Stefan Richter, MD PhD⁵ and David Ha, PharmD, BCIDP⁶; ¹Los Angeles County Department of Public Health, Los Angeles, California; ²UCLA, Los Angeles, California; ³LA Biomed, Torrance, California; ⁴La Biomed, Los Angeles, California; ⁵David Geffen School of Medicine UCLA, Los Angeles, California; ⁶KGI School of Pharmacy/Pomona Valley Hospital Medical Center, Los Angeles, California

Session: 59. HAI: MDRO: General

Thursday, October 3, 2019: 12:15 PM

Background. National surveillance for multidrug-resistant organisms (MDRO) are limited by narrow geographic sampling, few hospitals, and failure to account for local epidemiology. A Los Angeles County (LAC) regional antibiogram was created to inform public health interventions and provide a baseline for susceptibility patterns countywide. We present data to compare the 2015 and 2017 LAC regional antibiogram.

Methods. We conducted a cross-sectional survey of cumulative facility-level antibiograms from all hospitals in LAC; 83 hospitals (AH) and 9 Long-term Acute Care (LTAC). For 2015, submission was voluntary, 2017 data were collected by public health order. Non-respondents were contacted by phone and in person. Isolates from sterile sources were pooled. Countywide susceptibility was calculated by weighting each facility's isolate count by its reported susceptibility rate with minimum-maximim observed (2015) and Interquartile range (IQR) for 2017. Change from 2015 mean susceptibility is reported.

Results. Seventy-five (75) facilities submitted antibiograms for 2015 and 86 facilities for 2017. Among non-respondents in 2017, two facilities could not provide an adequate antibiogram and 4 were specialty hospitals with too few cultures to create an antibiogram. Regional summmary tables are presented in Tables 1–4. *Klebsiella pneumoniae* (n = 50 hospitals/19,382 isolates) % S to meropenem was 97% (IQR 94–100%), no change from 2015. *Pseudomonas aeruginosa* (PA) (n = 52 hospitals/17,770 isolates)% S to meropenem was 84% (IQR 74–93%), no change from 2015. Susceptibility to *Acinetobacter baumannii* (AB) was reported by 48 hospitals, including 1,4361 isolates, % S to meropenem was 39% (IQR 25–75%), 14% lower than 2015. *Streptococcus agalactiae* (n = 13 hospitals/647 isolates)% S to clindamycin was 43% (IQR 13–59%), a 22% increase from 2015.

Conclusion. LAC regional antibiograms identified stable patterns of antimicrobial resistance for most pathogens, but concerning results with *AB* and *PA*. Analysis of highly drug-resistant pathogens such as AB and PA would be improved with patient-level data to generate a combination antibiogram. We favor presenting IQR %S as done for 2017. Ongoing analysis will include multivariable analysis of observed changed S controlling for hospital characteristics.



Image: state state

S interpreted using non-meningitis (e.g., pneumonia) breakpoints; meningitis specific %S reported in detailed antibiogram Intrinsically resistant Not routinebt tested or not annitrable

Disclosures. All authors: No reported disclosures.

543. Biocide Resistance Genes in *Klebsiella* spp. Infections from Trauma Patients in Iraq and Afghanistan

John L. Kiley, MD¹; Dana M. Blyth, MD¹; Dana M. Blyth, MD¹; Miriam Beckius, MPH²; Susan Kaiser, BS²; M. Leigh. Carson, MS³; Dan Lu, MS³; Timothy Whitman, DO⁴; Joseph Petfield, MD⁵; David Tribble, MD, DrPH⁶ and Katrin Mende, PhD⁷; Brooke Army Medical Center, San Antonio, Texas; ²Brooke Army Medical Center, JBSA Fort Sam Houston, Texas, San Antonio, Texas; ³Infectious Disease Clinical Research Program, Department of Preventive Medicine and Biostatistics, Uniformed Services University of the Health Sciences, Bethesda, Maryland; ⁴Walter Reed National Military Medical Center, Bethesda, Maryland; ⁵Landstuhl Regional Medical Center, Landstuhl, Rheinland-Pfalz, Germany; ⁶Uniformed Services University, Bethesda, Maryland; ⁷Infectious Disease Clinical Research Program, Department of Preventive Medicine and Biostatistics, Uniformed Services University of the Health Sciences and Brooke Army Medical Center, JBSA Fort Sam Houston, San Antonio, Texas

Session: 59. HAI: MDRO: General

Thursday, October 3, 2019: 12:15 PM

Background. Biocides play an integral role in infection control. Paralleling concern about rising incidence of multidrug-resistant (MDR) organisms is a concern for resistance to biocides. In small studies, several genes involved in the production of efflux pump proteins have been identified as markers of biocide resistance in *Klebsiella* spp., namely *cepA*, *qacA*, *qacE*, *qacAE*, and *acrA*. This study aimed to analyze the *Klebsiella* spp. isolates of a previously defined military trauma group with a high incidence of MDR organisms for the presence of these genes and their correlation with other resistance.

Methods. All infecting *K. pneumoniae*, *K. variicola*, and *K. quasipneumoniae* isolates archived by the Trauma Infectious Disease Outcomes Study (June 2009–December 2014) were selected. Additionally, all colonizing isolates linked with infecting isolates were included; the remainder to total 50 MDR and 46 non-MDR colonizing isolates were chosen randomly. Antimicrobial identification and susceptibilities were determined by CLSI criteria using the BD Phoenix Automated Microbiology System. PCR according to published methods for *cepA*, *qacA*, *qacE*, *qacAE*, and *acrA* was accomplished in duplicate. MDR was defined as either resistance to \geq 3 classes of an ESBL or KPC.

Results. A total of 237 isolates (221 K. pneumoniae, 10 K. variicola, 6 K. quasipneumoniae) met inclusion criteria, of which 149 (63%) were MDR. All isolates had been exposed to antimicrobials prior to isolation. Of all isolates, 234 (98%) carried cepA: 218 (98%) K. pneumoniae carried cepA, 10 (100%) K. variicola carried cepA, and 6 (100%) of K. quasipneumoniae carried cepA. In addition, 148 (62%) isolates with cepA were MDR. One (10%) K. variicola isolate carried qacE along with cepA. This isolate was the only MDR K. variicola. None of the isolates carried qacA, qacAE, or acrA.

Conclusion. We confirmed the near universal presence of the *cepA* biocide resistance gene in *Klebsiella* spp. isolated from trauma patients in Iraq and Afghanistan. In the largest evaluation of biocide resistance genes in *Klebsiella* spp. to our knowledge, the presence of *qacA*, *qacE*, *qac*\Delta*E*, and *acrA* was less common than has been reported elsewhere.

Disclosures. All authors: No reported disclosures.

544. Clonal Spread of Two Sequence Types of Carbapenem-Resistant *Acinetobacter baumannii* Blood Isolates at a Tertiary Care Hospital in South Korea Over 2.5 Years

Seong Eun Kim, MD¹; Su-Mi Choi, MD, PhD²; Yohan Yu, MD³; Sung un Shin, MD¹; Tae hoon Oh, MD¹; Uh Jin Kim, MD⁴; Seung-Ji Kang, MD, PhD³; Hee-Chang Jang, MD, PhD⁴; Kyung-Hwa Park, MD, PhD⁵ and Sook In Jung, MD, PhD¹; ¹Chonnam National University hospital, Kangju, Kwangju-jikhalsi, Republic of Korea; ²Division of Infectious Diseases, Department of Internal Medicine, College of Medicine, The

Catholic University of Korea, Seoul, Korea, Seoul, Seoul-t'ukpyolsi, Republic of Korea; ³Infectious Diseases, Kangju, Kwangju-jikhalsi, Republic of Korea; ⁴Chonnam