Table 2: Carbapenemase Enzymes and Antimicrobial Susceptibilities of CNS to Novel Beta-Lactam-Beta-Lactamase Agents

| Isolate | Organism | Carbapenemase* | Cefazolin-Antimethicillin MIC | Meropenem-Vancomycin MIC |
|---------|----------|---------------|-----------------------------|-------------------------|
| RS102   | C. freundii | KPC           | 0.05                        | 0.05                     |
| RS103   | C. freundii | KPC           | 0.05                        | 0.05                     |
| RS116   | C. freundii | KPC           | <0.05                       | <0.05                    |
| RS236   | C. freundii | -             | 2                           | 0.5                      |
| RS237   | C. freundii | KPC           | >64                         | >64                      |
| RS240   | C. freundii | KPC           | 8                           | 8                        |
| RS259   | C. freundii | KPC           | >256 [R]                    | >8 [R]                   |
| RS289   | C. koseri   | KPC           | 2                           | 0.12                     |
| RY27    | C. freundii | KPC           | 0.5                         | 0.05                     |
| YODC58  | C. freundii | KPC           | >256 [R]                    | >8 [R]                   |
| YODC68  | C. freundii | KPC           | 4                           | 0.06                     |
| YODC68-3 |          |               | 2                           | 0.06                     |
| YODC45  | C. freundii | KPC           | >256 [R]                    | >8 [R]                   |
| YODC81  | C. freundii | KPC           | 4                           | 0.06                     |
| YODC86-7|          |               | 4                           | 0.12                     |
| YODC86-9| C. koseri   | KPC           | 4                           | 0.12                     |
| YODC93  | C. freundii | KPC           | 4                           | 0.12                     |
| YODC95  | C. freundii | KPC           | 4                           | 0.12                     |
| YODC97-2| C. freundii | KPC/OXA-48    | 4                           | 0.12                     |
| YODC730 |          |               | 0.5                         | 0.12                     |
| YODC849-1|         |               | >256 [R]                    | 16 (R)                   |

Abbreviations: R: Resistant
*Carbapenemase gene presence was evaluated by multiplex-PCR. Genomic DNA from isolates was used in 50 p. reactions containing BlueTaq DNA Polymerase (Bioneer). Each multiplex-PCR reaction contained PCR primers (forward TTTGTCCTTTGCTTCTTCTTCTTCTGT and reverse AGACATGGCGCGCCACACTT), NDM primers (forward AATGCTCTCGTTCTTATTTTTTCT and reverse AGACATGGCGCGCCACACTT), VIM primers (forward ATGTCCGGTTTAAATCTTT and reverse GAGGTGCTTGTGCTGTT), IMP primers (forward ATGCACGCTTGTGCTGTT and reverse GAGGTGCTTGTGCTGTT), and KhN primers (forward ATGCACGCTTGTGCTGTT and reverse GAGGTGCTTGTGCTGTT).

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487. Prevalence of Antimicrobial Resistance in Gram-Negative Bacilli Bloodstream Infections at a Tertiary Teaching Hospital in the Dominican Republic Alfredo J. Mena Lora, MD; Julia Rodriguez Abreu, MD MPH; Claudia Blanco, MD; Jacquelin de Lara, MS and Susan C. Bleasdale, MD; 1University of Illinois at Chicago, Chicago, Illinois; 2CEDIMAT, Santo Domingo, Distrito Nacional, Dominican Republic Session: 53. HAI: MDRO – GNR Epidemiology, Other Thursday, October 3, 2019: 12:15 PM

Background. Bloodstream infections (BSI) with gram-negative bacilli (GNB) are a major cause of morbidity and mortality worldwide. Sepsis due to GNB can carry a mortality rate as high as 40%, with higher mortality in developing nations. Early and appropriate empiric therapeutic selection plays an important role in survival. The rising incidence of antimicrobial resistance (AMR) limits empiric treatment options. Local susceptibility patterns can vary per region, institution or setting. Understanding local AMR may help guide empiric treatment choices. We seek to describe resistance rates for GNB BSI in the Dominican Republic (DR).

Methods. This is a retrospective review of antimicrobial susceptibility patterns from bloodstream infections in a tertiary hospital in the DR. Susceptibility data from all adult inpatient blood cultures were collected from January 1 to December 31, 2017.

Results. A total of 124 blood cultures were reported. The most common organisms were Escherichia coli (43%) and Klebsiella pneumoniae (23%). Fluoroquinolone resistance was present in 70% of E. coli. Phenotypic susceptibility patterns consistent with extended-spectrum β-lactamase (ESBL) producing GNB were present in 46% of isolates. Carbapenem resistance was found in 4 samples and was most common in P. aeruginosa. Susceptibility results are described on Table 1.

Conclusion. AMR was high in GNB BSI in the DR. High rates of ESBL render common cefepime sub-optimal for empiric treatment. PTZ retains in vitro susceptibilities despite cephalosporin resistance but clinical efficacy is controversial. CTX-M ESBLs may cause these resistance pattern in vitro. Further studies are needed to determine genetic mechanisms of resistance. Establishing antimicrobial stewardship programs with rapid diagnostic testing that identify mechanisms of resistance may promote judicious use of carbapenems and reduce further the risk of further development of AMR.

Table 1. Susceptibility patterns for GNB BSI (%)

| Organism   | E. coli | K. pneumonia | P. aeruginosa | E. cloacae | A. baumanii |
|------------|---------|--------------|---------------|------------|------------|
| Susceptible| 47%     | 37%          | 97%           | 79%        | 86%        |
| Resistant  | 53%     | 63%          | 3%            | 21%        | 14%        |

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488. Epidemiology and Outcomes for Stenotrophomonas maltophilia Infections at a Tertiary Care Center in Detroit, MI Erin Goldman, DO; Justin Oring, DO; Reda Awali, MD, MPH; and Teenah Chopra, MD, MPH; 1Wayne State University, Oak Park, Michigan; 2Detroit Medical Center, Wayne State University, Detroit, Michigan Session: 53. HAI: MDRO – GNR Epidemiology, Other Thursday, October 3, 2019: 12:15 PM

Background. Stenotrophomonas maltophilia is a gram-negative, biofilm forming bacterium. The increasing use of antibiotics has allowed this bacterium to become a predominant nosocomial pathogen with inherent resistance to several antibiotics. In this study, we describe the epidemiology and outcomes for patients treated for S. maltophilia infections who were admitted to Detroit Medical Center from January 1, 2010 to August 31, 2018.

Methods. This was a retrospective cohort study that included S. maltophilia cultures isolated from sterile body sites from January 1, 2010 to August 31, 2018. Nonsterile body sites and tissue cultures were excluded, as well as cultures that were deemed to be colonization based upon clinical evaluation. Appropriate empiric antibiotic therapy was defined as a regimen administered three days prior to or four days following the S. maltophilia culture date. Appropriate definitive therapy was defined as antibiotic treatment administered five to fourteen days following the culture date. Patient data were extracted from the electronic medical record which included demographic information, length of stay and outcome data. Bivariate analysis was performed using SAS database.

Results. 126 patients with S. maltophilia infections were analyzed: 89 had bacteremia, 22 had lung infections, and 15 had other infections. The median length of stay was 16 days (IQR: 6 – 30 days). Sixty-one patients (48%) admitted to the ICU had a median length of stay of 10 days (Table 2). Among the patients that were followed after discharge, 21 were readmitted within 30 days. Table 1 highlights the bivariate analysis of patients who died within 30 days vs. survived. Patients who received definitive antibiotic therapy had lower 30-day mortality (Table 1; CI 95%, OR=0.37, P = 0.03).

Conclusion. Carabapenemases were rarely the cause of carbapenem resistance but were found at EIP sites with high and low CRPA incidence. The emergence of mobile carbapenemases in P. aeruginosa has the potential to increase the incidence of CRPA. Increased detection and early response to carbapenemase-producing CRPA is key to prevent further emergence.

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addition, patients who were bacteremic had a lower 30-day mortality (Table 1; CI 95%, OR = 0.40, P = 0.04). There was no significant difference in mortality among patients who received appropriate empiric antibiotic therapy (P = 0.67).

Conclusion. This study demonstrates that nonbacteremic patients infected with Stenotrophomonas have higher 30-day mortality than those with bacteremia. This necessitates that diseases associated with this bacterium should be taken seriously and treated with definitive appropriate antibiotics.

490. High Prevalence of Rectal Carriage of blaKPC – Mediated Carbapenem-Resistant Enterobacteriaceae Among Community Food Handlers in Kuwait

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Session: 54. HAI: MDRO – GNR Epidemiology, CRE
Thursday, October 3, 2019: 12:15 PM

Background. Carbapenemases are diverse enzymes which inactivate the carbapenems. KPC-producing carbapenemase-producing Enterobacteriaceae have disseminated to many regions in the world, however, anecdotal reports of KPC-producing CPE in some GCC countries excluding Kuwait. In this study we report the first emergence of the KPC-producing CPE isolated from healthy food handlers in our community.

Methods. Rectal swabs were collected from 405 food handlers. Isolates were identified by VITEK 2 and their susceptibility to 21 antibiotics performed by MIC determination using Etest. Genes encoding carbapenemase production were characterized by PCR and cloning of isolates was determined by MLST.

Results. A total of 36 CPE were isolated from 31 participants, of which 15 (41.7%) were Escherichia coli and 8 (22.2%) Klebsiella pneumoniae. All isolates were susceptible to amikacin and tigecycline and an alarmingly high percentage (38.9%) were non-susceptible to colistin. A very high proportion of the CPE harbored blaKPC (58.3%), followed by blaOXA-48 (25%), blaNDM (5.6%) and blaVIM (2.8%). Carbapenemases were co-produced with ESBLs in 30.6% of the isolates. Sequencing of the KPC revealed that KPC-18 represented 45%, KPC-2 36% and KPC-29 18%. Considerable genetic diversity among the isolates was identified by MLST assays demonstrating the emergence of new clones. Five diverse new CPE clones were detected from three Bangladeshi citizens and 2 Indians.

Conclusion. Our finding demonstrates a relatively high colonization rate (8.9%) of healthy food handlers by CPE of which KPC-producing CPE were predominant; this is an unusual finding in Kuwait representing the first of such findings in our country and GCC.

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491. Working Together: A Tale of Carbapenem-Producing Organism Investigations in Three New York City Nursing Homes

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Background. New York State Department of Health (NYSDOH) and Wadsworth Center (WC) participate in the Centers for Disease Control and Prevention’s Antibiotic Resistance Laboratory Network (AR Lab Network), including identification and characterization of specific blA genes in carbapenemase-producing organisms (CPO). Three investigations from November 2018–March 2019 illustrate the findings and challenges investigating CPO in a blA<sub>esc</sub> endemic setting.

Methods. NYSDOH WC testing includes organism identification, drug susceptibility testing, detection of carbapenemase production, detection of carbapenemase genes, and whole-genome sequencing (WGS). NYSDOH epidemiologic (epi) investigations of novel resistance mechanisms review demographic and exposure data, conduct contact tracing with targeted rectal screening to identify colonized persons, and assess infection control (IC) and public health (PH) practices and provide recommendations. NYSDOH identified nursing home residents infected with CPO with novel carbapenemase genes (Figure 1) with no travel history but multiple co-morbidities, including mechanical ventilation: blA<sub>esc</sub>, Klebsiella pneumoniae (KP) (Facility A), blA<sub>esc</sub> KP (Facility B and C). Epi investigations identified CPO in 48 of 106 residents screened for rectal colonization; most isolates other than the index gene. Facility A and Facility B each had no additional residents colonized with CPO with the index gene after screening; 14 and 10 residents, respectively from Facility A and B, had CPO with endemic blA<sub>esc</sub> gene. WGS analysis identified 2 clusters of blA<sub>esc</sub> KP within Facility A and no clusters of CPO were detected in Facility B. IC/PH recommendations were made after diagnosis at all 3 facilities; serial IC/PH assessments/recommendations and screening were needed to disrupt transmission at Facility C, where 24 residents were colonized with CPO, including 7 residents with CPO with the index gene (blA<sub>esc</sub>), and a subset of the blA<sub>esc</sub> isolates were related to the index case by both epi and WGS analysis.

Conclusion. Epi investigation and WGS were complementary to detect transmission, identify clusters within an endemic setting, and inform PH response and IC measures for these emerging CPO in NY Healthcare Facilities.

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