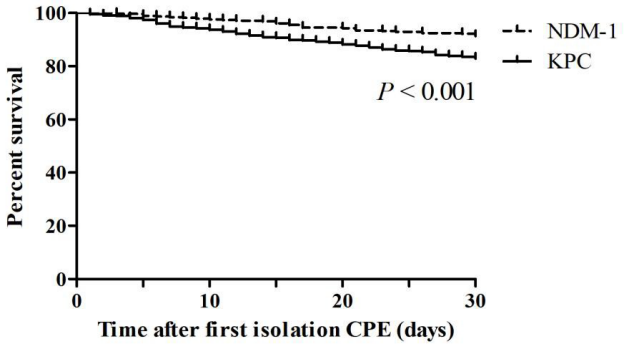
Figure 1. Kaplan–Meier survival estimates of patients with KPC or NDM-1-producing Enterobacteriaceae for 30-day mortality after first isolation: KPC (continuous line) versus NDM (dotted line). (log-rank test).



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

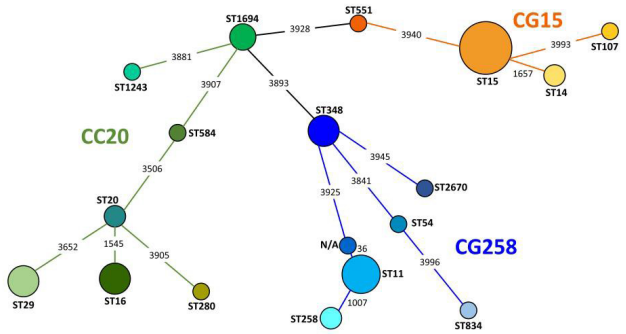
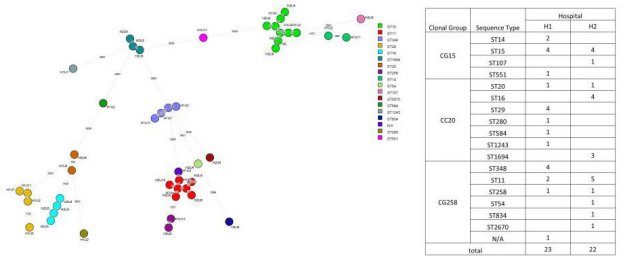


Figure 2. Minimum spanning tree (MST) of wgMLST profiles of Klebsiella pneumoniae isolates. Node labels indicate patients' hospital unit.



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.

Table. Four patient room drain CPE isolates (D1b, D4, D5, D12) and isolates from prior room occupants that they were related to by whole-genome sequencing.

Isolate ID[a]	Species and sequence type (ST)	Carbapenemase	Replicon type	Plasmid size (bp)	Percent coverage and identity of plasmids[b]	Time from room occupant CPE detection to drain sample (months)
D1b	*K. oxytoca* ST180	KPC-3	IncN3	53262	100% coverage	8
R1a	*C. freundii* STnovel	KPC-2	IncN3	64155	>99% identity	
R1b	*E. coli* ST69	KPC-2	IncN3	64157		
D4	*E. roggenkampii* ST41	KPC-3	IncN	58785	>99% coverage	9
R3	*K. pneumoniae* ST34	KPC-3	IncN	59316	>99% identity	
D5	*C. freundii* ST18[c]	KPC-2	IncFII	89208	>98% coverage	4
R4	*C. freundii* ST18[c]	KPC-2	IncFII	87520	>99% identity	
D12	*K. oxytoca* ST176	OXA-48	IncL/M	63589	>99% coverage	15
R11	*K. pneumoniae* ST147	OXA-48	IncL/M	63544	>99% identity	
R12	*K. pneumoniae* ST147	OXA-48	IncL/M	63544		

[a]D=Drain, R=Room Occupant. Each drain and room occupant is denoted by a number, and the letter following the number represents each unique isolate from that drain or room occupant. For example, room occupant R1 has two isolates, denoted R1a and R1b.
[b]Drain isolate carbapenemase gene-containing plasmid used as reference.
[c]Separated by 8 single nucleotide variants.

Conclusion. It was uncommon for drain CPE to be linked to prior patient exposure. This suggests contamination of most drains by undetected colonized patients and a need for more aggressive patient screening in our hospitals. This may also suggest retrograde (drain-to-drain) transmission, especially considering the 10 isolate drain cluster at one hospital. Reasons for the preponderance of *Enterobacter spp.* in drains requires further study.

Disclosures. **Allison McGeer, MD, FRCPC**, **GlaxoSmithKline** (Advisor or Review Panel member, Research Grant or Support)**Merck** (Advisor or Review Panel member, Research Grant or Support)**Pfizer** (Research Grant or Support)

838. Drivers of empiric carbapenem use: How important is history of extended-spectrum beta-lactamase (ESBL) infection?

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

Background. CARs are first line agents for serious infections caused by ESBL producers. Likelihood of developing subsequent ESBL infection is unknown. In patients (pts) with a history (hx) of ESBL positive (ESBLP) culture, empiric therapy with a CAR has become common in hospitals. The purpose of this study was to evaluate the microbiology of subsequent infections (SI) among pts with hx of ESBLP culture and determine risk factors associated with ESBLP SI that may justify an empiric CAR.

Methods. This retrospective observational study was conducted at a multicenter health system. The electronic medical record (EMR) was used to generate a report of all *E. coli* (EC) or *K. pneumoniae* (KP) ESBLP cultures during 2017, an analogous report was generated for ESBL-negative (ESBLN) EC or KP. These were termed index cultures (IC). Pts were randomly selected from each report until 200 total pts were enrolled. Inpatients, outpatients, and all culture specimens were included. Pts with an ESBLP culture prior to 2017 were excluded. The EMR was reviewed up to 1 year after the IC. Pt and culture characteristics were recorded. The primary outcome was proportion of pts who developed an ESBLP SI. Risk factors associated with ESBLP SI were determined. Relapsed infection (same site, same bacteria) that occurred within 2 weeks of the IC was excluded.

Results. 200 pts were included, 100 with ESBLP IC and 100 with ESBLN IC. The mean age was 58 years, 84% were female, and 69% were outpatients. 86% of IC were EC and 86% were urine specimens. Within 1 year of IC, 100 pts (50%) developed a SI. 22 of these were ESBLP, 43 were ESBLN, and 35 had no or negative culture. The mean time since IC for ESBLP SI and ESBLN SI was 85 (26-226) days and 140 (15-363) days, respectively (p=0.014). When comparing time to SI, 21 (96%) ESBLP and 26 (61%) ESBLN occurred < 6 months after IC (p=0.003). Among SI with culture data (n= 65), the number of ESBLP SI was higher if the IC was ESBLP (22 vs 0, p< 0.001). Incidence of ESBLP or ESBLN SI in all pts with an ESBLP IC was similar (22 vs 18, p=0.428). Factors associated with ESBLP SI were hx of ESBLP IC, male gender, and time between IC and SI.

Table 1. Index Culture Characteristics of Culture Positive Subsequent Infections

Index Culture	Culture Positive Subsequent Infections	
	ESBL-positive (n=22)	ESBL-negative (n=43)
ESBL-positive (n=100)	22 (100)	18 (42)
ESBL-negative (n=100)	0 (0)	25 (58)

Data presented as n (%)

Figure 1. Cumulative rate of ESBL-positive SI in 180 days (6 months) following IC

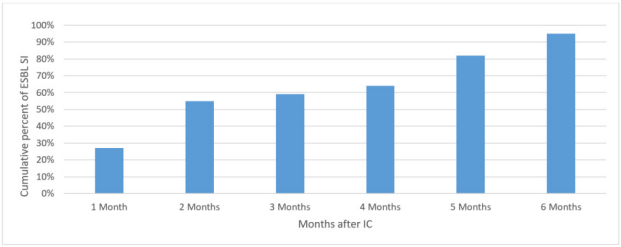

Table 2. Univariate Analysis of Patient Characteristics Comparing ESBL-positive and ESBL-negative Culture Positive Subsequent Infections

Factor	Culture Positive SI		*p*-value
	ESBLP (n=22)	ESBLN (n=43)	
Age, years, mean (SD)	67	60	0.091
Male	7 (32)	3 (7)	0.009
Immunocompromised	0 (0)	3 (7)	0.700
Charlson Comorbidity Index Score, mean (SD)	3.5 (3.12)	2.58 (2.36)	0.098
History of ESBLP IC	22 (100)	18 (42)	<0.001
Days between IC and SI, mean (SD)	85 (64.6)	140 (103.9)	0.014
Antibiotics received in previous 90d	17 (77)	25 (58)	0.127

Data presented as n (%) unless indicated otherwise

Conclusion. Hx of positive culture for ESBL-producing EC or KP is associated with SI caused by ESBLP EC or KP. Pts presenting < 6 months after ESBLP IC are at increased risk for ESBLP SI, justifying empiric CAR therapy.

Disclosures. **Tyler J. Stone, PharmD**, **Paratek** (Research Grant or Support) **Elizabeth Palavecino, MD**, **Paratek** (Grant/Research Support)**Paratek** (Grant/Research Support) **John Williamson, PharmD**, **Paratek** (Research Grant or Support)

839. Epidemiology of Extended-Spectrum Beta-lactamase (ESBL) Producing Enterobacteriaceae in the South East Tennessee, October-December 2017

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

Background. The increasing spread of drug resistant gram-negative organisms is one of the major public health challenges. ESBL-producing Enterobacteriaceae has become the most common multi drug resistant pathogen in the last three decades. These organisms confer resistance to most beta-lactam antibiotics, including penicillins, third generation cephalosporins, monobactams and tazobactam.

Methods. The Tennessee Health Department (TDH) collaborated with CDC to pilot population based surveillance of ESBL producing organisms in Maury, Wayne, Lewis and Marshall Counties during October to December 2017. A case was defined as isolation of *Escherichia coli, Klebsiella pneumoniae,* or *Klebsiella oxytoca* resistant to at least one extended-spectrum cephalosporin (ceftazidime, cefotaxime or ceftriaxone) and non-resistant to all carbapenem antibiotics from urine or normally sterile body sites from a resident of the surveillance catchment area. A line list of ESBL-producing organisms was received from the labs that serve the catchment population. Case report forms were completed for the first ESBL culture collected from a single patient in a 30 day-period.

Results. A total of 154 cases were identified during the study period. *E.coli* constitutes 92.2% of the ESBL producing organisms followed by *Klebsiella pneumonia* (5.2%) *and K. oxytoca* (2.6%). The estimated annual incidence rate was 400.7 per 100,000 population which is more than twice of the average rates of other sites that conducted similar studies. The most common isolate source was urine (97%), and 81.2% of all cases were female. Patient ages ranged from 3-99 years, with average of 67 years. Thirty-two isolates underwent additional sequence typing and 76.7% (23) of the isolates were ST 131. 21 (91.3%) of ST-131 isolates were resistant to ciprofloxacin.

Conclusion. The study revealed that the incidence of ESBL producing organisms is very high in the Tennessee study area compared to other sites. The most common ESBL-producing pathogen was found to be ST 131 and most of these were resistant to ciprofloxacin suggesting that resistance to fluoroquinolone may be co-transmitted in ESBL producing pathogens through plasmids. Continued surveillance of molecular epidemiology is important to guide the prevention of the spread of drug resistant pathogens.

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