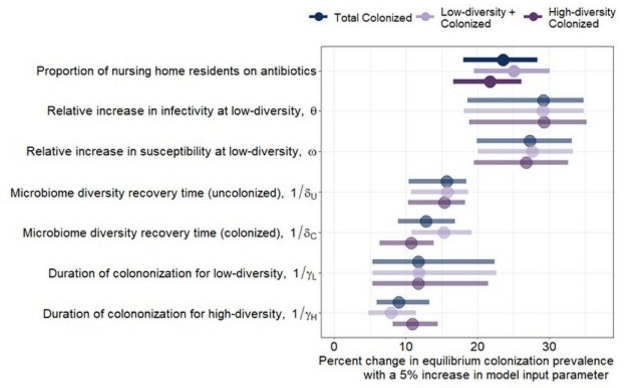

Figure 2. A standardized comparison showing percent change in the equilibrium proportion of colonized individuals out of the total nursing home resident population when model input parameters were individually increased by 5% (e.g., increase population-level antibiotic use by 5%). Parameter values were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