Presentation Type:
Oral Presentation

Identifying Opportunities to Improve Accuracy of NHSN Reporting: Lessons Learned From State Health Department Validations.

Suparna Bagchi, Centers for Disease Control and Prevention; Bonnie Norrick, Centers for Disease Control and Prevention; Nigel Lewis, CACI

Background: State Health Departments (SHDs) have systematically studied the validity of healthcare-associated infection (HAI) surveillance data submitted by healthcare facilities in their jurisdictions to the Centers for Disease Control and Prevention's (CDC's) National Healthcare Safety Network (NHSN) for central-line–associated bloodstream infections (CLABSIs), catheter-associated urinary tract infections (CAUTIs), surgical site infections following colon and abdominal hysterectomy procedures (SSI COLO and HYST), methicillin-resistant *Staphylococcus aureus* and *Clostridioides difficile* laboratory identified (MRSA and CDI LabID respectively) events. These studies are a key source of information about data quality and completeness serving as an impetus and a guide for improving the caliber of NHSN's HAI data. **Methods:** We contacted SHD HAI coordinators in all states for an inventory of HAI validation studies. We used data from these studies to calculate pooled mean sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) for HAI case determinations. HAI case reporting "error rates" were computed as the proportion of mismatches (underreport and overreport) among the medical records reviewed by SHDs and reasons for misclassification were categorized. **Results:** SHD validation studies varied by HAI type (range, 4 studies for MRSA LabID and 23 for CLABSI). Pooled mean sensitivity of HAI reporting ranged from 73.1% (COLO SSI) to 92.7% (CDI LabID). Pooled mean specificity and PPV exceeded 90% for all HAIs. LabID event validations demonstrated the lowest NPV (58.8% for MRSA and 55.1% for CDI). Error rates of HAI reporting to NHSN ranged from 2.5% (HYST SSI) to 13.6% (MRSA LabID). Common errors identified during CLABSI and CAUTI validations were incorrect application of general NHSN and CLABSI- and CAUTI-specific definitions. Incorrect secondary BSI attribution was the most frequently identified reason by CLABSI SHD validations (64.7%). Of all operative procedure-associated misclassifications, inconsistent surveillance practices (66.6%), incorrect NHSN operative procedure category assignment (55.5%), and misapplication of general organ-space and/or site-specific infection criteria (44.4%) were identified as the most common shortcomings. Among MRSA and CDI LabID validations, missed case finding due to failure to review candidate events and gaps in understanding the 14-day reporting rule of LabID protocol were identified as predominant reasons for inaccurate reporting. **Conclusions:** SHD HAI data validations identified specific targets for additional surveillance training, especially CLABSI determinations and application of the protocol rules for MDRO/CDI LabID case determinations. Further work is also needed to assure that data sources in addition to wound cultures are used for SSI determinations and that postdischarge SSI surveillance is more vigorous and comprehensive.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.522

Presentation Type:
Oral Presentation

Incorporating Telementorship Into Laboratory Capacity Building Initiatives for Improved AMR Surveillance in Ethiopia

Martin Evans, American Society for Microbiology; Rajiha Abubeker, Ethiopian Public Health Institute; Surafel Fentaw Dinku, Ethiopian Public Health Institute;Thuria Adem, American Society for Microbiology; Abera Abdeta, Ethiopian Public Health Institute; Amete Teshale, Ethiopian Public Health Institute; Dawit Assefa, Ethiopian Public Health Institute; Gebrie Alebachew, Ethiopian Public Health Institute; Mequanit Mitiku, Tikur Anbessa Specialized Hospital, Addis Ababa, Ethiopia; Estifanos Tsige, Ethiopian Public Health Institute; Maritza Urrego, American Society for Microbiology; Amare Berhanu, CDC-Ethiopia, CDC/DDPHSIS/CGH/DGHP; Carmen Hazim, CDC/DDID/NCEZID/DHQP; Daniel VanderEnde, Centers for Disease Control; Theresa Kanter, Centers for Disease Control/DDPHSIS/CGH/DGHP; Michele Parsons, Centers for Disease Control/DDPHSIS/CGH/DGHP; Michael Omondi, Centers for Disease Control and Prevention

Background: In July 2017, recognizing the threat that antimicrobial resistance poses to the population, the Ethiopian Public Health Institute (EPHI) launched the Ethiopia AMR Surveillance Network at 4 sentinel laboratories. Simultaneously, laboratory capacity building was initiated to ensure the reporting of quality laboratory data to the surveillance system. One initiative, Project ECHO (Extension for Community Healthcare Outcomes) was used to virtually connect subject matter experts with participating laboratories in remote settings to provide ongoing education and telementoring and to foster peer-to-peer learning and problem solving in microbiology. The 10-month project was supported by the Centers for Disease Control and Prevention (CDC) and the American Society for Microbiology (ASM).
Methods: Biweekly 1-hour sessions were held by ASM for 2 sentinel sites, Tikur Anbessa Specialized Hospital and the EPHI Clinical Microbiology and Mycology Laboratory, using a videoconferencing platform. Each virtual session consisted of a didactic session, a case presentation by a participating laboratory, open discussion and feedback. Case presentations focused on technical challenges and problems encountered in the preanalytical, analytical, and postanalytical phases of microbiology testing. Experts from CDC and ASM provided feedback along with a summation of key learning objectives. Sessions were recorded and post session reports were shared with participants. To assess participants' baseline knowledge, a comprehensive pretest was administered prior to the first session. The same instrument was administered as a posttest 2 weeks after the final session. Unstructured interviews were also conducted to assess participants' perceptions of the value of ECHO to their work. **Results:** Mean pretest scores were 69.25% and the posttest scores were 71.04%, a difference of 1.79% (P = NS). Participant interviews revealed perceived benefits of ECHO participation to include enhanced critical thinking and problem resolution in microbiology, increased communication and improved working relationships between participating sites, and improved understanding and application of CLSI standards. As a result of Ethiopia's participation in Project ECHO, 23 case presentations have been added to ECHO Box, a resource bank and web portal, which allows members of the ECHO community to share and access didactics, documents, and learning materials. **Conclusions:** Despite minimal difference between pretest and

posttest scores, the Project ECHO experience of virtual case-based learning and collaborative problem solving has encouraged critical thinking, peer-to-peer learning, networking among participants, and has provided microbiologists with the resources for improved bacterial isolation, identification, and antibiotic susceptibility testing. The lessons learned could be applied as this project is expanded to additional laboratories in the AMR Surveillance Network.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.523

Presentation Type:
Oral Presentation

Longitudinal Characterization and Transmission Dynamics of Antibiotic-Resistant Organisms in an ICU (LOCATE AROs)

Kimberley Sukhum, Washington University School of Medicine; Candice Cass, Washington University School of Medicine; Meghan Wallace, Washington University School of Medicine; Caitlin Johnson, Washington University School of Medicine; Steven Sax , Washington University School of Medicine; Carey-Ann Burnham, Washington University School of Medicine; Gautam Dantas, Washington University School of Medicine; Jennie H. Kwon, Washington University School of Medicine

Background: Healthcare-associated infections caused by antibiotic-resistant organisms (AROs) are a major cause of significant morbidity and mortality. To create and optimize infection prevention strategies, it is crucial to delineate the role of the environment and clinical infections. **Methods**: Over a 14-month period, we collected environmental samples, patient feces, and patient bloodstream infection (BSI) isolates in a newly built bone marrow transplant (BMT) intensive care unit (ICU). Samples were collected from 13 high-touch areas in the patient room and 4 communal areas. Samples were collected from the old BMT ICU, in the new BMT ICU before patients moved in, and for 1 year after patients moved in. Selective microbiologic culture was used to isolate AROs, and whole-genome sequencing (WGS) was used to determine clonality. Antibiotic susceptibility testing was performed using Kirby-Bauer disk diffusion assays. Using linear mixed modeling, we compared ARO recovery across time and sample area. **Results:** AROs were collected and cultured from environmental samples, patient feces, and BSI isolates (Fig. 1a). AROs were found both before and after a patient entered the ICU (Fig. 1b). Sink drains had significantly more AROs recovered per sample than any other surface area ($P < .001$) (Fig. 1c). The most common ARO isolates were *Pseudomonas aeruginosa* and *Stenotrophomonas maltophila* (Fig. 1d). The new BMT ICU had fewer AROs recovered per sample than the old BMT ICU ($P < .001$) and no increase in AROs recovered over the first year of opening ($P > .05$). Furthermore, there was no difference before versus after patients moved into the hospital ($P > .05$). Antibiotic susceptibility testing reveal that *P. aeruginosa* isolates recovered from the old ICU were resistant to more antibiotics than isolates recovered from the new ICU (Fig. 2a). ANI and clonal analyses of *P. aeruginosa* revealed a large cluster of clonal isolates (34 of 76) (Fig. 2b). This clonal group included isolates found before patients moved into the BMT ICU and patient blood isolates. Furthermore, this clonal group was initially found in only 1 room in the BMT ICU, and over 26 weeks, it was found in sink drains in all 6 rooms sampled (Fig. 2b). **Conclusions:** AROs are present before patients move into a new BMT ICU, and sink drains act as a reservoir for AROs over time. Furthermore, sink-drain *P. aeruginosa* isolates are clonally related to isolates found in patient BSIs. Overall, these results provide insight into ARO transmission dynamics in the hospital environment.

Funding: Research reported in this publication was supported by the Washington University Institute of Clinical and Translational

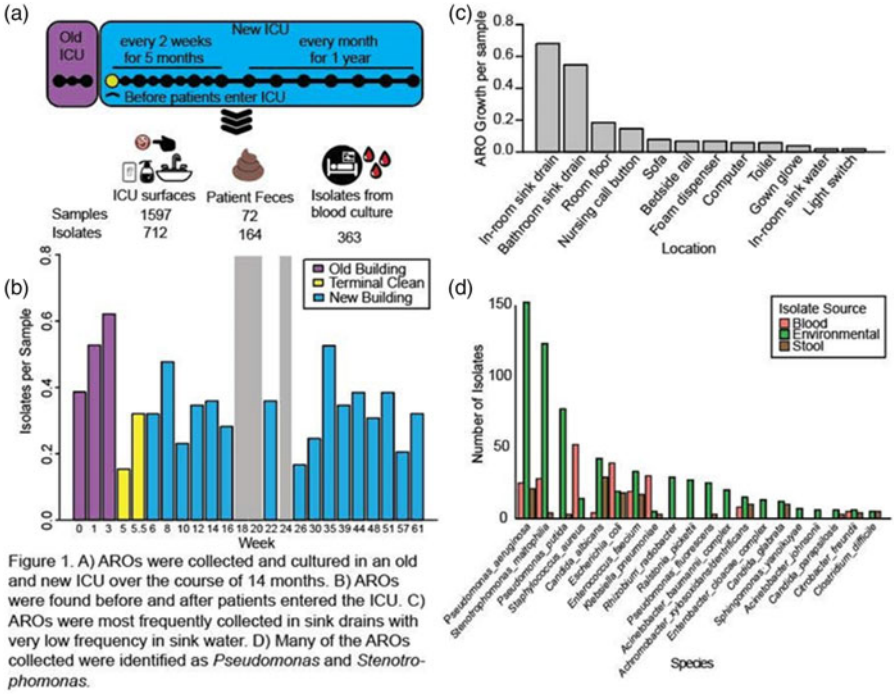

Figure 1. A) AROs were collected and cultured in an old and new ICU over the course of 14 months. B) AROs were found before and after patients entered the ICU. C) AROs were most frequently collected in sink drains with very low frequency in sink water. D) Many of the AROs collected were identified as *Pseudomonas* and *Stenotrophomonas*.

Fig. 1.