guide patient placement. Screening was conducted by collecting a composite swab from the bilateral axilla and groin. Samples were incubated in salt dulcitol broth for 5 days at 40°C then subcultured onto Sabouraud dextrose agar. Colony identification was performed using a Vitek 2 system (bioMérieux). **Results:** In total, 177 patients were placed in single-patient rooms under contact precautions during May–August 2019. We conducted 123 environmental cleaning observations, and the percentage of missed surfaces decreased from 71% (10 of 14) in June to 7% (1 of 16) in August. Hand hygiene compliance among ICU and HDU staff was 79% (204 of 257) in May, 71% (159 of 223) in June, 73% (170 of 233) in July, and 81% (534 of 657) in August. In total, 283 screening swabs from 234 patients were processed during May–August 2019. Overall, 18 of 88 PPS swabs (20%), 13 of 180 admission screening swabs (7%), and 0 of 15 contact screening swabs (0%) were positive for *C. auris*. The PPS results showed a rapid decrease in colonization: 6 of 14 (43%) in May, 12 of 54 (22%) in June, 9 of 98 (9%) in July, and 1 of 70 (2%) in August. No new *C. auris* infections were identified from June to October 2019. **Conclusions:** The control of *C. auris* in a hospital outbreak requires multimodal interventions, including enhanced IPC interventions, PPS, admission and contact screening for colonization, rigorous monitoring, and team effort.

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Candidemia: Predisposing Factors, Antifungal Susceptibility, Clinical Outcome and Connotations for Management

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Objective: We conducted this study to investigate the epidemiology of candidemia in our setting and to quantify the risk factors associated with disease, overall outcome, and mortality associated with candidemia. **Methods:** In this prospective observational study, we conducted lab-based surveillance with clinical correlation of all cases of candidemia within our ICUs during the period (2016–2018). Clinical assessment was done on day 5 and day 30, and comorbidities, clinical features, and outcome were observed within 30 days after the diagnosis. The diagnosis was made on the basis of positive blood culture for *Candida* spp and a compatible clinical picture. The demographic characteristics, sequential organ failure assessment (SOFA) scores, comorbidities, use of invasive devices, antibiotics administered were observed, and antifungal susceptibility testing was performed according to CLSI guidelines. Type and duration of antifungal administered and outcomes were noted. **Results:** In total, 48 episodes of candidemia, with 29 (60%) males and 19 (40%) females, were identified during the study period. *C. albicans* was the most common specie responsible for candidemia, causing 17 of the cases (~35%), whereas rest of the cases were caused by non–*albicans* spp, which included *C. auris*, accounting for 9 (19%) *C. parapsilosis* and *C. tropicalis* 7 (15%) each, *C. glabrata* and *C. famata* 2 (6%), and *C. krusei* was isolated in only 2 cases (4%). Among modifiable risk factors, CVC insertion and antibiotic exposure were the leading factors, seen in 100% of patient. *Candida* colonization was observed in 26 patients (28%), of whom 2 (4%) had multifocal *Candida* colonization. Among evaluable patients, 17 (35%) died within 30 days of the onset of candidemia. *C. tropicalis* was associated with the highest mortality rate, 27% (n = 4) in this cohort. Regarding the crude mortality in the different units, patients in medical ICU had the highest mortality rate (54%). In vitro activity of 3 systemically active antifungal agents was tested against 48 isolates of *Candida* spp. Based on CLSI break points, the susceptibility to voriconazole was 98%; only 1 isolate was resistant to voriconazole. Among candidemia-positive cases, 28 patients (58%) had taken the antifungals for >14 days, whereas 18 (37.5%) were treated for <14 days and 2 (4%) died before the initiation of therapy. **Conclusions:** In our study, *C. albicans* was the most common specie responsible for candidemia, but non–*albicans* spp are also emerging, with higher in vitro resistance to antifungals.

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Carbapenem-resistant Enterobacteriaceae carriage risk for parameterization of a regional healthcare network agent-based model

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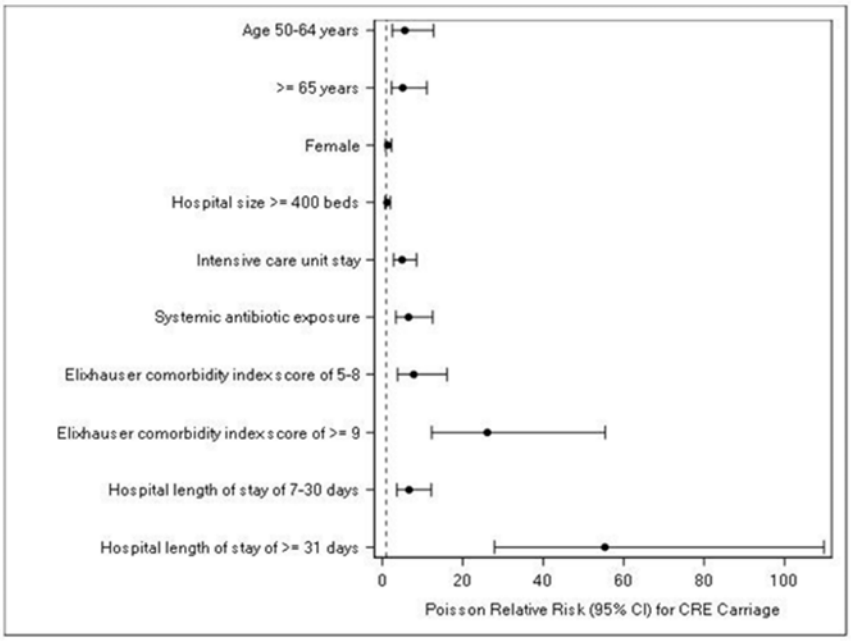
Background: Carbapenem-resistant *Enterobacteriaceae* (CRE) are increasingly common in the United States and have the potential to spread widely across healthcare networks. Only a fraction of patients with CRE carriage (ie, infection or colonization) are identified by clinical cultures. Interventions to reduce CRE transmission can be explored with agent-based models (ABMs) comprised of unique agents (eg, patients) represented by a synthetic population or model-generated representation of the population. We used electronic health record data to determine CRE carriage risk, and we discuss how these results can inform CRE transmission parameters for hospitalized agents in a regional healthcare network ABM. **Methods:** We reviewed the laboratory data of patients admitted during July 1, 2016–June 30, 2017, to any of 7 short-term acute-care hospitals of a regional healthcare network in North Carolina (N = 118,022 admissions) to find clinically detected cases of CRE carriage. A case was defined as the first occurrence of *Enterobacter* spp, *Escherichia coli*, or *Klebsiella* spp resistant to any carbapenem isolated from a clinical specimen in an admitted patient. We used Poisson regression to estimate clinically detected CRE carriage risk according to variables common to data from both the electronic health records and the ABM synthetic population, including patient demographics, systemic antibiotic administration, intensive care unit stay, comorbidities, length of stay, and admitting hospital size. **Results:** We identified 58 (0.05%) cases of CRE carriage among all admissions. Among these cases, 30 (52%) were ≥65 years of age and 37 (64%) were female. During their admission, 47 cases (81%) were administered systemic antibiotics and 18 cases (31%) had an intensive care unit stay. Patients administered systemic antibiotics and those with an

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

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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