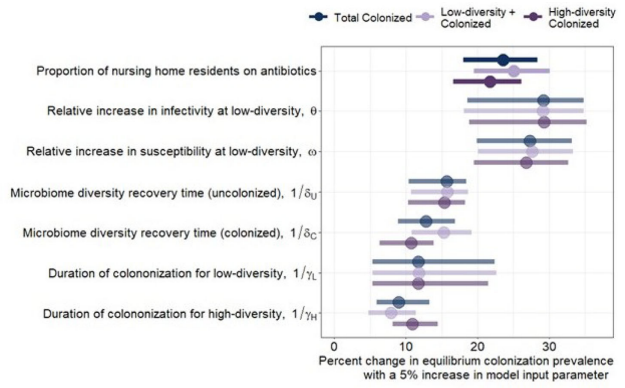

Figure 2. A standardized comparison showing percent change in the equilibrium proportion of colonized individuals out of the total nursing home resident population when model input parameters were individually increased by 5% (e.g., increase population-level antibiotic use by 5%). Parameter values were 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.

Disclosures: None

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

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.

Disclosures: None

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Presentation Type:
Poster Presentation - Poster Presentation
Subject Category: VAE

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

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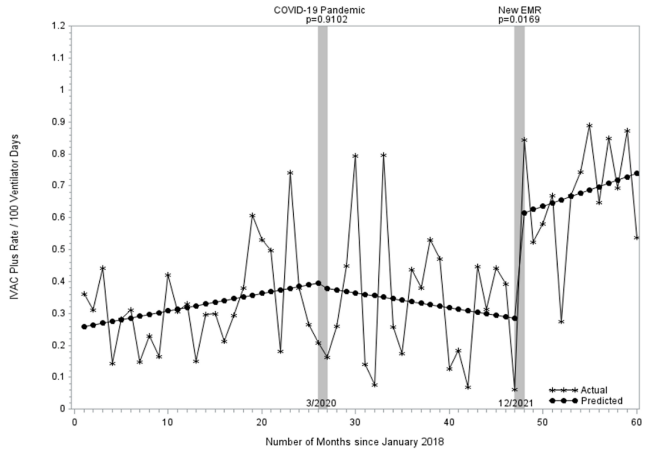
Background: Rates of ventilator-associated events (VAEs), including infection-related ventilator-associated complications (IVACs) and probable ventilator-associated pneumonia (PVAPs) have increased nationwide since the onset of the COVID-19 pandemic. In December 2021, our health system adopted a new 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

Figure 1: Interrupted Time Series Analysis of Infection-Related Ventilator Associated Events and Probable Ventilator Associated Pneumonias (IVAC Plus) Rates from January 2018 – November 2022



compared across periods using the χ^2 test. All analyses were performed using SAS version 9.4 software. **Results:** COVID-19 has been implicated in the increasing number of VAEs since the pandemic began: 6% of patients in 2020, 18% in 2021, and 23% in 2022 ($P < .001$). The percentage of patients meeting criteria for VAE by positive end-expiratory pressure (PEEP) decreased from 2018 to 2022 (92%, 95%, 93%, 85%, 85%, respectively; $P = .0004$). Patients meeting criteria for VAE by fraction of inspired oxygen (FiO_2) increased from 2018 to 2022 (9%, 6%, 11%, 17%, 19%, respectively; $P = .0002$). Manual review of 2022 data indicated opportunities for test stewardship in 8 of 65 patients with cultures (12%). ITS analysis revealed that IVAC+ rates were climbing prior to the onset of the COVID-19 pandemic (Fig. 1). We observed a marked increase in rates with the implementation of our new EMR and the changes to our surveillance process (0.32 cases per 100 ventilator days). Manual review of records from 2022 revealed 5 patients in which documentation of ventilator settings to meet VAE diagnosis could not be retrieved from flow sheets. **Conclusions:** COVID-19 continues to affect VAE despite vaccine availability and may partially account for elevated rates nationwide. However, changes in EMR-automated VAE surveillance may also affect rates. Our findings suggest that automated surveillance captures transient or spurious changes in ventilator machine settings that do not accurately represent clinical status. These data may contribute to spurious increases in VAE. More studies are needed to better understand the impact of both COVID-19 and automated surveillance on VAE.

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Presentation Type:
Poster Presentation - Oral Presentation

Subject Category: Antibiotic Stewardship

Validation of an electronic algorithm to identify appropriate antibiotic use for community-acquired pneumonia in children

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Background: Community-acquired pneumonia (CAP) is a common indication for antibiotic use in hospitalized children and is a key target for pediatric antimicrobial stewardship programs (ASPs). Building upon prior work, we developed and refined an electronic algorithm to identify children hospitalized with CAP and to evaluate the appropriateness of initial antibiotic choice and duration. **Methods:** We performed a cross-sectional study including children 6 months to 17 years hospitalized for CAP between January 1, 2019, and October 31, 2022, at a tertiary-care children's hospital. CAP was defined electronically as an *International Classification of Disease, Tenth Revision* (ICD-10) code for pneumonia, a chest radiograph or chest computed tomography scan (CT) performed within 48 hours of admission, and systemic antibiotics administered within the first 48 hours of hospitalization and continued for at least 2 days. We applied the following exclusion criteria: patients transferred from another healthcare setting, those who died within 48 hours of hospitalization, children with complex chronic conditions, and those with intensive care unit stays >48 hours. Criteria for appropriate antibiotic choice and duration were defined based on established guidelines. Two physicians performed independent medical record reviews of 80 randomly selected patients (10% sample) to evaluate the performance of the electronic algorithm in (1) identifying patients treated for clinician-diagnosed CAP and (2) classifying antibiotic choice and duration as appropriate. A third physician resolved discrepancies. The electronic algorithm was compared to this medical record review, which served as the reference standard. **Results:** Of 80 children identified by the electronic algorithm, 79 (99%) were diagnosed with CAP based on medical record review. Antibiotic use was classified as the appropriate choice in 75 (94%) of 80 cases, and appropriate duration in 16 (20%) of 80 cases. The sensitivity of the electronic algorithm for identifying appropriate initial antibiotic choice was 94%; specificity could not be calculated because no events of inappropriate antibiotic choice were identified based on chart review. The sensitivity and specificity for determining appropriate duration were 88% and 97%, respectively (Table 1).

Table 1. Performance Characteristics of an Electronic Algorithm Evaluating Appropriate Antibiotic Choice and Duration

Appropriate Choice	
Sensitivity	94% (75/80)
Specificity	NA (0/0)
Positive Predictive Value	100% (75/75)
Negative Predictive Value	0% (0/5)
Appropriate Duration	
Sensitivity	88% (14/16)
Specificity	97% (62/64)
Positive Predictive Value	88% (14/16)
Negative Predictive Value	97% (62/64)

Conclusions: The electronic algorithm accurately identified children hospitalized with CAP and demonstrated acceptable performance for identifying appropriate antibiotic choice and duration. Use of this electronic algorithm may improve the efficiency of stewardship activities and could facilitate alignment with updated accreditation standards. Future studies validating this algorithm at other centers are needed.

Disclosures: None

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Presentation Type:
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Subject Category: Antibiotic Stewardship

Trends and duration of antibacterial drug supply chain issues in the United States, January 2017–June 2022

Katie Suda; Katherine Callaway Kim; Inma Hernandez and Mina Tadrous

Background: Drug manufacturing and distribution is a complex, global process. The global drug supply chain is prone to disruptions associated with geopolitical issues, trade, civil unrest, severe weather, and pandemics, all of which have the potential to affect medication supply and result in drug shortages. To our knowledge, the extent to which the supply of antimicrobials is threated due to disruptions in the drug supply chain in the United States is unknown. We examined trends and duration of disruptions to the drug supply chain for antimicrobials. **Methods:** Manufacturer reports of supply disruptions were extracted from the Food and Drug Administration (FDA) and the American Society for Health-Systems Pharmacists (ASHP) websites and merged on the agent-