Figure 1: Primary and Secondary Endpoints

Antimicrobial exposure	Cases n = 106 (%)	Controls n = 119 (%)	Odds Ratio (95% CI)	
≥ 48 hours of meropenem	21 (19.8)	5 (4.2)	5.63 (2.04 - 15.54)	
≥ 7 days of meropenem	15 (14.2)	4 (3.4)	4.74 (1.52 – 14.77)	
≥ 7 days of other antipseudomonal antibiotics	37 (34.9)	18 (15.1)	3.01 (1.59 - 5.71)	

Disclosures. All authors: No reported disclosures.

484. Metallo-β-Lactamase-Positive Carbapenem-Resistant Enterobacteriaceae and Pseudomonas aeruginosa in the Antibiotic Resistance Laboratory Network, 2017–2018

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

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Background. Infections with metallo-β-lactamase (MBL)-producing organisms are emerging in the United States. Treatment options for these infections are limited. We describe MBL genes among carbapenemase positive carbapenem-resistant Enterobacteriaceae (CP-CRE) and *Pseudomonas aeruginosa* (CP-CRPA) isolates tested during the first two years of the Antibiotic Resistance Laboratory Network (AR Lab Network).

Methods. State and local public health laboratories tested CRE and CRPA isolates for organism identification, antimicrobial susceptibility, and PCR-based detection of $bla_{\rm KPC}$, $bla_{\rm NDM}$, $bla_{\rm OXA-48, blc}$, $bla_{\rm VIM}$, and $bla_{\rm IMP}$ carbapenemase genes. All testing results were sent to CDC at least monthly.

Results. Since January 2017, the AR Lab Network tested 21,733 CRE and 14,141 CRPA. CP-CRE were detected in 37% of CRE; 2% of CRPA were CP-CRPA. Among CP-CRE, 9% (686/8016) were MBL-producers (NDM, VIM, or IMP). Among MBL-producers, a bla_{NDM} gene was detected most often (81%; 551/686). bla_{NDM} were most common among *Klebsiella* spp. (47%; 261/551), bla_{MP} were most common among *Providencia* spp. (53%; 40/75), bla_{VIM} was most common among *Enterobacter* spp. (19%; 25/62). Twelve percent (96) of MBL CP-CRE contained more than one carbapenemase gene. Among CP-CRPA, 73% (218/300) were MBL producers and bla_{VIM} was the most common gene (62%; 186). Three (1%) MBL CP-CRPA contained more than one carbapenemase.

Conclusion. Increased testing of CRE and CRPA isolates through the AR Lab Network has facilitated early and rapid detection of hard-to-treat infections caused by MBL-producing organisms across the United States. The widespread distribution of MBL genes highlights the continued need for containment strategies that help prevent transmission between patients and among healthcare facilities. To support therapeutic decisions for severe infections caused by MBL-producing organisms, the AR Lab Network is now offering rapid susceptibility testing against aztreonam/avibactam, using digital dispenser technology. This testing program aims to close the gap between the availability of new drugs or drug combinations and the availability of commercial AST methods, thereby improving patient safety and antimicrobial stewardship.



Disclosures. All authors: No reported disclosures.

485. Clinical and Molecular Epidemiology of Carbapenem Non-susceptible *Citrobacter* sp.

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Session: 53. HAI: MDRO - GNR Epidemiology, Other

Thursday, October 3, 2019: 12:15 PM

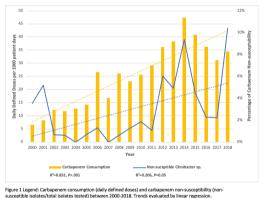
Background. Carbapenem non-susceptible *Citrobacter* sp. (CNSC) are becoming increasingly recognized as healthcare-associated (HA) pathogens, but data on clinical and molecular epidemiology, species diversity and mechanisms of carbapenem resistance are lacking.

Methods. We reviewed patients at University of Pittsburgh Medical Center with CNSC positive cultures from 2000 to 2018. The diversity of CNSC species among a subset of isolates from all UPMC sites was confirmed by 16S rRNA typing, and the presence of carbapenemase enzymes in the same isolates was determined by PCR amplificon. Minimum inhibitory concentrations (MICs) were determined by broth microdilution. Significance of epidemiological trends over time was determined by linear regression, and correlation with antibiotic consumption was determined by cross-correlation using STATA v15.

Results. Between 2000 and 2018, 3% (78/2817) of all *Citrobacter* sp. were CNS. CNSC rates increased from 4% in 2000 to 10% in 2018 ($R^2 = 0.206$, P = 0.05), as did carbapenem consumption (6.5–34.5 DDDs/1000, $R^2 = 0.831$, P < 0.001) (Figure 1). Twenty-one isolates from 19 patients were available for additional analysis. Patients had multiple comorbidities (84%), frequently acquired CNSC in the healthcare setting (84%), were colonized with other organisms (68%), and had high rates of in-hospital mortality/discharge to hospice (47%) (Table 1). *C. freundii* was the dominant species identified (16/21), followed by *C. farmeri* (2/21), *C. koseri* (2/21), and *C. werkmanii* (1/21). Carbapenemases were identified in 14 isolates, including KPC (n = 12), NDM (n = 2), and OXA-48 (n = 1) (Table 2). Isolates were frequently susceptible to ceftazidime-avibactam (MIC median [IQR]: 2[0.5,8]) 81%) and meropenem-vaborbactam (86%) (MIC median [IQR] 0.12[0.3,0.5]) (Table 2).

Conclusion. CNSC species are diverse, have emerged as an HA pathogen at our center, and cause high rates of mortality. Further studies, including ongoing genome sequencing and analysis, are required to better elucidate CNSC diversity and resistance mechanisms.

Figure 1: Rates of CNSC and Carbapenem Consumption from 2000-2018



ceptible isolates/total isolates tested) between 2000-2016. Trends evaluated by linear

Isolate ID	Age	Gender	Major Comorbid Conditions	Year	Source	Organism	Culture site	Clinical Infection	Polymicrobial culture (Y/N)	Other orgs	Outcome of hospitalizatio
RS-102	74	ŧ	ESLD, liver transplant	2018	HA	C. freundi	Rectal swab	Colonization	N	N/A	in-hospital death
RS-189	66	F	Diverticulosis	2017	HA	C. freundii	BAL	Pneumonia	N	N/A	Discharge to facility
R5226	56	Ł	Opiate dependency, CHF, HTN	2018	HA	C. freundi	Urine	Colonization	۷	E. coll	In-hospital death
R5236	70	м	Pancreatic cancer, COPD, DM, HTN	2018	HA	C. freundii	Peritoneal fluid	intra- Abdominal	Y	C. freundii (ESBL), E. faecium (VRE) C. tropicalis, C. parapsilasis	Transfer to hospice
RS237	80	F	Sinus OM	2018	Community	C. freundii	Urine	Colonization	N	N/A	Discharge to home
R5240	29	ŧ	Nephrolithiasis obstructive uropathy	2017	Community	C. freundV	Urine	Colonization	۲	5. maltophilia, 5. hemolyticus E. faecalis E. cloocae	Discharge to home
R5259	61	F	Metastatic lung cancer, COPD, DM	2018	HA	C. freundii	Peritoneal fluid	Intra- Abdominal	Ŷ	E. coli; P. aeruginosa	in-hospital death
R5289	92	м	Bladder cancer, dementia, CKD, COPD, CHF	2018	Community	C. koseri	Urine	UTI	¥	E. faecala	Discharge to home
R\$77	49	м	ESLD, liver transplant	2018	HA	C. freundi	Rectal swab	Colonization	N	N/A	Discharge to home
YDC582	54	м	ESLD, HCC	2012	HA	C. freundii	Abdominal drain	Intra- Abdominal	Y	E. aerogenes	in-hospital death
YDC608	57	м	HLD	2013	HA	C. freundV	BAL	Colonization	N	N/A	Transfer to hospice
YDC638-2	27	м	ESLD, Crohn's diseases, PSC, liver transplant	2013	HA	C. freundii	Billary drainage	intra- Abdominal	Ŷ	E. faecium (VRE)	Discharge to home
YDC645	67	F	CAD, CHF, DM, ESRD, dementia	2013	HA	C. freundi	Blood	SSTI/ Bacteremia/ Endocarditis	Y	Bacteroides, E. roffinosis	Transfer to hospice
YDC661	64	м	Heart transplant	2014	на	C. freundi	BAL	Pneumonia	۷	5. maitophilia	Discharge to facility
YDC667-1	73	м	CHF, DM, CAD, CKD	2014	HA	C. freundii	BAL	Pneumonia	Y	K. proemonioe (ESBL)	In-hospital death
YDC689-2	61	м	ESLD, liver transplant	2015	HA	C. koseri	BAL.	Pneumonia	N	N/A	Discharge to facility
YDC693*	65	м	SBT, adrenal insufficiency	2015	HA	C. freundii	BAL	Pneumonia	Y	ESBL E. coli	In-hospital death
YDC693-2*	65	м	SBT, adrenal insufficiency	2015	HA	C. freundi	BAL	Pneumonia	Ŷ	ESBL E. coll	in-hospital death
YDC697-2*	65	м	SBT, adrenal insufficiency	2015	HA	C. formeri	Tracheosto my site drainage	SSTI	¥	K. oxytoce (KPC)	in-hospital death
YDC730	71	м	Multiple myeloma	2015	HA	C. werkmani	Pelvic abscess fluid	Intra- Abdominal	۷	E. foecium (VRE)	Discharge ho
YDC849-1	26	F	CVID	2018	HA	C. freundi	Urine	UTI	Y	C. freundii (NDM)	in-hospital death
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Poster Abstracts • OFID 2019:6 (Suppl 2) • S237