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

Isolate	Organism	Carbapenemase*	Ceftazidime- Avibactam MIC	Meropenem- Vabrobactam MIC		
RS102	C. freundii	-	0.5	0.06		
RS189	C. freundii	NDM	0.5	0.015		
RS226	C. freundii	KPC	<0.25	0.015		
RS236	C. freundii	-	2	0.5		
RS237	C. freundii	-	64 (R)	0.5		
RS240	C. freundii	-	8	0.5		
RS259	C. freundii	KPC	>256 (R)	>8 (R)		
RS289	C. koseri	-	2	0.12		
RS77	C. freundii	KPC	0.5	0.015		
YDC582	C. freundii	KPC	>256 (R)	>8 (R)		
YDC608	C. freundii	KPC	4	0.06		
YDC638-3	C. freundii	KPC	2	0.06		
YDC645	C. freundii	KPC	<0.25	0.03		
YDC661	C. freundii	KPC	4	0.06		
YDC667-1	C. freundii	KPC	0.5	0.03		
YDC689-2	C. koseri	-	4	0.12		
YDC693	C. freundii	KPC	1	0.03		
YDC693-2	C. farmeri	KPC	4	0.12		
YDC697-2	C. farmeri	KPC/OXA-48	4	0.12		
YDC730	C. werkmanii	-	0.5	0.12		
YDC849-1	C. freundii	NDM	>256 (R)	16 (R)		

Abbreviations: R: Resistant

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486. Epidemiology of Carbapenem-Resistant Pseudomonas aeruginosa Identified Julian E. Grass, MPH<sup>1</sup>; Sandra N. Bulens, MPH<sup>1</sup>; Wendy M. Bamberg, MD<sup>2</sup>; Sarah J. Janelle, MPH<sup>2</sup>; Kyle Schutz, MS<sup>2</sup>; Jesse T. Jacob, MD, MSc<sup>3</sup>; Chris W. Bower, MPH<sup>4</sup>; Rebekah Blakney, MS<sup>4</sup>; Lucy E. Wilson, MD, ScM<sup>5</sup>; Elisabeth Vaeth, MPH<sup>6</sup>; Linda Li, MPH<sup>6</sup>; Ruth Lynfield, MD<sup>7</sup>; Paula Snippes Vagnone, MT(ASCP)<sup>8</sup>; Ginette Dobbins, MPH<sup>7</sup>; Erin C. Phipps, DVM, MPH<sup>9</sup>; Emily B. Hancock, MS<sup>9</sup>; Ghinwa Dumyati, MD<sup>10</sup>; Rebecca Tsay, MPH<sup>10</sup>; P Maureen. Cassidy, MPH<sup>11</sup>; Nicole West, MPH<sup>1</sup> Marion A. Kainer, MBBS, MPH, FRACP, FSHEA<sup>12</sup>; Jacquelyn Mounsey, RN<sup>12</sup>; Richard A. Stanton, PhD<sup>1</sup>; Gillian A. McAllister, BS<sup>13</sup>; Davina Campbell, MS<sup>1</sup>; Joseph D. Lutgring, MD<sup>1</sup>; Maria Karlsson, PhD<sup>13</sup> and Maroya S. Walters, PhD<sup>1</sup>; Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia; <sup>2</sup>Colorado Department of Public Health and Environment, Denver, Colorado; <sup>3</sup>Emory University, Atlanta, Georgia; <sup>4</sup>Georgia Emerging Infections Program, Decatur, Georgia; <sup>5</sup>University of Maryland Baltimore County, Baltimore, Maryland; <sup>6</sup>Maryland Department of Health, Baltimore, Maryland; <sup>7</sup>Minnesota Department of Health, Saint Paul, Minnesota; <sup>8</sup>Minnesota Department of Health Laboratory, St. Paul, Minnesota; <sup>9</sup>University of New Mexico, Albuquerque, New Mexico, <sup>10</sup>New York Rochester Emerging Infections Program at the University of Rochester Medical Center, Rochester, New York, <sup>11</sup>Oregon Health Authority, Portland, Oregon, <sup>12</sup>Tennessee Department of Health, Nashville, Tennessee, 13 Centers for Disease Control and Prevention, Atlanta, Georgia

Session: 53. HAI: MDRO - GNR Epidemiology, Other Thursday, October 3, 2019: 12:15 PM

Background. Pseudomonas aeruginosa is intrinsically resistant to many commonly used antimicrobials, and carbapenems are often required to treat infections. We describe the crude incidence, epidemiology, and molecular characteristics of carbapenem-resistant P. aeruginosa (CRPA) in the EIP catchment area.

Methods. From August 1, 2016 through July 31, 2018, we conducted laboratory and population-based surveillance for CRPA in selected areas in eight sites. We defined a case as the first isolate of P. aeruginosa resistant to imipenem, meropenem, or doripenem from the lower respiratory tract, urine, wounds, or normally sterile sites identified from a resident of the EIP catchment area in a 30-day period. Patient charts were reviewed. Analysis excluded cystic fibrosis patients. A random sample of isolates was collected. Realtime PCR to detect carbapenemase genes and whole-genome sequencing are in progress.

We identified 4,209 cases in 3373 patients. The annual incidence was Results. 14.50 (95% CI, 14.07–14.94) per 100,000 persons and varied among sites from 4.89 in OR to 25.21 in NY. The median age of patients was 66 years (range:  $<1{-}101$ ), 42.1% were female, and nearly all (97.5%) had an underlying condition. Most cases were identified from urine (42.8%) and lower respiratory tract (35.7%) cultures. Nearly all (93.3%) occurred in patients with inpatient healthcare facility stay, surgery, chronic dialysis, or indwelling devices in the prior year; death occurred in 7.2%. Among 937 isolates tested, 847 (90.4%) underwent PCR; six (0.7%) harbored a carbapenemase, from four sites (CO, MD, NY, and OR):  $bla_{VIM}$  (3),  $bla_{KPC}$  (2), and  $bla_{IMP}$  (1). Of 612 (65.3%) isolates sequenced, the most common ST types were ST235 (9.2%) and ST298 (4.9%).

Conclusion. Carbapenemases 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. Disclosures. All authors: No reported disclosures.

## 487. Prevalence of Antimicrobial Resistance in Gram-Negative Bacilli Bloodstream Infections at a Tertiary Teaching Hospital in the Dominican Republic

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Background. Bloodstream infections (BSI) with gram-negative bacilli (GNB) are a major cause of morbidity and mortality worldwide. Sepsis due to BSI 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 profile is described on Table 1.

Conclusion. AMR was high in GNB BSIs in the DR. High rates of ESBL render common cephalosporins sub-optimal for empiric treatment. PTZ retains in vitro susceptibilities despite cefepime 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 (%)

Organisms	Ampicillin- Sulbactam	Cefazolin	Cefepime	Ceftazidime	Ceftriaxone	Ciprofloxacin (FQ)	Ertapenem	Gentamicin	Imipenem	Piperacillin- tazobactam (PTZ)
E. coli	47	47	48	48	48	30	100	59	100	97
K. pneumoniae	29	37	37	37	37	52	97	50	97	82
P. aeruginosa		-	92	97		87		92	79	75
E. cloacae	-	-	90	81	81	81	100	100	100	86
A. baumannii	86	-	86	86		86	-	86	100	100

Disclosures. All authors: No reported disclosures.

## 488. Epidemiology and Outcomes for Stenotrophomonas maltophilia Infections at a Tertiary Care Center in Detroit, MI

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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). In