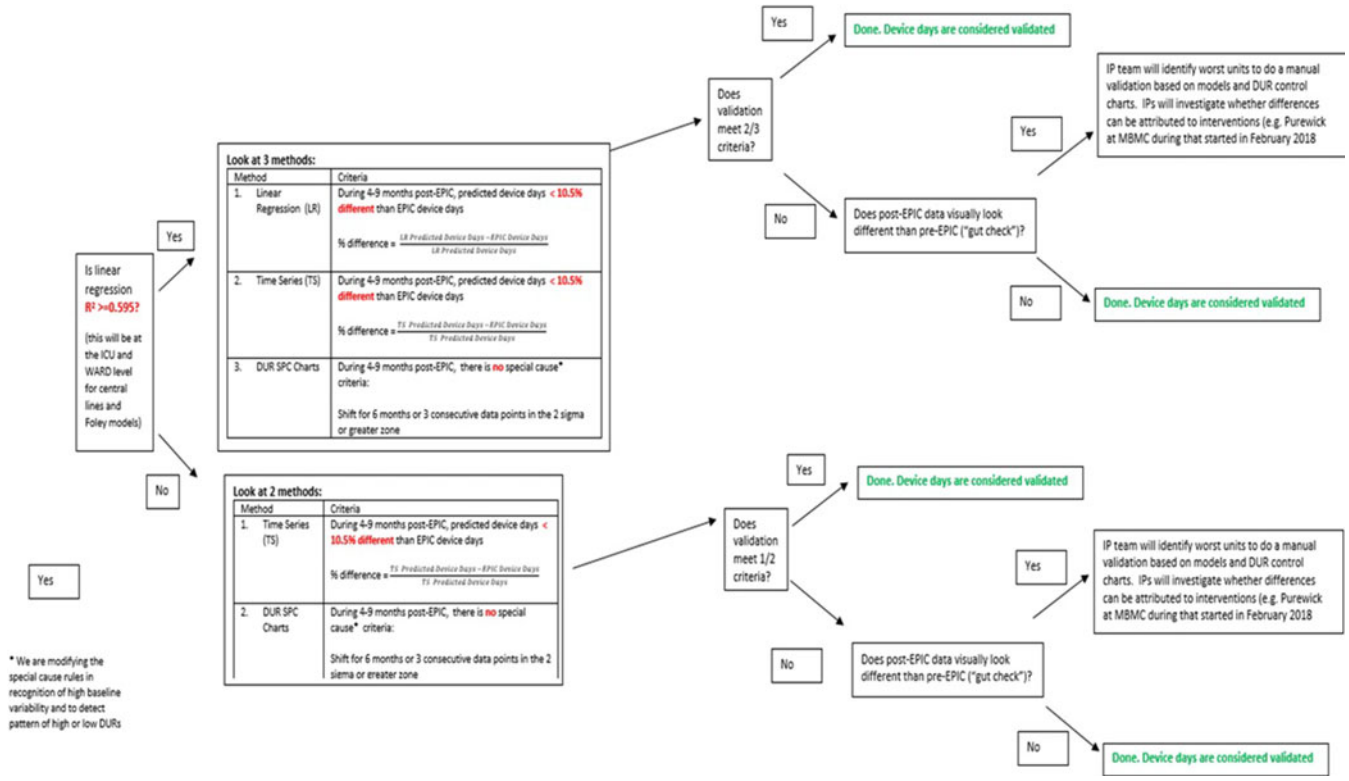

Fig. 1.

Clinical Excellence; Hilary Babcock, Washington University School of Medicine

Background: From August 2017 to June 2018, 11 hospitals within a large healthcare system switched from multiple different electronic medical records (EMRs) to 1 EMR. At the time of this transition, the NHSN provided guidelines to validate healthcare-associated infection (HAI) denominators when switching from manual denominator collection to electronic denominator collection, but the NHSN did not give guidelines for validation when switching from 1 EMR to another. We aimed to build a validation process to ensure the accuracy of central-line and urinary catheter days reported to the NHSN after switching EMRs. **Methods:** Our validation process began with a statistical phase followed by a targeted manual validation phase. The statistical phase used 3 prediction methods (linear regression, time series analysis, and statistical process control [SPC] charts) to forecast device days after the EMR switch for units within hospitals. Models were developed using baseline data from the old EMR (January 2015 through the new EMR implementation). Using prespecified criteria for each method to determine discrepancies, we built a decision tree to identify units needing manual validation. Any unit that failed the statistical phase would need to participate in the manual validation phase, using a midnight census and direct visualization of devices. The manual validation process was composed of 14-day blocks. At the end of each block, if manual device days were within ±5% of EMR device days, they were considered validated. Manual validation would be repeated in 14-day blocks until 2 consecutive blocks passed within ±5%. **Results:** Overall, 157 units were evaluated for urinary catheter days and central-line days. Among them, 143 units passed the statistical validation test for urinary catheter days and 151 passed for central-line days. There was no specific pattern when comparing forecasted versus actual device days. The manual validation process for the 20 failing units (14 urinary catheter and 6 central-line units) is ongoing; preliminary results identified issues with missing nursing documentation in the EMR and with inaccurate manual counting of device days. There were no systematic discrepancies associated with the new EMR. **Conclusions:** We developed a novel validation process using statistical prediction methods supplemented with a targeted manual process. This process saved resources by identifying the units that need manual validation. Discrepancies were largely related to nursing documentation, which the infection prevention team addressed with additional training.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.1090

Presentation Type:
Poster Presentation

Value of Nontargeted Screening for Highly Resistant Microorganisms: The MOVE Study

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Background: In the Erasmus MC University Medical Center, Rotterdam, the Netherlands, patients considered at risk for carrying highly resistant microorganisms (HRMO) are placed in isolation on admission, until tested negative for HRMO (ie, targeted screening). Patients without risk factors are not routinely screened (ie, nontargeted screening). However, nontargeted screening could identify patients colonized with HRMO missed by targeted screening. To determine the additional value of nontargeted screening, we compared the outcomes of the nontargeted screening approach with all available clinical cultures. **Objective:** We aim to identify patients colonized with HRMO, but missed by targeted screening, and to determine whether non-targeted screening has additional value. **Methods:** For the MOVE study, nontargeted admission and discharge cultures (nose and perianal) were obtained from randomly selected patients admitted to specific wards, regardless of HRMO risk factors. This study was part of a research initiative to identify the relation of a contaminated environment with the risk of becoming infected or colonized on a patient level. All bacteriological clinical samples positive for at least 1 HRMO from January 1, 2018, until August 31, 2019, were compared with the nontargeted screening samples. Samples were screened for methicillin-susceptible *Staphylococcus aureus* (MSSA) and methicillin-resistant *Staphylococcus aureus* (MRSA) as well as highly resistant *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Enterococcus faecium*, and Enterobacteriales. Broth enrichment was used for all cultures. **Results:** During the study period, 50,653 patients were admitted. 706 patients (1%) had a clinical sample positive for at least 1 HRMO during their hospital stay. 936 (1.8%) patients were included in the nontargeted screening for the MOVE study, and 40 patients were found to have at least 1 culture positive for HRMO (4.3%). Among these 40 patients, 28 were positive at admission and 12 were positive at discharge. Extended-spectrum β-lactamase (ESBL)–producing Enterobacteriales were most prevalent (n = 36, 90.0%) both at admission and discharge (n = 26 and n = 10, respectively). At admission, 1 patient was identified with MRSA and 1 patient was positive for vancomycin-resistant *E. faecium* (VRE). At discharge, 1 patient was identified with VRE and 1 had Verona Integron-encoded Metallo-β-lactamase (VIM)–positive *P. aeruginosa*. **Conclusions:** Our results show that the current targeted screening does not identify all HRMO carriers. Furthermore, patients who acquire an HRMO during admission are missed. The nontargeted screening identified 40 unknown carriers (4.3%). The limitations of the study are the restricted number of sample sites and the fact that we were unable to culture all patients. Therefore, it is likely that our study shows an underestimation of the true number of patients with HRMO.

Funding: None
Disclosures: None
Doi:10.1017/ice.2020.1091

Presentation Type:
Poster Presentation

Variability and Trends in Blood Culture Utilization, US Hospitals, 2012–2017

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Background: Microbiology data are utilized to quantify epidemiology and trends in pathogens, antimicrobial resistance, and bloodstream infections. Understanding variability and trends in rates of hospital-level blood culture utilization may be important for interpreting these findings. Methods: We used clinical microbiology results and discharge data to identify monthly blood

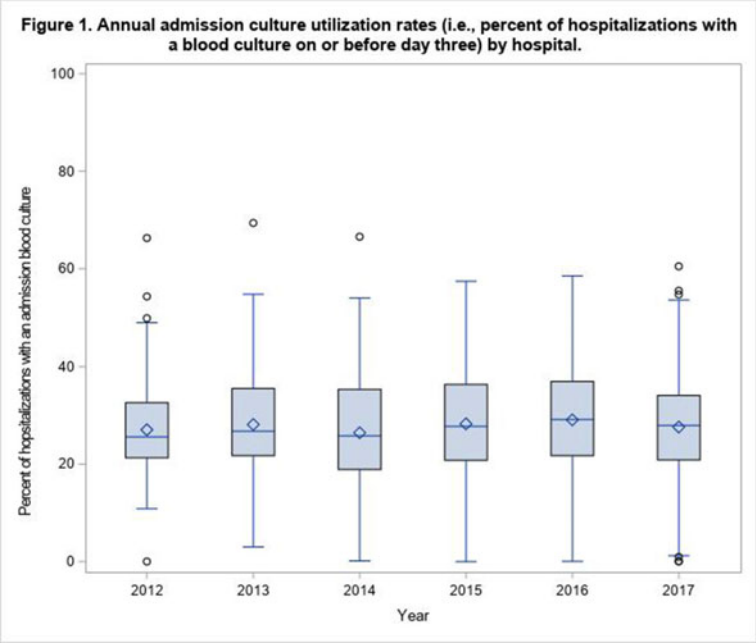

Fig. 1.