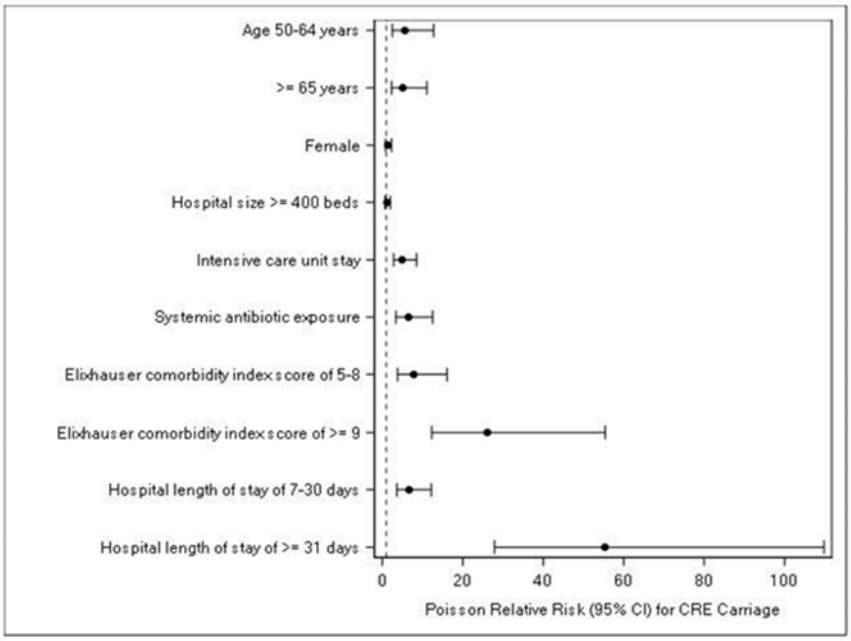
Figure. Carbapenem-resistant Enterobacteriaceae (CRE) carriage risk (95% CI) according to select variables among patients admitted during July 1, 2016-June 30, 2017 to any of seven short-term acute care hospitals of a regional healthcare network in North Carolina (N=118,022 admissions)



Note[1]: Age - reference category is 0-49 years

Note[2]: Intensive care unit stay - current Procedural Terminology code of 99291 or 99292

Note[3]: Systemic antibiotic exposure - ≥ 1 dose of any systemic antibiotic(s) during admission

Note[4]: Elixhauser comorbidity index score - International Classification of Diseases, Tenth Revision, Clinical Modification codes were mapped to comorbid components of the Elixhauser Comorbidity Index, each operationalized as a binary variable. Each admission's total Elixhauser Comorbidity Index score could range from 0-30. Reference: 0-4

Note[5]: Hospital length of stay - reference category is 0-6 days

Fig. 1.

intensive care unit stay had CRE carriage risk 6.5 times (95% CI, 3.4–12.5) and 4.9 times (95% CI, 2.8–8.5) higher, respectively, than patients without these exposures (Fig. 1). Patients ≥50 years of age and those with a higher Elixhauser comorbidity index score and with longer length of stay also had increased CRE carriage risk. **Conclusions:** Among admissions in our dataset, CRE carriage risk was associated with systemic antibiotic exposure, intensive care unit stay, higher Elixhauser comorbidity index score, and longer length of stay. We will use these risk estimates in the ABM to inform agents' CRE carriage status upon hospital admission and the CRE transmission parameters for short-term acute-care hospitals. We will explore CRE transmission interventions in the parameterized regional healthcare network ABM and assess the impact of CRE carriage underestimation.

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Disclosures: None

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Presentation Type:
Poster Presentation

Carbapenemase Gene Profiles in Carbapenem-Resistant Enterobacteriaceae—United States, January 2018–August 2019

Jennifer Huang, Centers for Disease Control; Amanda Pettinger, Oak Ridge Institute for Science and Education (ORISE); Katie Bantle, Oak Ridge Institute for Science and Education (ORISE); Amelia Bhatnagar, Goldbelt C6, Juneau, AK; Sarah Gilbert, Goldbelt C6, Juneau, AK; Sarah Malik, Centers for Disease Control and Prevention; Allison Brown

Background: Carbapenem-resistant Enterobacteriaceae (CRE) cause significant morbidity and mortality each year in the United States. Treatment options for these infections are often limited, in part due to carbapenemases, which are mobile β-lactam-hydrolyzing enzymes that confer multidrug resistance in CRE. As part of the CDC's Containment Strategy for Emerging Resistance, public health laboratories (PHLs) in the CDC Antibiotic Resistance Laboratory Network (AR Lab Network) have worked to characterize clinical isolates of CRE for rapid identification of carbapenemase genes. These data are then used by public health and healthcare partners to promote patient safety by decreasing the spread of resistance. We summarize carbapenemase gene profiles in CRE, by genus and geography, using data collected through the AR Lab Network from January 2018 through August 2019. **Methods:** CRE isolates were submitted to 55 PHLs, including those of all 50 states, 4 large cities, and Puerto Rico, in accordance with each jurisdiction's reporting laws. PHLs performed phenotypic and molecular testing on isolates to detect targeted, emerging carbapenemase genes and reported results to submitters. Carbapenemase-positive (CP) isolates were defined as PCR positive for ≥1 carbapenemase gene tested: *bla*KPC, *bla*NDM, *bla*VIM, *bla*IMP, *bla*OXA-48–LIKE. PHLs submitted results to

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Figure 1. Carbapenemase Genes in CRE, by Genus and Geographic Region—Antibiotic Resistance Laboratory Network, January 2018–August 2019

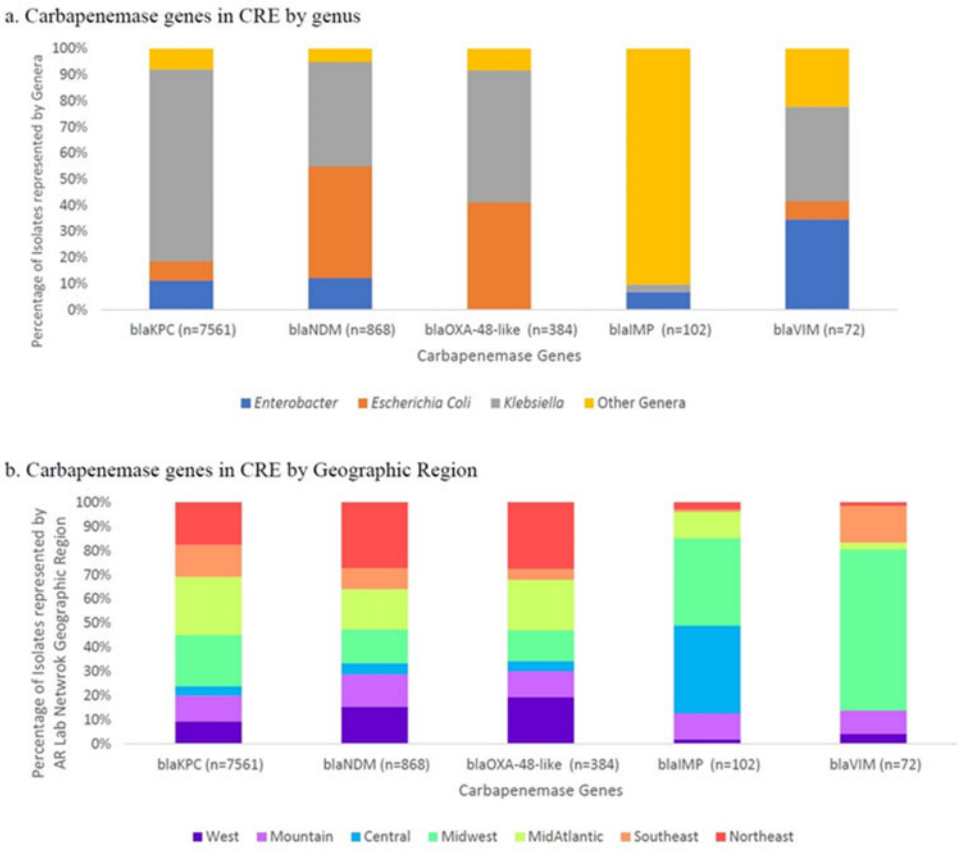

Fig. 1.

CDC monthly. Genera other than *Enterobacter*, *Klebsiella*, and *Escherichia coli* are categorized as other genera in this analysis. Data were compiled and analyzed using SAS v 9.4 software. **Results:** From January 2018 to August 2019, the AR Lab Network tested 25,705 CRE isolates; 8,864 of 25,705 CRE (34%) were CP. *Klebsiella* spp represented the largest proportion of CP-CRE at 68% (n = 6,063), followed by *E. coli* (12%, n = 1,052), *Enterobacter* spp (11%, n = 981), and other genera (9%, n = 768). Figure 1a shows the composition of CP-CRE carbapenemase genes by genus. The most common carbapenemase and genus profiles were *bla*KPC in *Klebsiella* (74%; 5,562 of 7,561 *bla*KPC-positive) blaNDM in *E. coli* (43%; 372 of 868 *bla*NDM-positive) *bla*VIM in *Enterobacter* spp (35%; 25 of 72 *bla*VIM-positive), and *bla*IMP among other genera (90%; 92 of 102 *bla*IMP-positive). Common CP-CRE genes and genera also varied by geography (Fig. 1b). **Conclusions:** The AR Lab Network has greatly enhanced our nation's ability to detect and characterize CP-CRE. Our data provide a snapshot of the organisms and regions where mobile carbapenemase genes are most often detected in CRE. Geographic variation in CP gene profiles provides actionable data to inform local priorities for detection and infection control and provide clinicians with situational awareness of the genes and organisms that are circulating in their region.

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Disclosures: In this presentation, the authors discuss the drug combination aztreonam-avibactam and acknowledge that this drug combination is not currently FDA-approved.

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Carbapenemase Production and Mortality Risk Among Carbapenem-Resistant Enterobacteriaceae Cases in Tennessee, United States

Rany Octaria, Vanderbilt University; Allison Chan, Tennessee Department of Health; Marion Kainer, Western Health

Background: Carbapenem-resistant Enterobacteriaceae (CRE) are an urgent public health threat associated with poor patient outcomes. CRE that produce carbapenemase (CP-CRE) are of particular concern because the mechanism-conferring genes in plasmids can be transferred to other bacteria. CRE are reportable in Tennessee (TN); isolate submission is required for CP production and resistance mechanism testing. We aimed to compare patient characteristics and outcomes between CP-CRE and non–CP-CRE patients to guide potential public health interventions. **Methods:** A retrospective cohort study to compare 30-day mortality, and clinical characteristics of CP-CRE to non–CP-CRE

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