Figure 1. Trends in CRBSI according to site of insertion (period 2008-2018)

Fig. 1.

Presentation Type:
Poster Presentation

Training to Improve Clinical Specimen Collection and Antimicrobial Resistance (AMR) Diagnostics and Surveillance in Ethiopia

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Background: Antimicrobial resistance (AMR) is an increasingly critical global public health challenge. An initial step in prevention is the understanding of resistance patterns with accurate surveillance. To improve accurate surveillance and good clinical care, we developed training materials to improve the appropriate collection of clinical culture samples in Ethiopia. **Methods:** Specimen-collection training materials were initially developed by a team of infectious diseases physicians, a clinical microbiologist, and a monitoring and evaluation specialist using a training of trainers (ToT) platform. Revisions after each training session were provided by Ethiopian attendees including the addition of regional and culturally relevant material. The training format involved didactic presentations, interactive practice sessions with participants providing feedback and training to each other and the entire group as well as assessments of all training activities. **Results:** Overall, 4 rounds of training were conducted from August 2017 to September 2019. The first 2 rounds of training were conducted by The Ohio State University (OSU) staff, and Ethiopian trainers conducted the last 2 rounds. Initial training was primarily in lecture format outlining use of microbiology laboratory findings in clinical practice and steps for collecting specimens correctly. Appropriate specimen collection was demonstrated and practiced. Essential feedback from this early audience provided input for the final development of the training manual and visual aids. The ToT for master trainers took place in July 2018 and was conducted by OSU staff. In sessions held in February and August 2019, these master trainers provided training to facility trainers, who provide training to personnel directly responsible for specimen collection. In total, 144 healthcare personnel (including physicians, nurses, and laboratory staff), from 12 representative Ethiopian public and academic hospitals participated in the trainings. Participants were satisfied with the quality of the training (typically ranked >4.5 of 5.0) and strongly agreed that the objectives were clearly defined and that the information was relevant to their work. Posttraining scores increased by 23%. **Conclusions:** Training materials for clinical specimen collection have been developed for use in low- and middle-resource settings and with initial pilot testing and adoption in Ethiopia. The trainings were well accepted, and Ethiopian personnel were able to successfully lead the trainings and improve their knowledge and skills regarding specimen collection. The materials are being finalized in an online format for easier open access dissemination. Further studies are planned to determine the effectiveness of the trainings in improving the quality of clinical specimen submissions to the microbiology laboratory.

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Transmission of Carbapenemase-Producing Hypervirulent *Klebsiella pneumoniae* in Georgia, 2018–2019

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Figure. Relatedness of seven NDM-producing *Klebsiella pneumoniae* carrying hypervirulence markers, and associated epidemiology and molecular features.

Fig. 1.

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Background: In April 2019, the Georgia Department of Public Health (DPH) initiated whole-genome sequencing (WGS) on NDM-producing Enterobacteriaceae identified since January 2018. The WGS data analyzed at CDC identified related *Klebsiella pneumoniae* isolates with hypervirulence markers from 2 patients. Carbapenemase-producing hypervirulent *K. pneumoniae* (CP-hvKP) are rarely reported in the United States, but they can to cause serious, highly resistant, invasive infections. We conducted an investigation to identify cases and prevent spread. **Methods:** We defined a case as NDM-producing *K. pneumoniae* with ≥4 hypervirulence markers identified by WGS, isolated from any specimen source from a Georgia patient. We reviewed the case patient's medical history to identify potentially affected facilities. We also performed PCR-based colonization screening and retrospective and prospective laboratory-based surveillance. Finally, we assessed facility infection control practices. **Results:** Overall, 7 cases from 3 case patients (A, B, and C) were identified (Fig. 1). The index case specimen was collected from case-patient A at ventilator-capable skilled nursing facility 1 (vSNF1) in May 2018. Case-patient A had been hospitalized for 1 month in India before transfer to the United States. Case-patient B's initial isolate was collected in January 2019 on admission to vSNF2 from a critical access hospital (CAH). The CAH laboratory retrospectively identified case-patient C, who overlapped with case-patient B at the CAH in October 2018. The CAH and the vSNF2 are geographically distant from vSNF1. Case-patients B and C had no known epidemiologic links to case-patient A. Colonization screening occurred at vSNF1 in May 2018, following detection of NDM-producing *K. pneumoniae* from case-patient A ~1 year before determining that the isolate carried hypervirulence markers. Among 30 residents screened, 1 had NDM and several had other carbapenemases. Subsequent screening did not identify additional NDM. Colonization screening of 112 vSNF2 residents and 13 CAH patients in 2019 did not reveal additional case patients; case-patient B resided at vSNF2 at the time of screening and remained colonized. At all 3 facilities, the DPH assessed infection control practices, issued recommendations to resolve lapses, and monitored implementation. The DPH sequenced all 27 Georgia NDM–*K. pneumoniae* isolates identified since January 2018; all were different multilocus sequence types from the CP-hvKP isolates, and none possessed hypervirulence markers. **Conclusions:** We hypothesize that CP-hvKP was imported by a patient hospitalized in India and spread to 3 Georgia facilities in 2 distinct geographic regions through indirect patient transfers. Although a response to contain NDM at vSNF1 in 2018 likely limited CP-hvKP transmission, WGS identified hvKP and established the relatedness of isolates from distinct regions, thereby directing the DPH's additional containment activities to halt transmission.
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Treatment Outcomes and Subsequent Healthcare Utilization Among Patients With Injection Drug Use–Associated Endocarditis

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Background: Addiction medicine consultation and medication-assisted treatment (MAT) have been promoted as a way to improve outcomes for patients hospitalized with injection drug use–associated endocarditis (IDU-IE). However, IDU-IE outcomes have not been evaluated in settings where these services are commonplace. **Objective:** In this study, we evaluated IDU-IE outcomes in a setting where involvement of addiction medicine consultants and use of MAT is well integrated into patient care. **Methods:** Medical records of patients hospitalized with a diagnosis of bacteremia or infective endocarditis (IE) between October 1, 2015, and December 31, 2017, at a safety-net hospital in Boston were screened for evidence of active injection drug use (IDU) within 6 months of hospitalization (as documented by providers or as supported by urine toxicology assays) for suspected or definite IE using modified Duke criteria. Patients without active IDU or IE were excluded, as were those with a diagnosis of IDU-IE over the 6 months prior to the index hospitalization. Demographic parameters, receipt of antibiotics and MAT, other clinical information, and details of rehospitalizations were recorded. Analyses of descriptive statistics were performed. **Results:** Of 567 subjects screened for inclusion, 47 patients met inclusion criteria. All had opiate use disorder (OUD); 41 patients (87.2%) had polysubstance abuse. Addiction medicine consultation was completed for 41 patients (87.2%). Of the 47 subjects, 23 patients (54.8%) received MAT (methadone or buprenorphine/naloxone) over their entire hospitalization, and 31 patients (73.8%) received MAT for