1168. Role of Extended-Spectrum Cephalosporin-Resistance in Recurrent Enterobacteriaceae Urinary Tract Infections
Judy A. Anesi, MD; Ebbing Lautenbach, MD, MPH, MSCE, FIDSA, FSHEA; Irving Nachman, DrPH, MPH, FSHEA; Charles B. Barragan, MD; Warren Bilker, PhD; Jacqueline Omonoroge, BS; Lois Dankwa, BA; Mary K. Wheeler, MBE; Pam Tolomeo, MPH; Jennifer Han, MD, MSCE and CDC Prevention Epicenters; Division of Infectious Diseases, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania, Department of Pathology and Laboratory Medicine, Perelman School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania.

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Background. Recent data have shown an increase in bacterial resistance to first-line antibiotics used to treat community-onset urinary tract infections (UTIs). A better understanding of the clinical outcomes associated with drug-resistant UTIs in the community is needed. We sought to determine the association between community-onset extended-spectrum cephalosporin-resistant (ESC-R) Enterobacteriaceae (EB) UTI and the risk for recurrent UTI.

Methods. A retrospective cohort study was performed. All patients presenting to the Emergency Departments (EDs) or outpatient practices with EB UTIs between 2010 and 2013 were included. Exposed patients had ESC-susceptible EB UTIs and were matched to exposed subjects 1:1 on study year. Multivariable Cox proportional hazard regression analyses were performed to evaluate the association between ESC-R EB UTI and time to recurrent UTI within 12 months. Patients were censored at the time of first recurrent UTI or at the end of follow-up.

Results. A total of 302 patients with an index community-onset EB UTI were included, with 151 exposed and unexposed. Within 12 months of the index UTI, 163 (54%) patients experienced a recurrent UTI. The median time to recurrence was 69 days (interquartile range 25–183 days). On multivariable analyses, a UTI due to an ESC-R EB was associated with an increased hazard of recurrent UTI (hazard ratio [HR] 1.39, 95% confidence interval [CI] 1.07–1.81, P < 0.01) and presence of a urinary catheter at the time of the index UTI diagnosis (HR 1.59, 95% CI 1.06–2.38, P = 0.03).

Conclusion. Community-onset UTI due to an ESC-R EB organism is associated with a significantly increased hazard of recurrent UTI within 12 months even after adjusting for baseline factors that predispose patients to UTI recurrence. This study raises the question of whether patients with an ESC-R EB organism may require modified treatment regimens. Further study is needed to better elucidate the cause of recurrence among these patients.

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1169. Surveillance of Antibiotic-Resistant Bacteria Reported Among Healthcare-Associated Infections, California, 2011–2017
Kyle Rizzo, MPH, Sam Horwich-Scholefield, MPH, CIC and Erin Epston, MD, Healthcare-Associated Infections Program, California Department of Public Health, Richmond, California

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Background. Antibiotic-resistant healthcare-associated infections (HAI) threaten patient safety and public health. HAI reported by California hospitals to the National Healthcare Safety Network include pathogen and antibiotic susceptibility information. We analyzed HAI data to measure regional changes in antibiotic resistance (AR) over time among select bacteria.

Methods. We analyzed central line-associated bloodstream infection (CLABSI) data using log binomial regression models to estimate annual change in the proportion of pathogens resistant to carbapenems, extended-spectrum cephalosporins, methicillin/oxacillin, and multidrug (MDR) combinations for the reporting years 2011–2017. We aggregated HAI CLABSI, catheter-associated urinary tract infection (CAUTI), and surgical site infection (SSI) data in 2-year increments (i.e., 2014–2015, 2016–2017) to assess changes in percent resistance by county when data for 30 or more pathogens were available.

Results. Among CLABSI reported from 2011 to 2017, there were no significant changes in the proportion of carbapenem-resistant Enterobacteriaceae (CRE) (Figure 1; risk ratio [RR]: 0.97, 95% CI: 0.92, 1.03; P = 0.32), methicillin/oxacillin-resistant S. aureus (MRSA) isolates (RR: 0.98, 95% CI: 0.96, 1.00; P = 0.06) or Pseudomonas aeruginosa with an MDR phenotype (RR: 1.02, 95% CI: 0.95, 1.10; P = 0.54). The proportion of E. coli with MDR and extended-spectrum β-lactamase (ESBL) phenotypes increased by 7% (RR: 1.07, 95% CI: 1.02, 1.12; P < 0.01) and 4% (RR: 1.04, 95% CI: 1.01, 1.08; P = 0.02) per year, respectively. Percentages of AR among aggregated CAUTI, CLABSI and SSI pathogens varied by county and time period (Figures 2 and 3).

Conclusion. Increases in antibiotic resistant phenotypes among E. coli, and unchanged prevalence of MDR Pseudomonas aeruginosa, CRE, and MRSA among reported HAI underscore the need for continued infection prevention and antibiotic stewardship efforts in California. Local public health departments can use these analyses to target coordinated AR prevention initiatives with healthcare facilities in their regions.

Figure 1.

Figure 2.

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1170. Applying Machine Learning Algorithms to Predict Multi-Drug-Resistant Bacterial Infections From Prior Drug Exposure
Elizabeth Lendrum, B.S.1, David Hadam, M.D.2 and Lilliam Ambroggio, PhD1, MPH1, College of Medicine, University of Cincinnati, Cincinnati, Ohio, 1Infectious Disease, Cincinnati Children's Hospital, Cincinnati, Ohio and 2Division of Hospital Medicine, Cincinnati Children's Hospital Medical Center, Cincinnati, Ohio

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Background. Multi-drug-resistant (MDR) infection in the acute care setting prolongs hospital stay and causes high mortality, especially in the pediatric population. Being able to predict MDR infection risk upon or during admission could help prevent and reduce morbidity and mortality in children requiring acute care in the future. This study aimed to develop and validate a predictive model for MDR infection in the pediatric population using machine learning (ML) analysis.

Methods. The study population included hospitalized pediatric patients diagnosed with MDR infection between January 1, 2010 and March 8, 2018. All positive cultures during that period were coded as growing either an MDR or non-MDR organism. ML was performed with random forest (RF) analysis to determine whether hospital drug exposure in the 90 days prior to culture was able to accurately classify cultures as positive for an MDR or non-MDR organism.

Results. During the study period, 7,551 positive cultures were defined as MDR out of a total of 26,913 cultures (28% of all positive cultures). When all cultures were included in the analysis, RF was modestly successful at classifying MDR vs. non-MDR organisms. Significant improvements in classification accuracy were obtained by subdividing cultures based on growth of individual species. RF was able to classify MDR Enterococcus with accuracy = 0.87, positive predictive value of 0.81, and negative predictive value of 0.88. Surprisingly, exposure to many nonantibiotic drugs were important in predicting antibiotic resistance, indicating either that these drugs altered risk directly, or were correlated with MDR risk indirectly.

Conclusion. Drugs without known antimicrobial activity were important predictors of MDR status. Nonantimicrobial drug exposure may be a marker for disease types or therapeutic interventions that place patients at higher risk of MDR infection. Monitoring antimicrobial and nonantimicrobial drug exposure may accurately identify patients at highest risk of MDR infection.

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1171. Impact on Mortality, Length of Stay, and Antibiotic Use in Allogenic and Autologous Stem Cell Transplant Patients Colonized With Carbapenemase-Producing Enterobacteriaceae
Rohima Ghanii, MBBS1; Siddarth Mookerjee, MPH1; Benjamin Mullish, MBBS1; Mark Thruser, MBBS1; Julian Marchesi, PhD1; Jiri Pavlu, MBBS1 and Frances Davies, MBBS1, Imperial College, London, UK, 1Imperial College Healthcare NHS Trust, London, UK

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Background. Carbapenemase producing Enterobacteriaceae (CPE) are increasingly impacting on patient management and hospital infection control practice. Stem cell transplant patients are among the most susceptible to invasive infections. Here we explored how this cohort are affected by CPE colonization.

Methods. All patients who underwent an autologous or allograft stem cell transplant (SCT) between September 15 and December 17 at a large tertiary hospital who were CPE positive on routine rectal screening were reviewed. Length of stay (LoS) post