(FEP), ceftazidime (CAZ) and piperacillin-tazobactam (TZP). Outcomes of patients with CRPA susceptible to FEP, CAZ and TZP are unclear.

Methods. The Georgia Emerging Infections Programed performs active, population-based surveillance for CRPA (minimum inhibitory concentration [MIC] ≥ 8 μg/mL for doripenem, imipenem or meropenem) isolated from sterile sites, urine, lower respiratory tracts and wounds in metropolitan Atlanta. We created a retrospective cohort of adults without cystic fibrosis with their first episode of CRPA while hospitalized or hospitalized within 1 week, from 8/2016 – 7/2018. We compared patients with CRPA that remained susceptible to FEP, CAZ and TZP ("susceptible CRPA") to those that were not ("resistant CRPA") including multivariable logistic regression for 30-day mortality.

Results. Among 643 patients, 638 had susceptibility results available for FEP, CAZ or TZP. 60% were male, median age was 65 years, and median Charlson comorbidity index was 2 (Table 1). Most (66%) resided in a hospital or long-term care facility 4 days prior to culture. The most common source was urine (38%). Non-susceptibility to multiple antibiotic classes was common: 523 (81%) for 3 classes and 214 (33%) for 5 classes (Table 2). 220 (34%) patients had susceptible CRPA and compared to patients with resistant CRPA, were more likely to have lived in a private residence, have a community-associated infection, and less likely to be in the ICU previously (Table 1). Patients with susceptible CRPA had a similar crude 30-day mortality (16% vs 12%, p = 0.15) to those with resistant CRPA, but in a multivariable analysis had an increased 30-day mortality (OR 1.9; 95% CI 1.1–3.2).

Table 1 (Part 1/2): Characteristics and outcomes of hospitalized patients with carbapenem-resistant Pseudomonas aeruginosa (CRPA) in metropolitan Atlanta, stratified by antipseudomonal β-lactam susceptibility

Table 1: Characteristics and outcomes of hospitalized patients with carbapenem-resistant *Pseudomonas aeruginosa* (CRPA) in metropolitan Atlanta, stratified by antipseudomonal β-lactam susceptibility

	All CRPA (n = 638)[1]	Susceptible CRPA[2] (n = 220)	Resistant CRPA[3] (n = 418)	P-value[4]
Age category (years)				0.09
19 – 49	125 (20)	37 (17)	88 (21)	
50 – 64	187 (29)	64 (29)	123 (29)	
65 – 79	231 (36)	76 (35)	155 (37)	
>79	95 (15)	43 (20)	52 (12)	
Male (n = 637)	385 (60)	127 (58)	258 (62)	0.36
Race				0.01
Black	335 (56)	98 (48)	237 (60)	
White	249 (42)	101 (49)	148 (38)	
Multiracial, other or unknown	54 (8)	21 (10)	33 (8)	
Charlson comorbidity index > 2	310 (49)	99 (45)	211 (50)	0.19
Residence 4 days prior to culture				<0.01
Inpatient	279 (44)	81 (37)	198 (47)	
Long-term facility (LTCF or LTACH)	145 (23)	42 (19)	103 (25)	
Private residence	214 (34)	97 (44)	117 (28)	
Epidemiologic class[5]				<0.01
Community associated	20 (3)	11 (5)	9 (2)	
Healthcare associated, community onset	332 (52)	128 (58)	204 (48)	
Hospital onset	286 (45)	81 (37)	205 (49)	
ICU in 7 days prior to culture	203 (32)	51 (23)	152 (36)	<0.01
Culture source				
Sterile site	52 (8)	17 (8)	35 (8)	0.09
Lower respiratory tract	226 (35)	64 (29)	162 (39)	
Urine	243 (38)	94 (43)	149 (36)	
Wound	117 (18)	45 (20)	72 (17)	
Location where culture was collected				0.14
Outpatient or ER	134 (21)	50 (22)	84 (20)	
Hospital inpatient (excluding ICU)	278 (44)	105 (48)	173 (41)	
ICU	209 (33)	59 (27)	150 (36)	
Long-term facility (LTCF or LTACH)	17 (3)	6 (3)	11 (3)	
Outcome at 30 days:				
Death	87 (14)	36 (16)	51 (12)	0.15
Alive and remained hospitalized	95 (15)	22 (10)	73 (17)	0.01
Alive and discharged to:	456 (71)	162 (74)	294 (70)	0.11
LTACH	58 (13)	21 (13)	37 (13)	
LTCF	145 (32)	41 (25)	104 (35)	
Private residence	233 (51)	94 (58)	139 (47)	
Other or Unknown	20 (4)	6 (4)	14 (5)	

Table 1 (Part 2/2): Characteristics and outcomes of hospitalized patients with carbapenem-resistant Pseudomonas aeruginosa (CRPA) in metropolitan Atlanta, stratified by antipseudomonal β-lactam susceptibility

Table 1 (continued)

All values are presented as number (%) unless otherwise stated

1. Had susceptibility results available for cefepime, ceftazidime or piperacillin-tazobactam
2. Susceptible to cefepime, ceftazidime and piperacillin-tazobactam (if tested)
3. Resistant to at least one of: cefepime, ceftazidime, and piperacillin-tazobactam
4. Compared susceptible versus resistant CRPA with Chi-square or Fisher's exact test as appropriate
5. Hospital onset is defined as the incident culture being obtained after hospital day 3; Healthcare associated, community onset is defined as not meeting criteria for hospital onset but having at least one of the following risk factors: Hospitalization, surgery, residence in LTCF or LTACH within the last year, chronic dialysis, or presence of a urinary catheter, central venous catheter or other indwelling device at the time of culture or within the 2 prior calendar days. Community onset is defined as not meeting criteria for hospital onset or healthcare associated, community onset

Abbreviations: CRPA, carbapenem-resistant *Pseudomonas aeruginosa*; LTCF, long term care facility; LTACH, long term acute care hospital; ICU, intensive care unit

Table 2: Antibacterial susceptibility results for hospitalized patients with carbapenem-resistant Pseudomonas aeruginosa in metropolitan Atlanta

Table 2: Antibacterial susceptibility results for hospitalized patients with carbapenem-resistant *Pseudomonas aeruginosa* in metropolitan Atlanta

Antibiotic (n = number tested)	Number susceptible (%)[1]
Amikacin (n = 543)	467 (86)
Gentamicin (n = 635)	373 (59)
Tobramycin (n = 610)	428 (70)
Ciprofloxacin (n = 555)	61 (11)
Levofloxacin (n = 496)	41 (8)
Cefepime (n = 623)	318 (51)
Ceftazidime (n = 570)	327 (57)
Piperacillin-tazobactam (n = 572)	264 (46)
Ceftazidime-avibactam (n = 38)	28 (74)
Ceftolozane-tazobactam (n = 47)	42 (89)
Aztreonam (n = 424)	141 (33)
Colistin (n = 85)[2]	66 (78)
Polymyxin B (n = 60)[2]	55 (92)
Meropenem (n = 598)	25 (4)
Doripenem (n = 66)	10 (15)
Imipenem (n = 296)	3 (1)

1. Antibiotic susceptibility was determined by automated testing instruments or through chart review. An isolate was non-susceptible if the MIC exceeded the Clinical and Laboratory Standards Institute 2020 susceptible breakpoint on any testing modality.
2. Based off medical record documentation or E-test only

Conclusion. Over 1/3 of hospitalized patients with CRPA retained susceptibility to other antipseudomonal β-lactams, but had an increased mortality compared to CRPA resistant to other β-lactams. Further research into mechanisms of resistance or antibiotics received might help explain this unexpected finding.

Disclosures. **Jessica Howard-Anderson, MD**, **Antibacterial Resistance Leadership Group (ARLG)** (Other Financial or Material Support, The ARLG fellowship provides salary support for ID fellowship and mentored research training)

835. Comparison of the outcomes of patients with KPC and NDM-1-producing *Enterobacteriaceae*

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. Carbapenemase-producing *Enterobacteriaceae* infections are associated with high mortality. We aimed to compare the clinical outcomes of patients with *Klebsiella pneumoniae* carbapenemase (KPC)-producing *Enterobacteriaceae* and those with New-Delhi-Metallo-beta-lactamase-1 (NDM-1)-producing *Enterobacteriaceae*.

Methods. We performed a retrospective cohort study of all adult patients (> 16 years old) with KPC or NDM-1-producing *Enterobacteriaceae* isolates in a 2,700-bed tertiary referral hospital in Seoul, South Korea between 2010 and 2019. Primary outcomes were infection within 30 days and 30-day mortality after the first isolation of KPC or NDM-1-producing *Enterobacteriaceae*.

Results. A total of 859 patients were identified during the study period. Of them, 475 (55%) were KPC group and 384 (45%) were NDM-1 group. KPC group tended to develop infection within 30 days after first isolation more frequently than NDM-1 group (31% vs. 26%; $P = 0.07$). Thirty-day mortality was significantly higher in KPC group compared to NDM-1 group (KPC, 17% (81/475) versus NDM-1, 9% (33/384), $P < 0.001$). Multivariate analysis revealed that APACHE II score (adjusted odds ratio [aOR], 1.12; $P < 0.001$), solid cancer (aOR, 2.56; $P < 0.001$), previous carbapenem therapy (aOR, 1.93; $P = 0.004$), development of infection of KPC or NDM-1-producing *Enterobacteriaceae* within 30 days (aOR, 2.63; $P < 0.001$), and KPC-producing *Enterobacteriaceae* (aOR, 1.62; $P = 0.045$) were independent risk factors for 30-day mortality.

Table 1. Results of analyses of risk factors for 30-day mortality from initial positive culture date in patients with KPC or NDM-1- producing Enterobacteriaceae

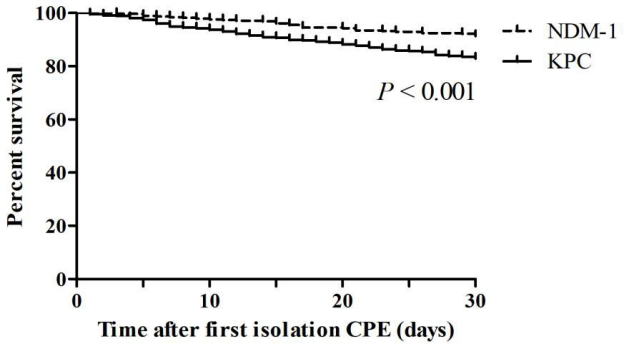
Table 1. Results of analyses of risk factors for 30-day mortality from initial positive culture date in patients with KPC or NDM-1- producing *Enterobacteriaceae*

	Univariate analysis		Multivariate analysis[a]	
Risk factor	**OR (95% CI)**	***P* value**	**Adjusted OR (95% CI)**	***P* value**
Age	1.03 (1.01–1.05)	< 0.001		
Male gender	0.73 (0.47–1.15)	0.17		
Healthcare-associated acquisition	1.04 (0.60–1.78)	0.89		
APACHE II score	1.13 (1.10–1.16)	< 0.001	1.12 (1.09–1.16)	< 0.001
Diabetes mellitus	0.83 (0.54–1.27)	0.39		
End-stage renal disease	1.52 (0.99–2.33)	0.06		
Solid cancer	1.87 (1.26–2.78)	0.002	2.56 (1.62–4.05)	< 0.001
Neutropenia	1.74(0.87–3.49)	0.12		
Indwelling device	1.73 (0.99–3.02)	0.054		
Previous carbapenem use within 3 months	2.56 (1.72–3.82)	< 0.001	1.93 (1.24–3.00)	0.004
Carbapenemase type (KPC)	2.19 (1.42–3.36)	< 0.001	1.62 (1.01–2.60)	0.045
Development of KPC or NDM-1-producing *Enterobacteriaceae* infection within 30 days	2.48 (1.62–3.81)	< 0.001	2.63 (1.69–4.10)	< 0.001

Abbreviations: CI, confidence interval; APACHE II, Acute Physiology and Chronic Health Evaluation II; KPC, *Klebsiella pneumoniae* carbapenemase; NDM-1, New-Delhi-Metallo-beta-lactamase-1

[a] Potential confounders identified to include in the multivariate analysis were age, male gender, APACHE II score, end-stage renal disease, solid cancer, neutropenia, indwelling device, previous carbapenem use within 3 months, development of KPC or NDM-1-producing *Enterobacteriaceae* infection within 30 days and carbapenemase type.

Figure 1. Kaplan–Meier survival estimates of patients with KPC or NDM-1-producing Enterobacteriaceae for 30-day mortality after first isolation: KPC (continuous line) versus NDM (dotted line). (log-rank test).



Conclusion. Our study suggests that KPC-producing *Enterobacteriaceae* is associated with poorer outcome compared to NDM-1-producing *Enterobacteriaceae*. Therefore, patients with KPC-producing *Enterobacteriaceae* colonization should be monitored carefully for development of infection, and appropriate antibiotics should be initiated as soon as possible.

Disclosures. **All Authors**: No reported disclosures

836. Complete genome sequencing reveals a melting pot of diverse *Klebsiella pneumoniae* pathogens in two Detroit hospitals

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. Klebsiella pneumoniae is one of the leading causes of healthcare-associated infections. Treatment of Klebsiella pneumonia is difficult due to the antibiotic resistance and high survival on environmental surfaces. Whole genome sequencing analysis of Klebsiella pneumoniae clinical isolates were performed to study the transmission of Klebsiella pneumonia in hospital settings.

Figure 1. Minimum spanning tree (MST) of wgMLST profiles of Klebsiella pneumoniae sequence types found in the two hospitals. Branch lengths reflect the number of allele differences between the isolates in the connected nodes

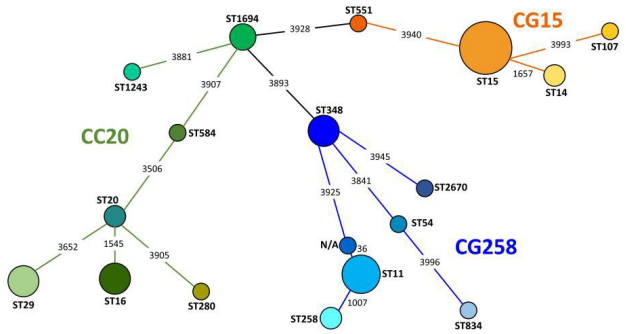
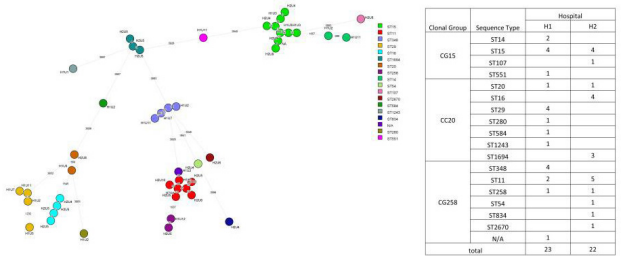


Figure 2. Minimum spanning tree (MST) of wgMLST profiles of Klebsiella pneumoniae isolates. Node labels indicate patients' hospital unit.



Clonal Group	Sequence Type	Hospital H1	Hospital H2
CG15	ST14	2	
	ST15	4	4
	ST107		1
	ST551	1	
CC20	ST20	1	1
	ST16		4
	ST29	4	
	ST280	1	
	ST584	1	
	ST1243	1	
	ST1694		3
CG258	ST348	4	
	ST11	2	5
	ST258	1	1
	ST54		1
	ST834		1
	ST2670		1
	N/A	1	
total		23	22

Methods. Clinical bacterial isolates from patients admitted to two disparate, geographically distinct tertiary care hospitals (H1, H2) in Detroit, Michigan, after 48 hours of admission from 2017- 2019 were collected and sequenced. Whole genome multilocus sequence typing (wgMLST) analysis was performed using Illumina NextSeq platform. De novo assembly of the contigs was performed using SPAdes assembler. WgMLST (assembly-free and assembly-based calls) was performed using calculation engine on the Bionumerics v7.6 platform. Minimum spanning tree with the isolates was constructed and arranged by their MLST Pasteur serotype and hospital/ward of the patient isolate collection.

Results. Total 17 different MLST Pasteur serotypes were observed from WgMLST analyzation of forty-five Klebsiella pneumoniae clinical patient isolates. All the Klebsiella pneumoniae isolates of HAI obtained from two hospitals were genetically distinct. As shown in Figure 1, there were three distinct clusters on the minimum spanning tree. Out of 17 STs, 4 were present in both hospitals. Though there was no predominant ST type, ST15 and ST11 were the most frequent isotypes (18% each). Both ST15 and ST11 were evenly spread across both hospitals, but the pattern was different. While ST15 was predominantly found in two units (H1U3 and H2U4), ST11 was found in multiple units. ST348 and ST29 were predominantly found in H1, whereas ST16 was found in H2.

Conclusion. Majority of Klebsiella pneumoniae infection is sporadic and there was no evidence of hospital spread. The WgMLST analysis showed the isolates distributed across the phylogeny of Klebsiella with diverse serotypes from the three main diverse evolutionary origin. Our study showed that the global spread of various serotypes of Klebsiella pneumoniae has already reached a significant level in these two Detroit hospitals possibly the catchment area.

Disclosures. **Chetan Jinadatha, MD, MPH**, **AHRQ** (Research Grant or Support)**Department of Veterans Affairs** (Other Financial or Material Support, Owner: Department of Veterans Affairs. Licensed to: Xenex Disinfection System, San Antonio, TX)**Inventor** (Other Financial or Material Support, Methods for organizing the disinfection of one or more items contaminated with biological agents)**NiH/NINR** (Research Grant or Support)**NSF** (Research Grant or Support)**Xenex Healthcare Services** (Research Grant or Support) **Mark Stibich, PhD MHS**, **Xenex Disinfection Services, Inc** (Board Member, Employee)

837. Contamination of Hospital Drains by Carbapenemase-Producing Enterobacterales (CPE) in Ontario, Canada

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Session: P-36. HAI: Gram-negatives (MDR-GNR)

Background. The hospital water environment is a CPE reservoir, and transmission of CPE from drains to patients is a risk.

Methods. We cultured sink and shower drains in patient rooms and communal shower rooms that were exposed to inpatients with CPE colonization/infection from October 2007 to December 2017 at 10 hospitals. We compared patient room drain CPE to prior room occupant CPE using Illumina and MinION whole-genome sequencing.

Results. Three-hundred and ten inpatients exposed 1,209 drains, of which 53 (4%) yielded 62 CPE isolates at 7 (70%) hospitals. Compared to room occupant CPE isolates, drain CPE isolates were more likely *Enterobacter* spp. (6, 10% vs. 25, 51%, p< 0.0001) or KPC-producers (9, 15% vs. 23, 47%, p=0.0002). Of the 49 CPE isolates in patient room drains, 4 (8%) were linked to a prior room occupant (Table), 24 (49%) had the same carbapenemase as a prior room occupant but isolates/carbapenemase gene-containing plasmids that were unrelated, and 21 (43%) did not share a carbapenemase with a prior room occupant. The 4 drains linked to prior room occupants were likely contaminated by these room occupants, who were CPE-colonized prior to drain exposure. Despite few links between drain and room occupant CPE, there were 10 isolates harbouring related bla_{NDM-1}-containing IncHI2A/HI2-type plasmids in 8 rooms on two units at one hospital. Nine of these were *Enterobacter hormaechei* ST66 isolates that were 0 to 6 SNVs apart and one was a *Klebsiella oxytoca* STnovel isolate.