Definition#	Total N for which AST data was available for drugs evaluated in the definition	True positive: Meets definition and CP gene present	False positive: Meets definition and CP gene absent	False Negative: Does not meet definition and CP gene present	True Negative: Does not meet definition and CP gene absent	Sensitivity	Specificity
R to 2 or more carbapenems (excluding ertapenem)	5445	175	3371	8	1891	96%	36%
R to Imipenem, Meropenem, or Doripenem AND:							
R Cefepime	6211	131	1480	70	4530	65%	75%
NS to Cefepime	6211	166	2805	35	3205	83%	53%
R Ceftazidime	5338	110	1544	42	3642	72%	70%
NS to Ceftazidime	5338	142	2041	10	3145	93%	61%
NS to Cefepime or Ceftazidime	6444	183	3046	20	3195	90%	51%
R to Aztreonam	6138	99	2947	90	3002	52%	50%
NS to Aztreonam	6138	124	4126	65	1823	66%	31%
R to Levofloxacin or Ciprofloxacin	1989*	153	981	6	849	96%	46%
NS to Levofloxacin or Ciprofloxacin	1989*	153	1111	6	719	96%	39%
R to Piperacillin/tazobactam	1989*	75	684	84	1146	47%	57%
NS to Piperacillin/tazobactam	1989*	129	1013	30	817	81%	41%
R to Gentamicin	1989*	77	377	82	1453	48%	73%
NS to Gentamicin	1989*	88	518	71	1312	55%	66%

CLSI interpretative criteria were applied to designate isolates as susceptible (S), intermediate (I), or resistant (R); Non-susceptible isolates (NS) include isolates designated as I or R.

*Only isolates from New York and Texas were included in this analysis because susceptibility data for these drugs was only available from these two states.

laboratories for carbapenemase testing and antimicrobial susceptibility testing (AST) and (2) laboratory and population-based surveillance for CRPA in 8 sites through the Emerging Infection Program (EIP). **Objective:** We used data from ARLN and EIP to identify AST phenotypes that can help detect CP-CRPA. **Methods:** We defined CRPA as *P. aeruginosa* resistant to meropenem, imipenem, or doripenem, and we defined CP-CRPA as CRPA with molecular identification of carbapenemase genes (*bla*KPC, *bla*IMP, *bla*NDM, or *bla*VIM). We applied CLSI break points to 2018 ARLN CRPA AST data to categorize isolates as resistant, intermediate, or susceptible, and we evaluated the sensitivity and specificity of AST phenotypes to detect CP among CRPA; isolates that were intermediate or resistant were called nonsusceptible. Using EIP data, we assessed the proportion of isolates tested for a given drug in clinical laboratories, and we applied definitions to evaluate performance and number needed to test to identify a CP-CRPA. **Results:** Only 203 of 6,444 of CRPA isolates (3%) tested through AR Lab Network were CP-CRPA harboring *bla*VIM (n = 123), *bla*KPC (n = 53), *bla*IMP (n = 16), or *bla*NDM (n = 13) genes. Definitions with the best performance were resistant to ≥1 carbapenem AND were (1) nonsusceptible to ceftazidime (sensitivity, 93%; specificity, 61%) (Table 1) or (2) nonsusceptible to cefepime (sensitivity, 83%; specificity, 53%). Most isolates not identified by definition 2 were sequence type 111 from a single-state *bla*VIM CP-CRPA outbreak. Among 4,209 CRPA isolates identified through EIP, 80% had clinical laboratory AST data for ceftazidime and 96% had clinical laboratory AST data for cefepime. Of 967 CRPA isolates that underwent molecular testing at the CDC, 7 were CP-CRPA; both definitions would have detected all 7. Based on EIP data, the number needed to test to identify 1 CP-CRPA would decrease from 135 to 42 for definition 1 and to 50 using definition 2. **Conclusions:** AST-based definitions using carbapenem resistance combined with ceftazidime or cefepime nonsusceptibility would rarely miss a CP-CRPA and would reduce the number needed to test to identify CP-CRPA by >60%. These definitions could be considered for use in laboratories to decrease the testing burden to detect CP-CRPA.

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Disclosures: In the presentation we will discuss the drug combination aztreonam-avibactam and acknowledge that this drug combination is not currently FDA approved.

Amelia Shiori Bhatnagar

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Presentation Type:
Poster Presentation

Nosocomial Rabies Encephalitis: Lessons Learned From Exposures in a Large Healthcare System

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Background: In October 2018 a patient presented to hospital A's emergency department (ED) for a work injury, arm spasms, and inability to drink liquids. He developed rapid neurologic decline and was transferred to hospital B for neurocritical care. He developed a fever, was intubated, and had an unrevealing infectious diseases (ID) consultation. He became comatose, had refractory seizures, and was transferred to hospital C. A second ID consultation revealed that he had many bats in his home, and his symptoms were consistent with rabies encephalitis. Antemortem specimens of serum, CSF, skin biopsy, and saliva were all positive for rabies virus PCR, and/or rabies serologies. **Objective:** We describe the response of a multihospital system to the exposure of employees across 3 facilities to rabies-infected body fluids. **Methods:** Three hospitals in 1 system (222 caregivers) cared for the index patient (hospital A, n = 8; hospital B, n = 107; hospital C, n = 107; 19 students and residents), as did 2 additional facilities outside the system. These included physicians (n = 21), registered nurses (n = 57), respiratory therapists (n = 29), imaging technicians (n = 24), phlebotomists (n = 12), laboratorians (n = 8) and others (n = 71). Infection prevention, employee health, and pharmacy leadership created a centralized team to ensure that all exposed caregivers were screened, and if exposed, were vaccinated. An electronic screening tool developed and administered by the Utah Department of Health via Research Electronic Data Capture (Redcap), rapidly assessed caregiver body fluid exposure risks (saliva, tears, neurologic tissue), and use of personal protective equipment in patient care. After completion, caregivers received notification that he or she (1) had no exposure (no further action), (2) had exposure and should report to employee health for vaccination, or (3) had unclear exposure and should contact the employee health department. **Results:** Caregivers feared that the tool underestimated exposure risk. Many caregivers (n = 48), repeated the assessment more than once, changing answers. The most common reasons cited were incomplete forms (n = 21), caregiver did not recall using personal protective equipment with contact with saliva (n = 8) or did not understand rabies transmission (n = 3). All vaccinations were initiated by 11 of 26 care givers, 18 days after initial deployment of the tool. All exposed caregivers completed the course. No caregivers developed symptoms of rabies encephalitis. **Conclusions:** An online tool can safely assess large healthcare exposure such as rabies. A team comprising infection preventionists, employee health representatives, pharmacists, and public health department representatives made the assessment of many geographically dispersed caregivers rapid and effective. Caregivers should employ the basic tenets of standard precautions in the daily care of patients to avoid unknown exposures to common bodily fluids.

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Novel Method to Detect Cardiac Device Infections by Integrating Electronic Medical Record Text with Structured Data in the Veterans Affairs Health System

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Background: Cardiovascular implantable electronic device (CIED) infections are highly morbid, yet infection control resources dedicated to preventing them are limited. Infection surveillance in outpatient care is also challenging because there are no infection reporting mandates, and monitoring patients after discharge is difficult. **Objective:** Thus, we sought to develop a replicable electronic infection detection methodology that integrates text mining with structured data to expand surveillance to outpatient settings. **Methods:** Our methodology was developed to detect 90-day CIED infections. We tested an algorithm to accurately flag only cases with a true CIED-related infection using diagnostic and therapeutic data derived from the Veterans Affairs (VA) electronic medical record (EMR), including administrative data fields (visit and hospital stay dates, diagnoses, procedure codes), structured data fields (laboratory microbiology orders and results, pharmacy orders and dispensed name, quantity and fill dates, vital signs), and text files (clinical notes organized by date and type containing unstructured text). We evenly divided a national dataset of CIED procedures from 2016–2017 to create development and validation samples. We iteratively tested various infection flag types to estimate a model predicting a high likelihood of a true infection, defined using chart review, to test criterion validity. We then applied the model to the validation data and reviewed cases with high and low likelihood of infection to assess performance. **Results:** The algorithm development sample included 9,606 CIED procedures in 67 VA hospitals. Iterative testing over 381 chart reviewed cases with 47 infections produced a final model with a C-statistic of 0.95 (Table 1). We applied the model to the 9,606 CIED procedures in our validation sample and found 100 infections of the 245 cases identified by the model to have a high likelihood of infection We identified no infections among cases the model as having low likelihood. The final model included congestive heart failure and coagulopathy as comorbidities, surgical site infection diagnosis, a blood or cardiac microbiology order, and keyword hits for infection diagnosis and history of infection from clinical notes. **Conclusions:** Evolution of infection prevention programs to include ambulatory and procedural areas is crucial as healthcare delivery is increasingly provided outside traditional settings. Our method of algorithm development and validation for outpatient healthcare-associated infections using EMR-derived data, including text-note searching, has broad application beyond CIED infections. Furthermore, as integrated healthcare systems employ EMRs in more outpatient settings, this approach to infection surveillance could be replicated in non-VA care.

Table 1. CIED Infection Detection Algorithm Logistic Regression Results for Development and Validation in 2016-2017 VA Data

	Development Sample (n=381 CIED procedures, 47 infections)	Validation Sample (n=295 CIED procedures, 100 infections)
Variables	OR (95%CI)	OR (95%CI)
Comorbidity		
Congestive heart failure	**0.12 (0.04-0.39)**	**0.52 (0.23-1.21)**
Coagulopathy	**7.76 (1.94-30.93)**	**0.74 (0.23-2.39)**
Pulmonary circulation disease		
Billing Data		
Emergent problem		
ICD10 code for SSI only	**12.09 (3.47-42.1)**	**24.63 (8.88-68.31)**
Pharmacy Data		
No Abx ≥ 3 days		
Abx ≥ 3 days to treat staph		
Abx ≥ 3 days – not related to staph		
Laboratory Data		
No Micro order	ref	ref
Micro order - Blood	**6.35 (1.85-21.77)**	1 (0.28-3.53)
Micro order - Cardiac	**5.7 (1.71-19.05)**	1.72 (0.79-3.74)
Misc Micro order	0.56 (0.05-6.47)	ERR
Text Note Data		
Diagnosis of infection	**25.99 (3.14-215.49)**	**7.63 (2.25-25.84)**
History of infection	**0.09 (0.02-0.32)**	**0.05 (0.02-0.15)**
Model c- statistic	0.96	0.90

ERR=error in model because there were too few cases with a misc micro order in our validation chart review sample.

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Novel Method to Evaluate Diagnostic Shifting After a Pediatric Antibiotic Stewardship Intervention

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Background: Audit-and-feedback interventions track clinician practice patterns for a targeted practice behavior. Audit and feedback of antibiotic prescribing data for acute respiratory infections (ARI) is an effective stewardship strategy that relies on administrative coding to identify eligible visits for audit. "Diagnostic shifting" is the misclassification of a patient's diagnosis in response to audit and feedback and is a potential unintended consequence of audit and feedback. Objective: To develop a method to identify patterns consistent with diagnostic shifting including both positive shifting (improved diagnosis and documentation) and negative shifting (intentionally altering documentation of diagnosis to justify antibiotic prescribing), after implementation of an audit-and-feedback intervention to improve ARI management. **Methods:** We evaluated the intervention effect on diagnostic shifting within 12 University of Utah pediatric clinics (293 providers). Data included 66,827 ARI diagnoses: pneumonia, sinusitis, bronchitis, pharyngitis, upper respiratory infection (URI), acute otitis media (AOM), or serous otitis with effusion (OME). To determine whether rates of ARI diagnoses changed after the intervention, we developed logistic generalized estimating equation (GEE) models with robust sandwich standard error estimates to account for clinic-wise clustering. Outcomes included the change in each ARI diagnosis relative to the competing 6 diagnoses included in audit-and-feedback reports before and after intervention implementation. Models tested for a change in outcomes after the intervention (ie, diagnostic shift) after adjustment for month of diagnosis. For each diagnosis, we estimated the population attributable fraction (PAF) for antibiotic prescriptions due to combined shifts in