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.

**Table 1.**

| Variables | Mean (SD) | Median (IQR) | p value |
|-----------|-----------|--------------|---------|
| Definitive Therapy | 61.47 (11.71) | 61.00 (58.00) | 0.04 |
| Appropriate Empirical Therapy | 56.12 (11.00) | 56.00 (54.00) | 0.02 |
| Bacteremia | 59.33 (11.47) | 58.00 (57.00) | 0.02 |

**Table 2. Length of Stay and Readmission**

| Number of patients (%) | Median (IQR) | p value |
|------------------------|--------------|---------|
| Length of Stay          | 18 (6-30)    | 0.71    |
| Length of Stay to Isolation | 14 (8-23) | 0.03 |
| 30 Day Readmission      | 21 (18-24)   | 0.01    |

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

### 498. 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

**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, 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 group (P=0.413). In the multivariate logistic regression, microbiologic failure (odds ratio [OR], 7.862; 95% confidence interval [CI], 3.448–17.931; p=0.001), previous use of immunosuppressants (OR, 3.309; 95% CI, 1.334–8.210; P=0.010), and Perioperative cardopulmonary 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.

### 499. 40. HAI: MDRO – GNR Epidemiology, Other

**Background.** Carabepenemases are diverse enzymes which inactivate the carbapenems. KPC-producing carabepenemase-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 & KPC producing 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 carabepemase production were characterized by PCR and cloning 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 bla*KPC* (58.3%), followed by bla*OXA*-48 (25%), bla*NDM* (5.6%) and bla*VIM* (2.8%). Carabepenemases were co-produced with ESBL 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 findings demonstrate 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 Carabepenemase-Producing Organism Investigations in Three New York City Nursing Homes**

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**Session:** 54. HAI: MDRO – GNR Epidemiology, CRE

**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 carabepenemase-producing organisms (CPO). Three investigations from November 2018-March 2019 illustrate the findings and challenges investigating CPO in a *KPC*-endemic setting.

**Methods.** NYSDOH WC testing includes organism identification, drug susceptibility testing, detection of carabepenemase production, detection of carabepenemase 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 nursing home residents infected with CPO with novel carabepenemase genes (Figure 1) with no travel history but multiple co-morbidities, including mechanical ventilation: *bla*isl-K. *Klebsiella pneumoniae* (KP) (Facility A), *bla*isl-KP (Facility B and C). Epi investigations identified CPO in 48 of 106 residents screened for rectal colonization; most *K. pneumoniae* infections were *KPC*-producing. Colonized Facility A and Facility B each had no additional residents colonized with CPO with the index gene after screening; 13 and 11 residents, respectively from Facility A and B, had CPO with endemic *bla*isl-K. WGS analysis identified 2 clusters of *bla*isl-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*isl-K); a subset of the *bla*isl-K 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.