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Session: 59. HAI: MDRO: General

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**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

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### Session: 59. HAI: MDRO: General

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**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.

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#### 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

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**Background.** The dissemination of carbapenem-resistant *Acinetobacter baumannii* (CRAB) became an urgent public health concern. A specific sequence type (ST) of *A. bauamannii* has been reported to be associated with severity of disease or mortality. This study aimed to determine the genetic relatedness of CRAB blood isolates cultured from patients at a tertiary care hospital and to investigate clinical characteristics and outcome of CRAB bacteremia.

*Methods.* CRAB blood isolates were collected between June 2016 and December 2018, and their clinical data were obtained. Multi-locus sequence test (MLST) was performed using the Oxford scheme, and the STs were assigned using the MLST database.

**Results.** Of the 126 CRAB blood isolates, 123 isolates which could be typed by MLST all belonged to clonal complex (CC) 92. During the entire period, ST369 (42.3%) was the most dominant, followed by ST191 (32.5%), ST784 (13.8%) and ST451 (4.1%). ST369 was firstly introduced in August 2017. ST191 (61.4%) was the most abundant during June 2016 to July 2017, whereas ST369 (65.8%) replaced ST191 (16.5%) since August 2017. The time interval between intensive care unit admission and bacteremia was shorter in ST369 than ST191 in multivariate analysis (day, median (Q1, Q3), ST369 (6 (3, 9.8), ST191 9 (6, 17), Odd Ratio 0.87 (95% CI 0.76–0.99) P = 0.048 logistic regression). According to the ST, the 7-day and 30-day mortality rates were as follows; 46% and 65% in ST191, 50% and 62% in ST369, and 10.7% and 46.4% in the other STs. Patients infected by ST191 or 369 had significant higher 7-day mortality rates (ST191/369, 48.3% vs. the other STs 10.7%, P = 0.001 by log-rank test) and 30-day mortality rates (ST191/369, 63.2% vs. the other STs, 46.4%, P = 0.045 by log-rank test).

**Conclusion.** This study demonstrates the clonal spread of two STs at a tertiary care hospital in South Korea over 2.5 years. After the introduction of ST369, it replaced ST 191 and widely disseminated within a hospital. Two predominant STs were associated with poor outcome. Continuous surveillance are necessary to monitor the dissemination of these strains.



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#### 545. Incidence of Carbapenem Non-Susceptible Acinetobacter spp. and Carbapenem-Resistant Pseudomonas aeruginosa Clinical Cultures among Patients in US Acute Care Hospitals, 2012–2017

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Session: 60. HAI: MDRO – GNR Epidemiology, Acinetobacter *Thursday, October 3, 2019: 12:15 PM* 

**Background.** Carbapenem-nonsusceptible Acinetobacter spp. (CNAB) and carbapenem-resistant Pseudomonas aeruginosa (CRPA) are recognized causes of severe and difficult to treat healthcare-associated infections. This study estimated and compared the incidence of CNAB and CRPA among patients admitted to US acute care hospitals in 2012–2017.

**Methods.** We measured the incidence of positive clinical cultures from inpatient encounters in a cohort of over 300 hospitals submitting data to the Premier Healthcare Database and Cerner Health Facts in 2012–2017. We included clinical cultures from any body site yielding *Acinetobacter* spp./*P. aeruginosa* non-susceptible/ resistant to imipenem, meropenem, or doripenem. Cultures collected on days 1–3 of hospitalization were considered community-onset (CO) and cultures from later were hospital-onset (HO). Duplicate isolates identified within 14 days of an incident culture and surveillance cultures were excluded. For each year, a raking procedure generated weights to extrapolate the sample estimate to match the American Hospital Association distributions based on US census division, hospital bed capacity, teaching status, and urban designation. We compared estimated rates in 2017 vs. 2012 using weighted multivariable logistic regression adjusting for hospital characteristics and hospital-level clustering.

**Results.** In 2017, the estimated rates of HO and CO CNAB rates were 0.77 and 1.39/10,000 discharges, and HO and CO CRPA rates were 3.14 and 6.57, respectively. Compared with 2017, rates of HO CNAB decreased 49% (Odds Ratio (OR) 0.51; 95% CI: 0.34–0.75) and rates of CO CNAB decreased 29% (OR 0.71; 95% CI: 0.54–0.92). For CRPA, the incidence of HO decreased (OR 0.66; CI: 0.49–0.88) with no change in CO rates (OR 0.93; CI: 0.79–1.11). Assessment of cultures from sterile sites alone showed similar results, but they did not reach statistical significance, Figure 1.

**Conclusion.** We estimate significant national decreases in the rates of HO and CO CNAB, and HO CRPA. Risk factors and effective interventions to reduce CO CRPA might differ from CNAB and HO CRPA. Additional prevention strategies are needed to address CO CRPA.





#### 546. Seasonal Changes in the Prevalence of Antibiotic-Susceptible Acinetobacter baumannii Results in Increased Multidrug Resistance Rates During Winter Months

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Session: 60. HAI: MDRO – GNR Epidemiology, Acinetobacter

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**Background.** Understanding the seasonal behavior of infections ("seasonality") caused by Gram-negative pathogens, including *Acinetobacter baumannii*, is essential for the design of effective healthcare policies; however, the factors mediating seasonality remain elusive.

*Methods.* Over 2,000 *A. baumannii* cases identified in the BJC Health System between 2007 and 2017, were retrospectively analyzed according to isolation month, hospital acquisition, anatomical source, and antibiotic susceptibility profile.

**Results.** Compared with quarter 1 (Q1, December–February), *A. baumannii* case incidence was similar in Q2 (March–May) but significantly higher in Q3 (June–August) and Q4 (September–November). This seasonality was exhibited by antibiotic-susceptible but not antibiotic-resistant isolates. This was independent of tested antibiotic, anatomic source, or hospital vs. community acquisition.

**Conclusion.** Seasonality is absent from antibiotic-resistant *A. baumannii* cases. Selective decrease of antibiotic-susceptible cases in Q1/Q2 results in 50–100% increase in resistance rates compared with Q3/Q4. *A. baumannii* seasonality is possibly linked to the increased use of antibiotics during winter. As resistance determinants tend to be genetically linked in *A. baumannii*, pressure from community antibiotics may have the inadvertent effect of selecting for multidrug resistance. This link must be further studied, as it may also explain seasonality in other, more antibiotic-susceptible Gramnegative pathogens.

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## 547. Multidrug-Resistant *Pseudomonas aeruginosa* in an Academic Regional Burn Intensive Care Unit

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