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.

Figure 1. Number of patients with *Stenotrophomonas maltophilia* bacteremia vs. other sites between January 2010-August 2018.

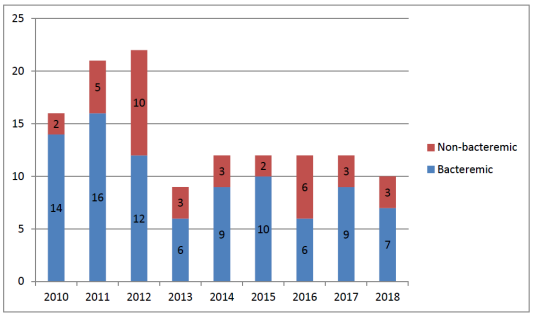

Table 1: Variables

	Died	Survived	Odds Ratio	Confidence Interval	*p* value
Definitive Therapy	19 (23)	64 (77)	0.37	0.14 – 0.89	0.03
Appropriate Empiric Therapy	34 (74)	12 (26)	0.79	0.34 – 1.84	0.67
Bacteremia	18 (23)	61 (77)	0.40	0.17 – 0.96	0.04

Table 2. Length of Stay and Readmission

	Number of patients (%)	Median Days (Interquartile Ranges)
Length of Stay	-	16 (6-30)
ICU Admission and Length of Stay	61 (48%)	10 (3-23)
Length of Stay to Isolation	-	2 (0-11)
30 Day Readmission	21 (18%)	-

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

489. Risk Factors for Mortality in Patients with *Elizabethkingia* and Clinical Impact of Antimicrobial Susceptibility Patterns

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

Background. *Elizabethkingia* spp. is a non-fermenting, non-motile, oxidase-positive gram-negative aerobic bacilli that is ubiquitous in the environment, found in freshwater, saltwater and soil. Nowadays, they are emerging as nosocomial pathogens. In this study, we analyzed *Elizabethkingia* spp infected cases clinically and microbiologically.

Methods. This study was performed to evaluate the risk factors for mortality and to study the impact of microbiologic response on clinical outcomes in patient with *Elizabethkingia* spp Data on 210 patient of *Elizabethkingia* pneumonia and bacteremia that have occurred between November 1, 2005, and May 31, 2016, in a teaching hospital (2000 beds) in Seoul, Korea, were analyzed. Furthermore, antimicrobial susceptibility testing of *Elizabethkingia* from sputum and blood cultures was performed by E test for rifampin, moxifloxacin and vancomycin.

Results. Among 210 patients, there were 157(74.8%) survivor and 53(25.2%) non-survivor. Among these patients, 129 patients (61.4%) were male and the median age was 66.5 years. There were no significant differences in the Charlson comorbidity index between survivor and non-survivor groups ($P = 0.413$). In the multivariate logistic regression, microbiologic failure (odds ratio [OR], 7.862; 95% confidence interval [CI], 3.448–17.931; *p*Elizabethkingia infection (OR, 1.032; 95% CI, 1.013–1.051; $P = 0.001$), previous use of immunosuppressants (OR, 3.309; 95% CI, 1.334–8.210; $P = 0.010$), and Percutaneous cardiopulmonary support system use at the time of *Elizabethkingia* infection (OR, 7.439; 95% CI,1.180–46.900; $P = 0.033$) were significantly associated with 28day mortality. Patients with moxifloxacin-resistant and vancomycin-resistant showed higher mortality rate but no statistically significant difference.

Conclusion. The early identification of these clinical factors in patients with *Elizabethkingia* infection is important to improve prognosis

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

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

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Session: 54. HAI: MDRO – GNR Epidemiology, CRE
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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 clonality 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 but 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.

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

491. Working Together: A Tale of Carbapenemase-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_{KPC} 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.

Results. NYSDOH identified three nursing home residents infected with CPO with novel carbapenemase genes (Figure 1) with no travel history but multiple co-morbidities, including mechanical ventilation: bla_{OXA-48} *Klebsiella pneumoniae* (KP) (Facility A), bla_{NDM} KP (Facility B and C). Epi investigations identified CPO in 48 of 106 residents screened for rectal colonization; most isolates had genes 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_{KPC} gene. WGS analysis identified 2 clusters of bla_{KPC} 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 interrupt transmission at Facility C, where 24 residents were colonized with CPO, including 7 residents with CPO with the index gene (bla_{NDM}), and a subset of the bla_{NDM} 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.

Figure 1- Summary of Characteristics of 3 Carbapenemase-Producing Organism (CPO) Investigations in NY, November 2018–March 2019

Index Case Gene and Organism	Age/ Sex of Patient with Infection	International Travel	Index patient on contact precautions?	Number of Point Prevalence Surveys to Screen Residents	Number of Residents Screened	Number of Residents Colonized with any CPO	Additional Residents Identified with Index Gene	PH/IC Assessment Recommendations	Clusters identified by Whole-Genome Sequence Analysis (Number of Clusters)	Gene Types for Clusters Identified
bla_{OXA-48} *Klebsiella pneumoniae*	72 male	No	No	1	37	14	No	-I/C/CP	Yes (2)	bla_{KPC}
bla_{NDM} *K. pneumoniae*	74 female	No	No	1	18	10	No	-I/C/CP	No	
bla_{KPC} *K. pneumoniae*	90 male	No	No	5	51	24	Yes	-I/C/CP -Enhancements to respiratory therapy & consulting provider IC over 5 serial IC visits	Yes (1)	bla_{NDM}
Totals				7	106	48*			Yes (3)	

* Some residents > 1 mechanism
PH=Public Health
IC= Infection Control
I/C/CP= Isolation, Cohorting and Contact precautions

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