SSI reporting. Methods: A retrospective multisite cohort study of IPC and NSQIP superficial, deep, and organ-space THR/TKR SSI data collected 30 days postoperatively from September 1, 2015, to March 31, 2018 was undertaken. To identify patients with procedures captured by both IPC and NSQIP, data were cleaned, duplicates removed, and patients matched 1:1 using year of birth, procedure facility, type, side, date, and time. Positive and negative agreement were assessed, and the Cohen κ values were calculated. The definitions and data capture methods used by both IPC and NSQIP were also compared. Results: There were 7,549 IPC and 2,037 NSQIP patients, respectively, with 1,798 matched patients: IPC (23.8%) and NSQIP (88.3%). Moreover, 17 SSIs were identified by both IPC and NSQIP, including 9 superficial and 8 complex by IPC and 6 superficial and 11 complex by NSQIP. Also, 7 SSIs were identified only by IPC, of which 5 were superficial, and 36 SSIs were identified only by NSQIP, of which 28 were superficial (positive agreement, 0.44; negative agreement, 0.99; $\kappa = .43$). Excluding superficial SSIs, 7 SSIs were identified by both IPC and NSQIP; 3 were identified only by IPC; and 12 were identified only by NSQIP (positive agreement, 0.48; negative agreement, 1.00; $\kappa = 0.48$). Conclusions: THR/TKR SSI rates reported by IPC and NSQIP were not comparable in this matched dataset. NSQIP identifies more superficial SSIs. Variations in data capture methods and definitions accounted for most of the discordance. Both surveillance systems are critically involved with improving patient outcomes following surgery. However, stakeholders need to be aware of these variations, and education should be provided to facilitate an understanding of the differences and their interpretation. Future work should explore other surgical procedures and larger data sets.

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Presentation Type:

Poster Presentation

Comparison of Metrics Used to Track CLABSIs and CAUTIS Across a Regional Network

Sonali Advani, Duke University Medical Center; Becky Smith, Duke University Medical Center; Jessica Seidelman, Duke University; Nicholas Turner, Duke Center for Antimicrobial Stewardship and Infection Prevention; Christopher Hostler, Duke University Health System; Deverick John Anderson, Duke University Medical Center; Sarah Lewis, Duke University

Background: The standardized infection ratio (SIR) is the nationally adopted metric used to track and compare catheter-associated urinary tract infections (CAUTIs) and central-line- associated bloodstream infections (CLABSIs). Despite its widespread use, the SIR may not be suitable for all settings and may not capture all catheter harm. Our objective was to look at the correlation between SIR and device use for CAUTIs and CLABSIs across community hospitals in a regional network. Methods: We compared SIR and SUR (standardized utilization ratio) for CAUTIs and CLABSIs across 43 hospitals in the Duke Infection Control Outreach Network (DICON) using a scatter plot and calculated an R^2 value. Hospitals were stratified into large (>70,000 patient days), medium (30,000-70,000 patient days), and small hospitals (<30,000 patient days) based on DICON's benchmarking for community hospitals. Results: We reviewed 24 small, 11 medium, and 8 large hospitals within DICON. Scatter plots for comparison of SIRs and SURs for CLABSIs and CAUTIs across our network hospitals are shown in Figs. 1 and 2. We detected a weak positive overall correlation between SIR and SUR for CLABSIs (0.33; $R^2 = 0.11$), but no correlation between SIR and SUR for CAUTIs (-0.07; $R^2 = 0.00$). Of 15 hospitals with SUR >1, 7 reported SIR <1 for CLABSIs, whereas 10 of 13 hospitals with SUR >1 reported SIR <1 for CAUTIs. Smaller



Fig. 1. **\$178** 41 Suppl 1: 2020



Fig. 2.

hospitals showed a better correlation for CLABSI SIR and SUR (0.37) compared to medium and large hospitals (0.19 and 0.22, respectively). Conversely, smaller hospitals showed no correlation between CAUTI SIR and SUR, whereas medium and larger hospitals showed a negative correlation (-0.31 and -0.39, respectively). **Conclusions:** Our data reveal a weak positive correlation between SIR and SUR for CLABSIs, suggesting that central line use impacts CLABSI SIR to some extent. However, we detected no correlation between SIR and SUR for CAUTIS in smaller hospitals and a negative correlation for medium and large hospitals. Some hospitals with low CAUTI SIRs might actually have higher device use, and vice versa. Therefore, the SIR alone does not adequately reflect preventable harm related to urinary catheters. Public reporting of SIR may incentivize hospitals to focus more on urine culture steward-ship rather than reducing device utilization.

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Comparison of Respiratory Microbiome Disruption Indices to Predict VAP and VAE risk at LTACH Admission

Erik Clarke, University of Pennsylvania; Kathleen None Chiotos, Childrens Hospital of Philadelphia; James Harrigan, University of Pennsylvania; Ebbing Lautenbach, Perelman School of Medicine, University of Pennsylvania; Emily Reesey, University of Pennsylvania; Magda Wernovsky, University of Pennsylvania; Pam Tolomeo , University of Pennsylvania Perelman School of Medicine; Zygmunt Morawski, University of Pennsylvania; Jerry Jacob, University of Pennsylvania; Michael Grippi, University of Pennsylvania; Brendan Kelly, University of Pennsylvania

Background: Healthcare exposure results in significant microbiome disruption, particularly in the setting of critical illness, which may contribute to risk for healthcare-associated infections (HAIs). Patients admitted to long-term acute-care hospitals (LTACHs) have extensive prior healthcare exposure and critical illness; significant microbiome disruption has been previously documented among LTACH patients. We compared the predictive value of 3 respiratory tract microbiome disruption indices-bacterial community diversity, dominance, and absolute abundance -as they relate to risk for ventilator-associated pneumonia (VAP) and adverse ventilator-associated events (VAE), which commonly complicate LTACH care. Methods: We enrolled 83 subjects on admission to an academic LTACH for ventilator weaning and performed longitudinal sampling of endotracheal aspirates, followed by 16S rRNA gene sequencing (Illumina HiSeq), bacterial community profiling (QIIME2) for diversity, and 16S rRNA quantitative PCR (qPCR) for total bacterial abundance. Statistical analyses were performed with R and Stan software. Mixed-effects models were fit to relate the admission MDIs to subsequent clinically diagnosed VAP and VAE. Results: Of the 83 patients, 19 had been diagnosed with pneumonia during the 14 days prior to LTACH admission (ie, "recent past VAP"); 23 additional patients were receiving antibiotics consistent with empiric VAP therapy within 48 hours of admission (ie, "empiric VAP therapy"); and 41 patients had no evidence of VAP at admission (ie, "no suspected VAP"). We detected no statistically significant differences in admission Shannon diversity, maximum amplicon sequence variant (ASV)-level proportional abundance, or 16S qPCR across the variables of interest. In isolation, all 3 admission microbiome disruption indices showed poor predictive performance, though Shannon diversity performed better than maximum ASV abundance. Predictive models that combined (1) bacterial diversity or abundance with (2) recent prior VAP diagnosis and (3) concurrent antibiotic exposure best predicted 14-day VAP (type S error < 0.05) and 30-day VAP (type S error < 0.003). In this cohort, VAE risk was paradoxically associated with higher admission Shannon diversity and lower admission maximum ASV abundance. Conclusions: In isolation, respiratory tract