

Fig. 2.

inappropriate prophylaxis; however, this was not statistically significant (1.10 vs 2.02; OR, 0.54; $P = .35$). The most common BSI pathogen was *E. coli* (2 (67%) before implementation and 10 (77%) after implementation). Also, 5 *E. coli* BSIs (50%) were fluoroquinolone resistant in the postimplementation group compared to 1 (33%) in the preimplementation group. Of 13 postimplementation BSIs, 6 occurred in patients who received aminoglycosides perioperatively; however, all 6 BSI pathogens were aminoglycoside sensitive. **Conclusions:** Compliance with our FQRE screening program and antimicrobial prophylaxis protocol was moderate. Although pre- and postimplementation differences in BSI rates were not statistically significant, the high failure rate among patients receiving aminoglycosides was concerning and led to a change in TRPB prophylaxis guidelines. Reasons for increased BSI risk among FQRE+ patients may include prophylaxis agent, dose, timing, or other confounding factors associated with drug-resistant pathogens. Facilities implementing FQRE screening protocols should evaluate the efficacy of their program and periodically review screening compliance, prophylaxis dosing and timing adherence, and impact on patient-level outcomes.

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Presentation Type:

Poster Presentation

Establishment of a Sink Gallery to Investigate Growth of Carbapenemase-Producing *Klebsiella pneumoniae* and Biofilms in P-Traps

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Background: Hand-hygiene sink drains in healthcare facilities may provide an environment for the survival and dissemination of various multidrug-resistant organisms (MDROs), including carbapenemase-producing *Klebsiella pneumoniae* (CPKP). We developed a sink model system to establish and test native drinking water biofilms containing CPKP in the p-traps of hand-hygiene sink drains. **Methods:** A handwashing sink gallery was designed to consist of 6-wall mounted stainless-steel sink basins connected to the same municipal water line. Each sink's plumbing included a chrome-plated brass p-trap. Healthcare facility conditions were simulated to include handwashing events with the addition of hand-soap and municipal water 4× per day, and nutritional shake (simulating liquid waste) 1× per day. Resultant biofilms in the p-traps of each sink were harvested after 28 days for community analysis. Microbial community analyses were performed on selected biofilm samples using 16S rRNA sequencing of the V4 hypervariable region of genomic DNA. Another experiment evaluated 28-day p-trap biofilm inoculated with CPKP CAV1016 (10 mL 7.0×10⁷ CFU/mL) and was assessed over 14 days. Heterotrophic plate counts (HPCs) were determined on R2A medium (7 days of incubation at 25°C). CPKP was quantified on mEndo selective medium (48 hours of incubation at 36°C). **Results:** Biofilms developed in all p-traps, but biofilm HPC (5.78 mean log CFU/cm², range 4.35–7.16) and community diversity (15–20 genera per p-trap) varied with sink position. Community analysis showed similarities in bacterial community composition and diversity between sinks 1 and 2, and between sinks 3, 5 and 6, but with differences between the 2 groups. The most abundant family in sinks 3, 5, and 6 was *Erythrobacteriaceae* (76%, 78%, and 55% of the total reads, respectively), whereas sinks 1 and 2 were dominated by *Sphingomonadaceae* (63% and 36%) and

Methylobacteriaceae (19% and 55%). Also, 16S sequencing revealed the presence of potential opportunistic pathogens in the biofilms, including reads attributed to *Pseudomonas* and *Acinetobacter*. CPKP CAV1016 inoculated into 28-day p-trap biofilms colonized and persisted in all 6 sinks for 12 days after inoculation. **Conclusions:** Despite all 6 sinks sharing an incoming water line, soap, and carbon and energy source, there was a significant variation in the bacterial community composition observed between the sinks. CPKP can colonize and persist in the p-trap biofilms; however, additional work is needed to achieve a reproducible model system. Once this is achieved, the sink gallery will be used to investigate interventions to mitigate colonization or persistence of CPKP in p-trap biofilms.

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Estimating the Impact of County Boundaries on State-wide Patient-Sharing Network Models

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Background: In the field of public health, network models are useful for understanding the spread of both information and infectious diseases. Collecting network data requires determining network boundaries (ie, the entities selected for data collection). These decisions, if not made carefully, have potential outsized downstream effects on study findings. In practice, collaboration and coordination between healthcare organizations are often dictated by historical or geopolitical boundaries (eg, state or county boundaries), which may distort the underlying network under study, and thereby affect the reliability and/or accuracy of the network model. **Objective:** We compared natural communities in a patient-sharing network with those induced by geopolitical boundaries. **Methods:** Using data from the Healthcare Cost and Utilization Project (HCUP), we constructed a patient-sharing network among hospitals in California, splitting the data into a training set and a holdout set. We performed edge-

betweenness clustering on the training set, and with the holdout set, we compared the resulting partition with the partition by counties using modularity. We also clustered contiguous counties that might function more cohesively together than individually. We performed spatially



Fig. 1.

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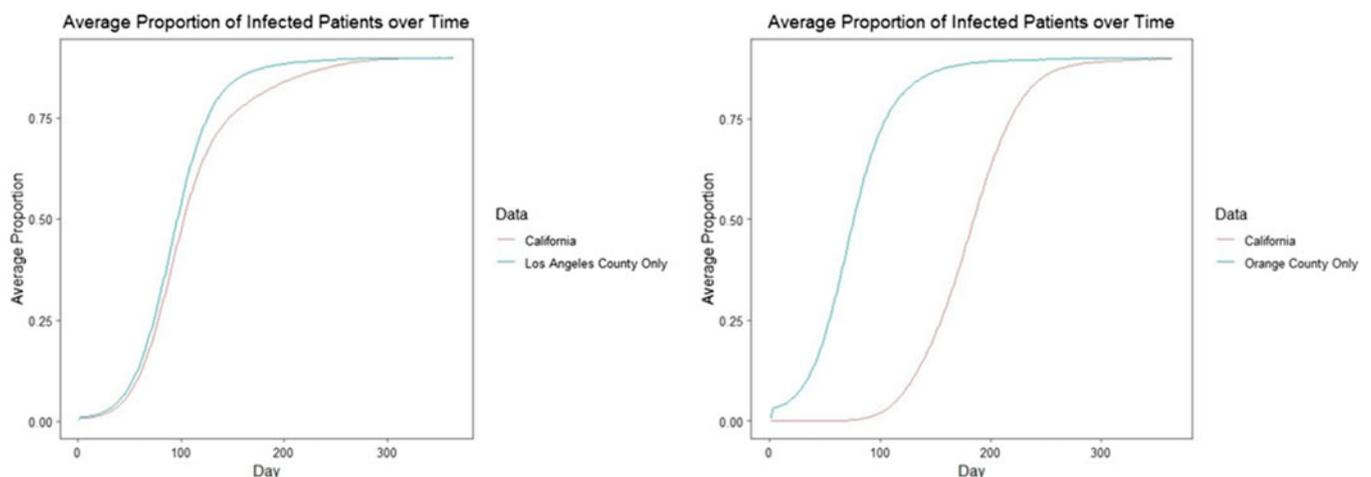


Fig. 2.