care and BMT patients 2016–2018.

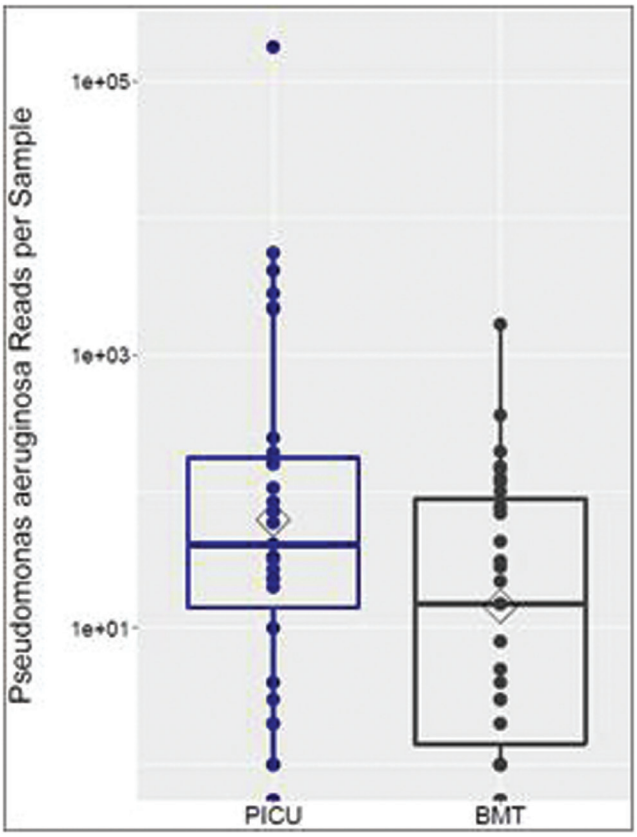

Figure 2. Boxplot of reads per sample of *Pseudomonas aeruginosa* from the oral microbiome in PICU and BMT patients.

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

2300. Molecular Epidemiology of Carbapenem-Resistant *Klebsiella pneumoniae* (CRKP) Causing Central Line Associated Blood Stream Infections (CLABSI) in Three ICU Units in Egypt

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Background. CLABSI caused by CRKP is associated with high mortality. Identification of the genetic basis for carbapenem resistance is crucial for selecting the proper antimicrobial therapy, and testing for bacterial clonality. We aimed to study the genetic basis of CRKP causing CLABSI in 3 ICUs, and use ERIC PCR to test for their clonality.

Methods. The study was conducted in a tertiary care hospital in Egypt from January 1, 2016 to December 31, 2017 after approval by the Institution Review Board. We enrolled all patients with CVCs in 3 ICUs. At least 2 sets of blood cultures were collected from each febrile patient by BACT/ALERT system (Bio Merieux, France), before starting an antibiotic. The pathogens and their antimicrobial susceptibility were detected by the VITEK 2 system (Bio Merieux, France). Phenotypic detection of carbapenemase activity was done by modified Hodge (MHT) test and Carba-NP test. Multiplex PCR was done to identify the carbapenemase genes. Molecular typing of carbapenem-resistant isolates was performed by ERIC–PCR.

Results. We enrolled 1,210 patients admitted for 17,785 ICU days. Central catheters were utilized in 53.3% of patients for a total of 11,014 central line days. Out of 130 Gram-negative CLABSI pathogens detected, we identified carbapenem resistance in 57 (43.8%); of which *K. pneumoniae* was the predominant pathogen (27 out of 57, 47.4%). By MHT and carba-NP, 63.79% of *K. pneumoniae isolates* were carbapenemase producers. Multiplex PCR revealed bla_{NDM} in 48.14% and bla_{KPC} in 33.33% of the *K. pneumoniae* isolates, whereas bla_{OXA-48} was not detected. ERIC-PCR analysis of 27 CRKP isolates showed genetic relatedness among only 5 KPC-positive and 2 producers, while most isolates were polyclonal.

Conclusion. We detected a high rate of carbapenem resistance among *K. pneumoniae* causing CLABSI showing bla_{NDM} in 48.14% and bla_{KPC} in 33.33%; and they were mostly polyclonal.

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2301. *Streptococcus pneumoniae* Serotyping: Assessing the Performance of a PCR- and Sequencing-Based Testing Algorithm

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Background. *Streptococcus pneumoniae* is a bacterium that causes significant morbidity and mortality worldwide. Its capsular polysaccharides have been used successfully as vaccine antigens, and to characterize *S. pneumoniae* into 92 different serotypes. Phenotypic (Quellung reaction) or genotopic (PCR or sequencing) methods can be used for serotype assignment, but the performance may vary between methods. This study compared the performance of the Quellung reaction, to an algorithm using PCR- and sequence-based serotyping technologies for vaccine-preventable or closely related serotypes.

Methods. A panel of geographically diverse isolates of *S. pneumoniae* spanning 92 different serotypes was provided by various references laboratories worldwide. Each isolate was subjected to conventional multiplex PCR methods, using previously established methods. Sanger sequencing was performed using genetic signatures defined in the PneumoCaT database. When discrepant, Quellung reaction were repeated, and next-generation sequencing and comparative genomics was used to evaluate the sequence composition of the *cps* loci.

Results. As expected, PCR was unable to assign serotype in some cases, and some serotype results were insufficiently discriminatory. Following sequencing, 86.3% (404/468) of isolates were concordant with the Quellung serotyping. Discrepant analyses are underway.

Conclusion. An algorithm based on PCR and sequencing, or next-generation sequencing alone, shows much promise for serotyping of *S. pneumoniae*. However, discrepant results were noted, suggesting either our current understanding of genetic signatures conferring serotype-specificity might not be complete, or the Quellung reaction results were incorrect. Accurate methods for serotyping are essential to monitor the impact of pneumococcal vaccines, and understand the epidemiology of *S. pneumoniae* diseases.

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2302. Bloodstream Infections Due to Carbapenem-Resistant Gram-Negative Bacteria in Pediatric Intensive Care Unit (PICU): Risk Factors and Outcomes

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Background. Bloodstream infections (BSI) caused by multidrug-resistant bacteria are associated with poor outcome and increased cost. We investigated risk factors for carbapenem resistance (CR) and outcome associated with the development of BSI due to Gram-negative (GN) bacteria in PICU patients, a very vulnerable population.

Methods. We reviewed the records of 1 month–15 year old patients with documented GN BSI hospitalized in a PICU from 2005 to 2017. Isolates with meropenem MIC ≥16 mg/L were considered as resistant. Demographics, clinical characteristics, potential risk factors for acquisition of resistant strains, treatment, potential source control and outcome were recorded. Outcome was determined as microbiological response (negative blood cultures) within 5 days and mortality within 30 days. Both univariate and multivariable logistic regression analysis was performed and odds ratios (OR) with 95% confidence intervals (CI) were presented.

Results. 81 patients with GN BSI were studied (34.6% *Pseudomonas aeruginosa*, 34.6% *Acinetobacter baumannii* and 30.9% *Enterobacteriaceae*), 21 with CR isolates. Risk factors for CR BSI were: prior carbapenem use (OR: 3.86, 95% CI: 1.10, 13.82) and renal replacement therapy (OR: 3.86, 95% CI: 1.10, 13.82). In multivariable outcome analysis, high levels of CRP (OR: 0.99, 95% CI: 0.99, 0.999), renal replacement therapy (OR: 0.11, 95% CI: 0.01, 0.71) and inotrope administration (OR: 0.30, 95% CI: 0.09, 0.91) were associated with poor microbiological response, whereas source control (OR: 2.99, 95% CI: 1.01, 9.43) with better microbiological response. High PRISM score III (OR: 1.15, 95% CI: 1.04, 1.29) and CR (OR: 5.07, 95% CI: 1.47, 19.36) were both independently associated with worse outcome, whereas source control was the only independent factor preventing death (OR: 0.24, 95% CI: 0.06, 0.78). In patients with CR BSI, administration of at least two active antimicrobials was associated with better outcome (OR: 10.80, 95% CI: 1.33, 237.05).

Conclusion. Prior carbapenem use is associated with carbapenem-resistant BSI development in PICU, which in turn is an independent risk factor for mortality. Source control is associated with better microbiological response within 5 days, as well as with decreased mortality.

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

2303. Differential Effects on MRSA and MSSA Epidemiology in a Neonatal Intensive Care Unit (NICU) During a Year-Long Surveillance and Decolonization Effort

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Background. *Staphylococcus aureus* (SA) causes morbidity and mortality in the NICU. While surveillance, with decolonization, is recommended for MRSA outbreak control, the impact of such strategies on endemic MSSA infections is less known. We compare the impact of a year-long surveillance and decolonization effort on MRSA and MSSA colonization dynamics and invasive infection rates in the NICU.

Methods. All infants hospitalized in our academically affiliated, regional perinatal NICU (1032 annual admissions) between January and December 2017 were screened twice monthly for SA colonization by culturing the anterior nares and three skin sites. Eligible patients with positive SA cultures underwent decolonization with mupirocin and/or chlorhexidine bathing. The following parameters for MRSA and MSSA were compared using frequencies and Fisher's exact tests: 1) Colonization density (proportion of positive surveillance cultures; 2) rates of effective decolonization (proportion of successful decolonization efforts); 3) rates of invasive infections; and 4) mupirocin resistance.

Results. Overall, 25 twice monthly surveillance efforts were undertaken from which 1351/1375 (98%) screening cultures were obtained. Screening identified newly detected MSSA vs. MRSA in 145 vs. 20 infants, respectively. Colonization density decreased more for MRSA (Q1 vs. Q4 decrease of 67%) vs, MSSA (Q1 vs. Q4 decrease of 5%). Decolonization was more effective for MRSA (78%) vs. MSSA (71%). Compared with 2016, rates of invasive infections decreased more for MRSA (2.4 vs. 1.6 /10,000 patient-days, 33%) than MSSA (9.4 vs. 7.8 /10,000 patient-days, 17%). Prevalence of mupirocin resistance through study period was higher for MSSA (24% vs. 10%). No outbreaks were detected.

Conclusion. A year- long surveillance and decolonization effort was more successful in decreasing MRSA colonization density and invasive infections compared with MSSA. These results are likely due to continual importation of MSSA into the NICU from the community. Since MSSA caused more invasive infections than MRSA, strategies primarily aimed to decrease the burden of MRSA need to be modified to decrease the burden of MSSA in NICUs.

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

2304. Decreased Incidence of Methicillin-Susceptible *Staphylococcus aureus* (MSSA) Infections after Implementation of Routine Surveillance and Decolonization in a Level IV Neonatal Intensive Care Unit (NICU)

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Background. *Staphylococcus aureus* (SA) is a leading cause of hospital-acquired infection, including bloodstream infection (BSI), in NICUs. In this study, we evaluated the effect of screening and decolonization of MSSA-colonized babies with mupirocin on the rate of MSSA infection.

Patients and Methods. *Study design:* Sequential time series. Pre-intervention period, January 2015–March 2017; wash out period, April 2017; intervention period, May 2017–March 2018. *Population:* Neonates admitted to a Level IV NICU with anticipated stay of greater than 2 days. *Intervention:* A single swab of the nares, umbilicus & groin was sent weekly for SA surveillance culture. MSSA-colonized neonates were decolonized with mupirocin application to nares, umbilicus and abraded skin twice daily for 5 days. *Outcome measures:* Comparison of rates of MSSA infections during pre- and post-intervention periods. Infections included BSI and skin/wound infections, excluding patients with MSSA from only eye or respiratory specimens. *Comparators:* Change in rates of Gram-negative and MRSA BSI. Change in rates of MSSA BSI in an affiliated NICU with the same medical staff but no intervention.