1757. Impact of Accelerate Phenom® Rapid Blood Culture Detection System on Laboratory and Clinical Outcomes in Bacteremic Patients

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Background. Molecular-based automated systems for the rapid diagnosis of bacterial infections have potential to improve patient care. The Accelerate Phenom® blood culture detection system (ACCEL) is an FDA approved platform that allows for identification (ID) and antimicrobial susceptibility testing (AST) 8 hours following growth in routine culture. Methods. This is a single-center retrospective chart review of bacteremic adult inpatients before and after implementation of ACCEL. Laboratory and clinical data were collected February–March 2018 (intervention) and compared with a January–April 2017 historical cohort (standard of care). Standard of care ID and AST were performed using VITEK MS (MALDI-TOF MS) and VITEK2, respectively. An active antimicrobial stewardship program was in place during both study periods. Patients with polymicrobial cultures, off-panel isolates, previous positive culture, or who were discharged prior to final AST report were excluded. Primary outcome was length of stay (LOS). Secondary outcomes were (a) inconsistent culture performance in ACCEL during intervention (18% were identified as on-panel organisms. Seventy-five (64%) of these 118 cultures and 79 (70%) of 113 reviewed standard of care cultures met inclusion criteria. Patient comorbidities (P = NS), MEWS severity score (P = 0.10), source of bacteremia (P = 0.43), and pathogen identified (P = 0.30) were similar between cohorts. Time from collection to ID (28.2 ± 12.7 hours vs. 53.8 ± 20.9 hours; P = 0.001) and AST (31.9 ± 11 hours vs. 71.8 ± 20 hours; P = 0.001) were shorter in the intervention arm.

Results.
Clinical Outcomes

| Standard of Care | Intervention |
|------------------|--------------|
| Mean (SD)        | Mean (SD)    |
| Clinical Outcomes | N = 75       | N = 75       |
| LOS (days)       | 12.1 (11.9)  | 9.1 (7.6)    | 0.03       |
| TTOT (hours)     | 73.5 (50.2)  | 37.5 (32.7)  | <0.001     |
| Total antibiotic DOT (days) | 9.0 (7.5) | 7.0 (4.6)    | 0.05       |
| Meropenem DOT (days) | 6.6 (3.7)  | 3.7 (2.1)    | 0.03       |

Conclusion. Compared with standard of care, ACCEL shortens laboratory turn-around time and improves clinical outcomes. The use of this system has resulted in decreased mean antibiotic DOT, TTOT, and LOS. Further studies are needed to verify these findings.

Disclosures. All authors: No reported disclosures.

1759. High Proportion of Discordant Results in Culture-Independent Diagnostic Tests (CIDT) for Shiga Toxin, Foodborne Disease Active Surveillance Network (FoodNet), 2012–2015

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Background. Molecular-based automated systems for the rapid diagnosis of bacterial infections have potential to improve patient care. The Accelerate Phenom® blood culture detection system (ACCEL) is an FDA approved platform that allows for identification (ID) and antimicrobial susceptibility testing (AST) 8 hours following growth in routine culture. Results. Of 118 cultures performed on ACCEL during intervention, 83% (136) were identified as on-panel organisms. Seventy-five (64%) of these 118 cultures and 79 (70%) of 113 reviewed standard of care cultures met inclusion criteria. Patient comorbidities (P = NS), MEWS severity score (P = 0.10), source of bacteremia (P = 0.43), and pathogen identified (P = 0.30) were similar between cohorts. Time from collection to ID (28.2 ± 12.7 hours vs. 53.8 ± 20.9 hours; P = 0.001) and AST (31.9 ± 11 hours vs. 71.8 ± 20 hours; P = 0.001) were shorter in the intervention arm.

Conclusion. Compared with standard of care, ACCEL shortens laboratory turn-around time and improves clinical outcomes. The use of this system has resulted in decreased mean antibiotic DOT, TTOT, and LOS. Further studies are needed to verify these findings.

Disclosures. All authors: No reported disclosures.

1760. Interferon Gamma Release Assay for Diagnosis of Lyme disease

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Background. The sensitivity of current antibody detection assays against Borrelia burgdorferi, the early stage of Lyme disease, is very low. Patients who commonly have febrile viral illnesses, manifestations of early Lyme disease can be misdiagnosed. We previously demonstrated that IFNy secretion could be detected in whole blood collected from Lyme disease patients at first clinical presentation following overnight incubation of the blood with peptides derived from B. burgdorferi. In the present study, we further evaluated the utility of IFNy release for the laboratory diagnostic of Lyme disease in children with varying stages of the illness.

Methods. Children ages 2-18 years with no prior history of Lyme disease and without infections of Lyme disease were enrolled. Serum samples for IgM and IgG and healthy controls were enrolled for comparison. We collected history and physical examination data and blood samples at the time of enrollment, at 1 month, and at 6 months. Standard 2-tier testing with ELISA (whole cell sonicate [WCS] and C6) and western blot were run in parallel to the IFNy release assay for all blood samples. Sensitivity and specificity of the study assay were determined for presentation at all stages of Lyme disease. Clinical data were summarized.

Results. Blood samples from 22 patients with Lyme disease and 7 controls (4 sick, 3 healthy) were obtained at the first visit. The IFNy release assay detected early and early disseminated Lyme disease with 78% sensitivity compared with 59% sensitivity of 2-tier testing in our study. For patients presenting with a single erythema migrans (EM) lesion, the IFNy release assay detected Lyme disease with 63% sensitivity compared with 14% sensitivity with 2-tier testing. The IFNy release assay had only 25% sensitivity for detecting late disease. A similar trend for both was the IFNy release assay and 2-tier serology.

Conclusion. A novel IFNy release assay demonstrated significantly increased sensitivity when compared with 2-tier testing in the laboratory diagnosis of Lyme disease in patients presenting with a single EM lesion. Future study is needed to determine the effect of Lyme disease in patients with nonspecific febrile illness in the absence of erythema migrans.

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1761. Effect of Carbapenem-Resistant Enterobacteriaceae (CRE) Surveillance Case Definition Change on CRE Epidemiology—Selected US Sites, 2015–2016

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Background. Carbapenem-resistant Enterobacteriaceae (CRE) are an urgent US public health threat. CDC reported CRE incidence to be 2,930/100,000 population in 2012–2013 in selected sites but changed the CRE surveillance case definition in 2016 to improve sensitivity for detecting carbapenemase-producing (CP) CRE. We describe CRE epidemiology before and after the change.

Methods. Eight CDC Emerging Infections Program sites (CO, GA, MD, MN, NM, NY, OR, TN) conducted active, population-based CRE surveillance in selected counties. A case was defined as having an isolate of E. coli, Enterobacter, or Klebsiella meeting a susceptibility phenotype (figure) at a clinical laboratory from urine or a normal sterile body site in a surveillance area resident in a 30-day period. We collected data from medical records and defined cases as community-associated (CA) if no healthcare risk factors were documented. A convenience sample of isolates were tested for carbapenemase genes at CDC by real-time PCR. We calculated incidence rates (per 100,000 population) by using US Census data. Case epidemiology and the proportion of CP-CRE isolates in 2015 versus 2016 were compared.

Results. In total, 442 incident CRE cases were reported in 2015, and 1,149 cases were reported in 2016. Most isolates were cultured from urine: 87% in 2015 and 92% in 2016 (P < .001). The crude overall pooled mean incidence in 2015 was 2.93 (range by site: 0.47–7.19) and in 2016 was 7.48 (range: 3.13–15.95). The most common CRE genus was Klebsiella (51%) in 2015, and in 2016 was Enterobacter (41% P < 0.001). Of the subset of CRE isolates tested at CDC, 109/227 (48%) were CP-CRE in 2015 and 109/551 (20%) were CP-CRE in 2016. In 2015, 52/442 (12%) of cases were CA CRE, and in 2016, 267/1,419 (23%) were CA CRE (P < 0.001). In 2016, 3/111 (2.7%) of CA CRE isolates tested were CP-CRE.

Conclusion. A large increase in reported CRE incidence was observed after the change in the case definition. The new case definition includes substantially larger number of Enterobacter cases. A decrease in CP-CRE prevalence appears to be driven by an increase in non-CP-CRE cases. Although CP-CRE in the community still appear to be rare, a substantial proportion of phenotype CRE appear to be CA, and CDC is undertaking efforts to further investigate CA CRE, including CP-CRE.

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1763. Estimating Median Survival Time to Central Line-Associated Bloodstream Infection (CLABSI) Among Patients in Intensive Care Units Reported to National Healthcare Safety Network (NHSN)

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Background. Duration of free line of central- associated bloodstream infection (CLABSI) in a hospital may vary by type of patient population. We estimated patients’ median time to CLABSI by intensive care unit (ICU) type among acute care hospitals.

Methods. The study population was ICU patients whose CLABSI data were reported to National Healthcare Safety Network (NHSN) in 2016 under the reporting requirement of the Centers for Medicare and Medicaid. The unit of analysis was ICU location, not an individual patient. We conducted counting process survival analysis method to compute time (day) to a CLABSI beginning from day 1 of first reporting month in 2016 in a given ICU location. Once a CLABSI occurred in a location, the start time of follow-up was reset to day 1 after the date of event. The Cox regression method was used to explore the hospital and location-level characteristics that are potentially associated with the daily hazard of CLABSI for an ICU. We also assessed the proportionality hazard assumption of these factors. Adjusting for the vector of means of covariates, we then estimated median time to CLABSI by ICU location type, which is defined as follow-up time (days) by which 50% of events have happened in a given ICU type.

Results. In 2016, 6,935 ICUs at 3,384 hospitals reported CLABSI data to NHSN, with a total of 10,985 CLABSIIs and 2,449,361 follow-up time in days. Factors associated with an increased daily hazard of CLABSI were the following: admission to a hospital with a large bed size, major teaching status, and admission to a patient care location with higher device utilization ratio (Table 1). Adjusted survival curves showed that median time to event (median CLABSI-free time) among ICUs ranged from 66 days (level III neonatal ICU), 90 days (burn units) to 275 days (oncology units), and 284 days (cardiothoracic units) (Table 2, Figure 1).

Conclusion. The study demonstrated that ICUs with level III care for neonatal patients and ICUs with burn patients were least likely to achieve the target of “zero” infection in a defined period and may warrant further targeted interventions. Similar research to investigate infection control performance through estimating median infection-free time is needed beyond ICUs and across multiple HAI type and facility settings.