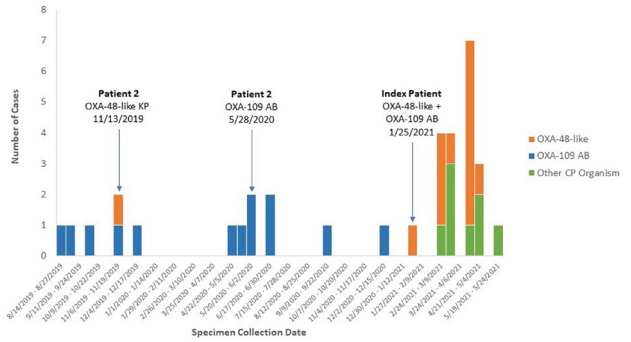
Figure 2. Epidemic Curve of OXA-109 AB, OXA-48-like AB, and Other CP Organism Cases, 2019-2021




***Conclusion.*** The first reported case of OXA-48-like AB in the US was identified through public health sentinel laboratory surveillance, allowing prompt response to contain spread of a novel multidrug-resistant organism (MDRO). WGS detected a rare OXA-48-like gene in AB and KP and provides evidence for possible interspecies transfer of this gene from KP to AB through plasmid transfer followed by chromosomal integration.

***Disclosures.*** **All Authors**: No reported disclosures

**180. Alterations to the Gut Microbiomes and Acquisition of Bacteria Resistance Elements among US International Travelers**

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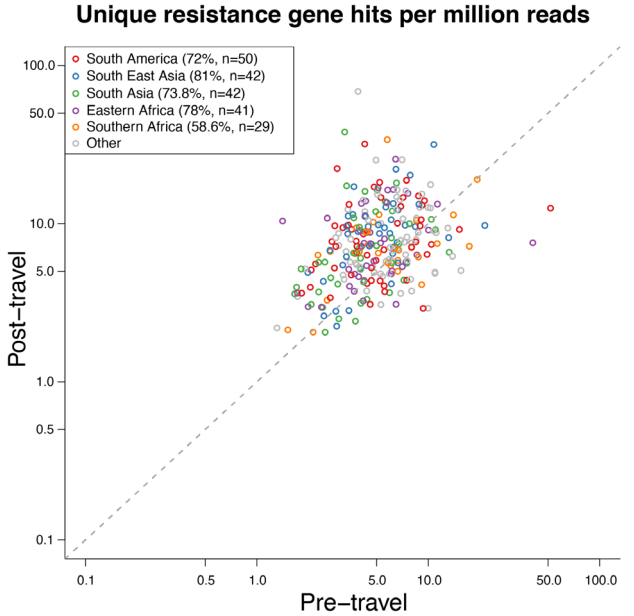
**Session:** O-35. Trends in Gram-negative Resistance

***Background.*** This study investigated the impact of international travel on the acquisition and carriage of antimicrobial resistance (AMR). We prospectively assessed U.S. international travelers for the acquisition of resistant *Enterobacterales* species and evaluated changes in travelers' gut microbiomes.

***Methods.*** Metagenomic sequencing was performed on DNA extracted from pre- and post-travel stool samples of 273 U.S. international travelers. We used Kraken2 to assess microbial gut composition and analyzed antibiotic resistance gene (ARG) content using the Resistance Gene Identifier (RGI) and ResFinder, and read mapping to ARG databases. We assessed the change in gut profile and resistome associated with (i) all international travel; (ii) travel to specific geographic regions; and (iii) traveler's diarrhea.

***Results.*** International travel resulted in a perturbation of the gut microbiome, which was greater in travelers receiving treatment for diarrhea during travel ($p$ = 4E-5). There was an overall loss in microbial diversity following travel, regardless of health outcome ($p$ = 0.011); this was most consistently observed in travelers to South East Asia (SEA) (loss of gut diversity in 81% of SEA travelers). 78% of all travelers had a higher relative abundance of *E. coli* after travel, including 85% of travelers who acquired AMR bacteria during travel. Travel to South Asia was also associated with a significantly greater increase of *E. coli* relative to other destinations ($p$ = 0.04). Additionally, the relative abundance of *Pasteurellales* was higher in the pre-travel samples of those who subsequently acquired AMR bacteria (FDR = 0.08). Furthermore, there was a significant increase in ARG content among the post-travel samples, with regional differences in the magnitude of acquisition (**Figure 1**). 72% of all travelers had a greater resistance burden post-travel. SEA was associated with the greatest increase in resistome diversity, while South America was associated with the greatest increase in overall ARG content.

Resistance genes present in the gut microbiome.




Genes mapping to the Comprehensive Antibiotic Resistance Database were measured pre- (x-axis) and post-travel (y-axis) to assess the acquisition of resistance genes in association with travel, distinguished by geographic region. Colors indicate geographic regions visited by travelers: South America (red), South East Asia (blue), South Asia (green), Eastern Africa (purple), Southern Africa (orange), Other (grey).

***Conclusion.*** International travel is associated with a perturbation in the gut microbial community, with the acquisition of AMR bacteria and genes, and an increase in the relative abundance of *E. coli*. These perturbations following travel may be important factors in the global spread of AMR.

***Disclosures.*** **All Authors**: No reported disclosures

**181. Potential Benefit of Masking and other COVID-19 Infection Prevention Measures on Late-Onset Infections in the NICU**

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MASKING STUDY GROUP

**Session:** O-36. Trends in Pediatric Bacterial Disease

***Background.*** Incidence of blood stream infections (BSI) among NICU admissions remains high, with associated mortality and morbidity. Due to COVID-19, there are increased infection prevention (IP) measures in NICUs including universal masking for all healthcare workers and families, social distancing, visitation restrictions, and increased attention to hand hygiene. These measures may also affect late-onset infection rates and offer understanding of novel interventions for prevention.

***Methods.*** We examined infection rates during the 24 months prior to implementation of COVID-19 IP measures (PRE-period) compared to the months after implementation from April 2020 (POST-period). Late-onset infections were defined as culture-confirmed infection of the blood, urine, or identification of respiratory viral pathogens. An interrupted time series analysis of infection per 1000 patient days was performed based on a change-point Poisson regression with a lagged dependent variable and the number of patient days used as offsets. Each month was treated as independent with additional analysis using an observation-driven model to account for serial dependence.

***Results.*** Multicenter analysis to date included all infants cared for at three centers (Level 3 and 4) from 2018-2020. Monthly BSI rates decreased in the POST-period at the three centers (**Figure 1).** At all centers actual BSI rate was lower than the expected rate in the POST-period (**Figure 2).** The combined BSI rate per 1000 patient days was 41% lower compared to the rate prior to implementation (95% CI, 0.42 to 0.84, P=0.004) (**Table 1**). In subgroup analysis by birthweight, infants< 1000g had a 39% reduction in BSI (P=0.023), for1000-1500g patients there was a 44% reduction (P=0.292) and in those > 1500g there was a 53% reduction (0.083).

Figure 1. PRE and POST MASKING and other COVID Infection Prevention Measures and Monthly BSI Rates.