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:
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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

Carol Davis; Youssoufou Ouedraogo; Christopher Evans and Christopher Wilson

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

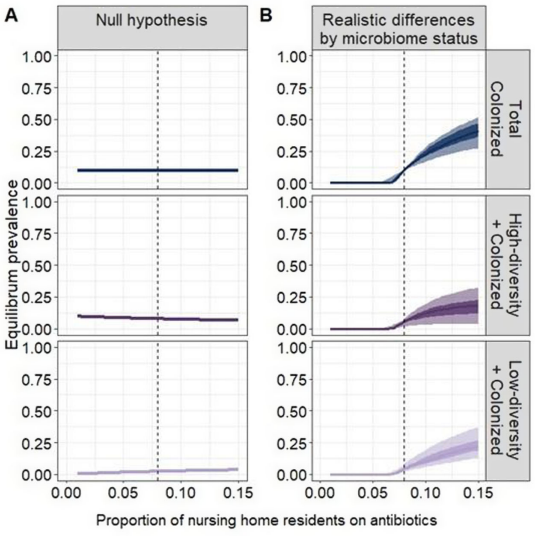

Figure 1. The relationship between population-level antibiotic use and long-term (equilibrium) prevalence of colonized individuals (total or separated by low or high microbiome diversity) differed if the model was parameterized to a "null hypothesis" (A) with no different processes by microbiome diversity 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.

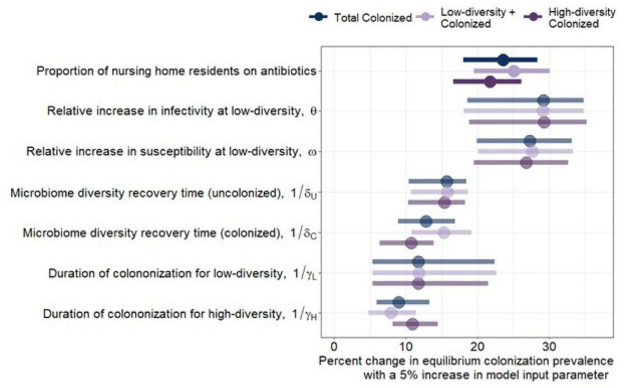

Figure 2. A standardized comparison showing percent change in the equilibrium proportion of colonized individuals out of the total nursing home resident population when model input parameters were individually increased by 5% (e.g., increase population-level antibiotic use by 5%). Parameter values were sampled from uniform distributions (the same ranges and methodology from the "realistic" scenario Fig 1B). A 5% increase in the population-level antibiotic use (top results highlighted in a darker shade) led to median increases of 24%, 25%, and 22% for the proportions of total colonized, low-diversity colonized, and high-diversity colonized individuals at equilibrium, respectively. Here, antibiotic use is modeled exclusively as antibiotics targeting pathogens other than Clostridioides difficile. Thus, changes in colonization proportion in relation to antibiotic use occur only through indirect effects modulated by the host microbiome. Points mark the median change in equilibrium value, and line ranges denote the 1st to 3rd interquartile ranges. Colors and ordering distinguish between different groupings of C. difficile colonization, with total (regardless of microbiome status), low-diversity microbiome only, and high-diversity microbiome only colonized individuals indicating the numerator for the equilibrium proportion calculation and appearing from top to bottom within a group respectively.

between the microbiome and the colonization process. Based on proportional abundance of microbial taxa, we classified individuals into high and low α diversity groups, each further stratified into uncolonized or colonized with *C. difficile*. The rate of transition from the high to low microbiome diversity group was proportional to the population-level rate of antibiotic use. Transmission dynamics followed a susceptible–infectious–susceptible framework with the possibility for increased susceptibility and infectivity for the low-diversity microbiome group. First, as a comparator, we used a "null model" in which microbiome diversity did not influence host susceptibility or infectivity. Next, we sampled from realistic (literature informed) parameter ranges to analyze how the microbiome mediates the effect of antibiotics on colonization in this population. **Results:** Our analysis suggests that antibiotic use can catalyze colonization with *C. difficile* through interactions with the host microbiome, resulting in a sharp increase in colonization with a modest increase in antibiotic use (Fig 1). Increasing the population-level antibiotic use by 5% led to a median 24% increase in long-term colonization prevalence in the model (Fig 2). In contrast, increasing susceptibility or infectivity rates by 5% resulted in slightly higher increases in total colonization (27% and 29%, respectively). However, there was considerable uncertainty around these estimates, with interquartile ranges of up to 20% for some parameters (Fig 2). **Conclusions:** Higher population-level antibiotic use likely increases colonization by *C. difficile* through indirect effects of the microbiome. The increased colonization burden attributable to increasing antibiotic use may be substantial. With high uncertainty around some estimates, conducting observational studies to better understand key colonization and microbiome parameters (eg, the relative increase in susceptibility or infectivity with lower microbiome diversity) is critical for future efforts to estimate the impact of antibiotic use on colonization with *C. difficile* and MDROs.

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Tecovirimat use among patients with monkeypox (mpox) in Alameda County, California, June–October 2022

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Background: Tecovirimat (TPOXX) is an antiviral drug only available via an Expanded Access Program (EAP) investigational new drug protocol and is recommended for treatment of select patients with monkeypox (mpox) infection. Alameda County Public Health Department prioritizes health equity but does not have a dedicated public health clinic. Therefore, we partnered closely with local healthcare providers that serve communities disproportionally impacted by mpox to ensure there was access to TPOXX. Using data collected during the outbreak we assessed whether populations in Alameda County most affected by mpox received treatment. **Methods:** We describe Alameda County patients with confirmed or probable mpox who received TPOXX during June–October 2022. Data were collected from case investigation interviews with patients and state-wide reportable disease database(s), which included demographic, clinical, and behavioral information. Confidence intervals (CIs) were calculated using the exact method for Poisson counts. We compared characteristics of mpox patients who received and did not receive TPOXX using the Pearson χ^2 or Fisher exact test. $P < .05$ was considered significant. **Results:** Mpox case rates in Alameda County were highest among Black or African-American residents (35.6 per 100,000, 95% CI, 26.7–46.4) and Hispanic or Latinx residents (25.2, 95% CI, 20.2–31.0) compared to Asian residents (3.9, 95% CI, 2.3–6.1) and white residents (10.4, 95% CI, 7.7–13.9) residents. Among 242 mpox patients, 69 patients (28.5%) received TPOXX. The distribution of demographic and clinical characteristics among patients who received TPOXX was not significantly different than among those who did not, including residents aged 31–40 years (36.2% vs 34.7%), Black or African-American residents (20% vs 26.3%), Hispanic or Latinx residents (38.5% vs 41%), male residents (89.9% vs 95.3%), gay, lesbian, or same-gender loving residents (67.2% vs 67.4%) in the city of Oakland (63.2% vs 61.5%), or residents with human immunodeficiency virus infection (43.5% vs 36.6%). **Conclusions:** During the Alameda County mpox outbreak, nearly one-third of patients received TPOXX. Demographic and clinical characteristics were similar among TPOXX recipients and nonrecipients. A proactive approach to obtaining TPOXX in Alameda County and strong relationships with local providers may have allowed for treatment to be accessible to mpox patients. Regular review of outbreak data can inform public health activities, ensure health equity, and help refine local response efforts.

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Increasing rates of ventilator-associated events: Blame it on COVID-19?

Aditee Dash; Kaila Cooper; Barry Rittmann; Michael Stevens; Gonzalo Bearman; L. Silvia Munoz-Price and Michelle Doll

Background: Rates of ventilator-associated events (VAEs), including infection-related ventilator-associated complications (IVACs) and probable ventilator-associated pneumonia (PVAPs) have increased nationwide since the onset of the COVID-19 pandemic. In December 2021, our health system adopted a new electronic medical record (EMR), which changed the way surveillance for VAEs is performed. We reviewed surveillance criteria, COVID-19 status, and culturing practices in attempts to understand why VAE rates continue to be elevated. **Methods:** We collected data on VAE type, culture data, COVID-19 status, and surveillance criteria for all patients meeting NHSN definitions for VAE from 2018 through November 2022. For all patients in 2022 (post-EMR transition), 2 physicians (A.D. and M.D.) manually reviewed documented ventilator settings from flow sheets to validate the automated EMR data, and they evaluated culture data for appropriateness. Cultures were defined as appropriate unless they were included in "pancultures" for leukocytosis without concern for pneumonia documented. Rates were compared using an interrupted time series (ITS) analysis before and after the onset of the COVID-19 pandemic and the EMR transition. Patient level data were