organizational risk factors and nosocomial transmission of CDI and MRSA. **Methods:** This retrospective observational study included 100 eligible acute-care inpatient units from 12 hospitals in British Columbia, Canada, from April 1, 2020, to September 16, 2021. The outcome variables included whether a unit was on the CDI or MRSA vulnerable unit list (ie, defined as having ≥5 CDI cases or ≥6 MRSA cases being attributed to the unit in the last 6 fiscal periods), the average CDI/MRSA rate, as well as the average CDI/MRSA standardized infection ratio (SIR). Independent variables included, but were not limited to, infection control factors (eg hand hygiene rate), infrastructural factors (eg, unit age, total beds on unit), and organizational factors (eg, hallway bed utilization, nursing overtime). Multivariable regression was performed to identify statistically significant risk factors using SAS, R Studio, and Stata software. **Results:** For CDI, older units were associated with higher odds of being on the CDI vulnerable unit list (aOR, 1.086; 95% CI, 1.024–1.175), higher CDI rate (adjusted relative risk [aRR], 0.012; 95% CI, 0.004–0.020), and higher CDI SIR (aRR, 0.011; 95% CI, 0.003–0.020). Larger unit size was associated with higher odds of being on the CDI vulnerable unit list (aOR, 1.210; 95% CI, 1.095–1.400) and higher CDI SIR (aRR, 0.013; 95% CI, 0.001–0.026). For MRSA, an increase in hand hygiene rate was associated with lower odds of being on the MRSA vulnerable unit list (aOR, 0.71; 95% CI, 0.53–0.897), lower MRSA rate (aRR, −0.035; 95% CI, −0.063 to −0.008), and lower MRSA SIR (aRR, −0.039; 95% CI, −0.069 to −0.008). Higher MRSA bioburden was associated with higher odds of being on the MRSA vulnerable unit list (aOR, >999; 95% CI, >999 to >999), higher MRSA rate (aRR, 9.008; 95% CI, 5.586–12.429), and higher MRSA SIR (aRR, 4.964; 95% CI, 1.971–7.958). Additionally, higher MRSA rates were associated increased utilization of hallway beds (aRR, 0.680; 95% CI, 0.094–1.267), increased nursing overtime rate (aRR, 5.018; 95% CI, 1.210–8.826), and not having a clean supply room with the door consistently closed (aRR, −0.283; 95% CI, −0.536 to −0.03). **Conclusions:** Several infrastructural and organizational factors were associated with nosocomial transmissions of CDI and MRSA. Further research is needed to investigate the mechanisms by which these factors are associated.

Disclosures: None

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: Surveillance/Public Health

Susceptibility results discrepancy analysis between NHSN antimicrobial resistance (AR) Option and NEDSS Base System in Tennessee, July 2020–December 2021

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Background: The NHSN Antimicrobial Resistance (AR) Option is an important avenue for acute-care hospitals to electronically report facility-wide antibiogram data. The NEDSS Base System (NBS) is the statewide surveillance system for mandatory reporting of all carbapenem-resistant Enterobacteriaceae (CRE) cases. The state health department (SHD) validated CRE case data reported through the AR Option to assess completeness and accuracy. **Methods:** NHSN AR Option data from July 2020–December 2021 for 24 facilities were validated by comparing reported CRE and susceptibility results to CRE isolates reported via the NBS. Isolates were matched based on specimen date, sex, birth month and day, pathogen, and specimen source. NHSN susceptibility results were dichotomized as "not resistant" and "resistant" to match the NBS results. Susceptibility discordance (differing proportions of resistant isolates) of matched pairs were evaluated using the McNemar exact test in SAS version 9.4 software. **Results:** The SHD identified 270 CRE cases from the NHSN and 1,254 unique CRE isolates from the NBS. Of the NHSN events, 72 (26.67%) were matched to the NBS. Among matched isolates, discordance was significant for doripenem (0 resistant isolates in the NHSN vs 13 in the NBS; $P < .001$) and imipenem (5 resistant isolates in the NHSN vs 23 in the NBS; $P < .0001$). Discordance was not significant for ertapenem nor meropenem. Sensitivity analyses maximized the match rate at 30.74% (83 matches) when NBS isolates from unknown sources were included and matching factors were specimen date and date of birth ± 1 day, and pathogen. Among all 6,325 CRE isolates in NBS, 290 (4.58%) did not have a specimen source provided. Of all 47,348 NHSN events, 7,624 (16.10%) had impossible patient birthdays. **Conclusions:** Many NHSN isolates could not be matched to NBS due to either isolates being missing from NBS or to data differences across the systems. This mismatch highlights the need for data validation and standardization at the point of entry for both systems. Discordant susceptibility outcomes raise concerns about using the NHSN as a method for facility and regional antibiogram data.

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Uncovering gut microbiota-mediated indirect effects of antibiotic use on *Clostridioides difficile* transmission

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Background: *Clostridioides difficile* and multidrug-resistant organisms (MDROs) pose challenges due to treatment complexities and substantial morbidity and mortality. Susceptibility to colonization with these organisms and potential onward transmission if colonized (ie, infectivity) is influenced by the human microbiome and its dynamics. Disruptive effects of antibiotics on the microbiome imply potential indirect effects of antibiotics on *C. difficile* colonization. Mathematical models can help explore the relative impact of key pathways linking antibiotic use to *C. difficile* colonization, including the relationship between population-level antibiotic use and colonization prevalence. **Methods:** We built a compartmental model of long-term *C. difficile* colonization prevalence of nursing home residents (though malleable for any MDRO), allowing interactions

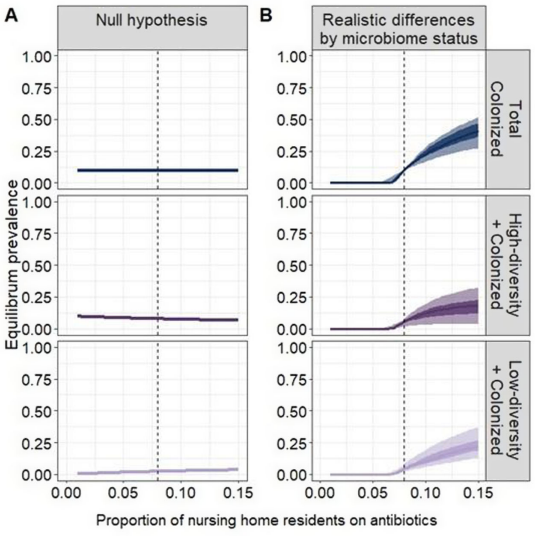

Figure 1. The relationship between population-level antibiotic use and long-term (equilibrium) prevalence of colonized individuals (total or separated by low or high microbiome diversity) differed if the model was parameterized to a "null hypothesis" (A) with no different processes by microbiome diversity group compared to a more realistic parameterization (B) where infectivity, susceptibility, and clearance of the pathogen could vary depending on the microbiome status. The population-level antibiotic use (x-axis) is the proportion of nursing home residents receiving antibiotics on a given day. In the realistic parameterization (B), the average rate at which an individual's microbiome recovers its high diversity (i.e., recovery from antibiotic disruption) could vary for uncolonized vs colonized individuals. For each parameter in the realistic parameterization, values were sampled from ranges derived from the literature and based on nursing home resident populations as much as possible. The transmission rate was fit such that each parameter combination had 10% of the total population colonized at equilibrium. The vertical dashed line at 0.08 on the x-axis marks the baseline amount of population-level antibiotic use. In (B), the lighter shaded regions show 95% confidence intervals, darker shaded regions show 50% confidence intervals, and colored lines show median values.