

Methods: A retrospective descriptive study was conducted in collaboration with the Michigan Department of Health and Human Services (MDHHS). CRE isolates submitted to MDHHS between April 2014 and July 2019 were tested for the presence of NDM using CDC PCR protocols. Additional information on case demographics, laboratory results, healthcare and antibiotic exposure history, and travel history were collected. **Results:** In total, 30 NDM cases were identified in Michigan during the study period. Of these 30 cases, 15 (50%) were men, and the median age was 73.5 years (range, 20–88 ±20). Also, 2 of these patients (6.6%) were immunocompromised; 2 patients (6.6%) had had extensive abdominal surgery, and 2 patients (6.6%) had recurrent hospitalization. Furthermore, 12 case isolates (40%) were collected in outpatient settings, whereas 16 (53%) were collected from inpatient settings. In addition, 13 (43%) patients were admitted from home and 4 (13%) presented from an extended-care facility. Urine was the most common site of isolation in 19 of 30 (63%) cases, followed by blood and tissue culture in 4 of 30 (13%) each. *Escherichia coli* was the most common organism (17 of 30, 57%), followed by *Klebsiella pneumoniae* (9 of 30, 30%). Also, 15 of 30 cases (50%) had a recent history of international travel, and of these, 9 of 15 (60%) reported travel to India. Among these 15 cases, 12 (80%) sought medical care in the countries they visited. Two cases (6.6%) had a documented history of multidrug-resistant organism colonization or infection. The mortality rate was 6.6% (2 of 30). The mean time from admission to implementation of contact precautions was 7.3 days (range, 0–20). **Conclusions:** Suspicion of NDM CRE strains should remain high in patients with a travel history from areas known as major reservoirs of NDM. Delay in implementing contact precautions, as noted in the present study, can lead to a greater risk of transmission. Early detection and subsequent isolation of NDM patients are essential strategies for preventing transmission within healthcare facilities. Future efforts include performing whole-genome sequencing of these isolates to assist in identifying potential epidemiological links among the affected patients.

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Presentation Type:

Poster Presentation

Epidemiology of Posttransrectal Prostate Biopsy Bloodstream Infections and Impact of a Screening Program

Dorothy Ling, Duke University Medical Center; Sarah Lewis, Duke University; Christina Sarubbi, Duke University Health System; Rebekah Moehring, Duke University Medical Center; Sonali Advani, Duke University Medical Center; Deverick John Anderson, Duke University Medical Center; Becky Smith, Duke University Medical Center

Background: Antibiotic prophylaxis choice for transrectal prostate biopsy (TRPB) has been affected by the emergence of fluoroquinolone-resistant *Escherichia coli* (FQRE). Prebiopsy FQRE screening and targeted antibiotic prophylaxis may reduce post-TRPB bloodstream infection (BSI). We assessed the impact of a FQRE screening program on post-TRPB BSIs at an academic medical center.

Methods: We implemented a FQRE screening program and targeted TRPB antimicrobial prophylaxis guidelines on May 1, 2017 (Fig. 1). We performed a retrospective cohort study of all TRPB and compared the incidence of post-TRPB BSI (within 7 calendar days) per 100 procedures before the intervention (January 1, 2016, to April 30, 2017) and to the incidence after the intervention (May 1, 2017, to August 31, 2019). We used a subanalysis to compare BSI incidence between patients with positive (+) and negative (–) FQRE screens and appropriate prophylaxis use, defined as administration of guideline-recommended antibiotics. The Fisher exact test of independence was used to analyze nominal data.

Results: The analysis included 2,157 TRPB procedures: 647 in the preintervention period and 1,510 in the postintervention period. FQRE screening compliance was 61% (n = 914) in the post-intervention group (Fig. 2); 168 FQRE screens (18%) were positive. The median time from FQRE screen to procedure was 40 days (IQR, 13–69). Postprocedure BSI rates were higher in than those in the preimplementation group; however, this difference was not statistically significant (0.86 vs 0.46; OR, 2.01; $P = .42$). Among FQRE-screened patients, BSI rates differed significantly between FQRE+ and FQRE– patients (2.98 vs 0.54; OR, 5.67; 95% CI, 1.21–28.94; $P = .01$). Screened patients receiving appropriate prophylaxis had lower BSI rates than those receiving

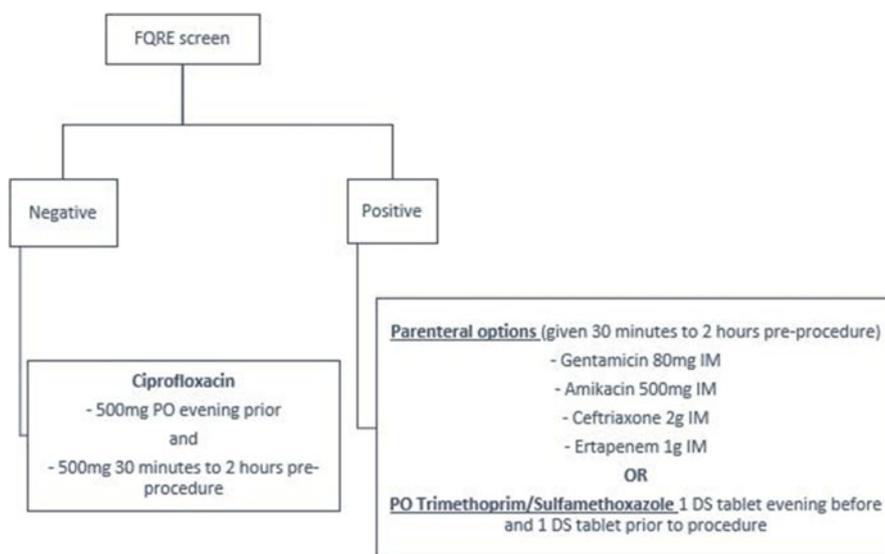


Fig. 1.

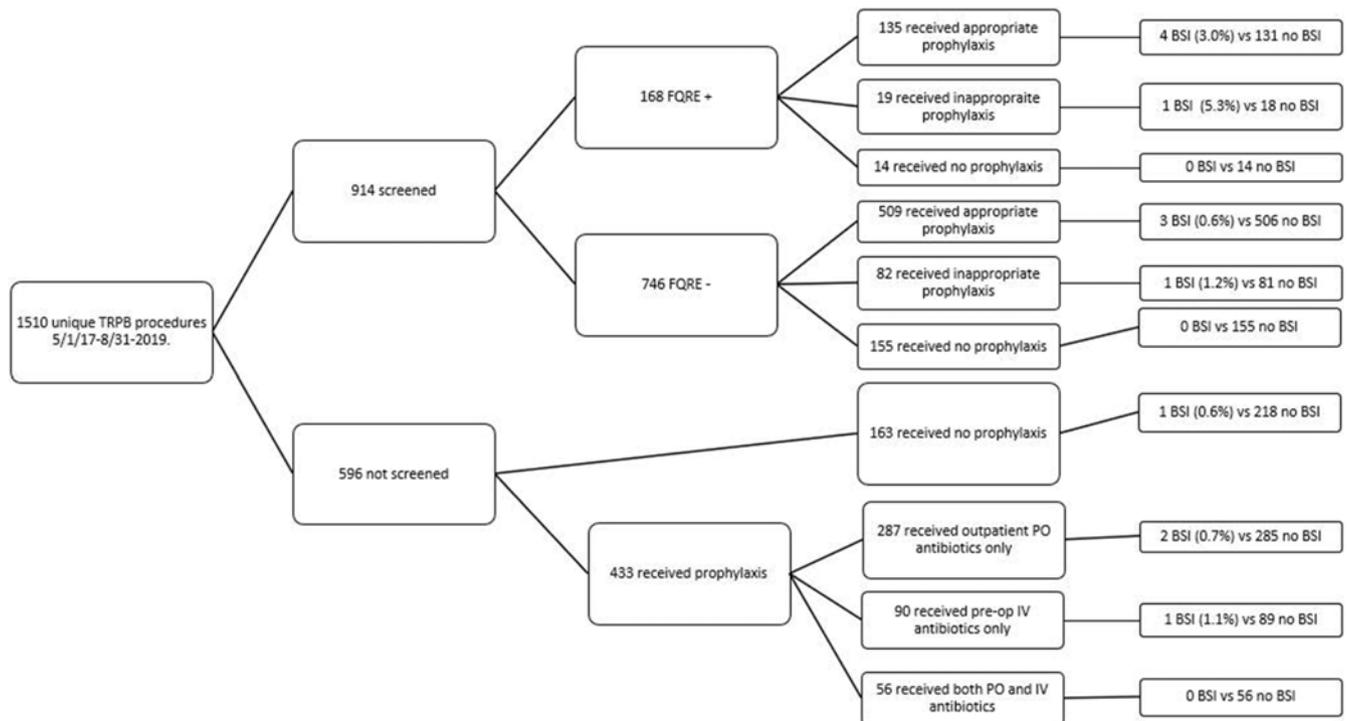


Fig. 2.

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

Christine Ganim, Centers for Disease Control and Prevention; Mustafa Mazher, HHS; Erin Breaker, Centers for Disease Control and Prevention; Rodney Donlan

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