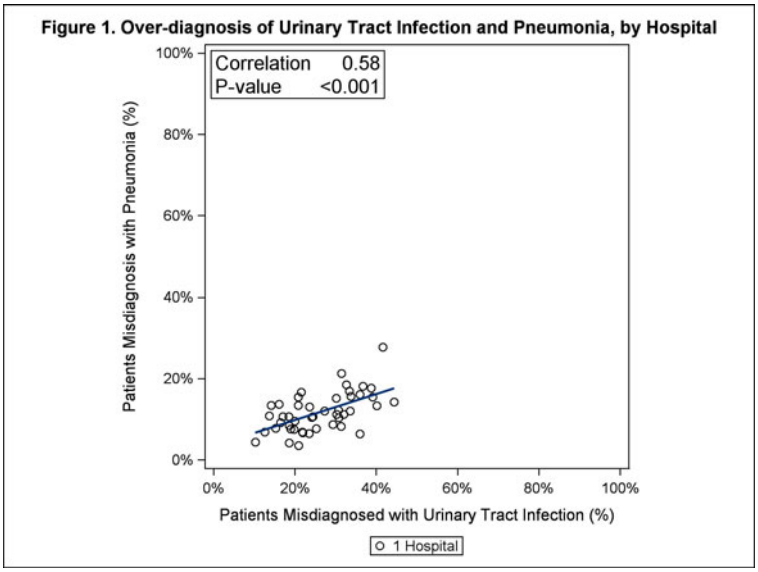

Fig. 1

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Presentation Type:
Poster Presentation

Molecular Epidemiology and Outcomes of Patients with Carbapenem-Resistant Enterobacteriaceae Bacteriuria, Atlanta 2012–2015

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Background: Carbapenem-resistant *Enterobacteriaceae* (CRE) represent a significant antibiotic resistance threat, in part because carbapenemase genes can spread on mobile genetic elements. Here, we describe the molecular epidemiology and outcomes of patients with CRE bacteriuria from the same city in a nonoutbreak setting.
Methods: The Georgia Emerging Infections Program performs active, population-based CRE surveillance in Atlanta. We studied a cohort of patients with CRE (resistant to all tested third-generation cephalosporins and ≥1 carbapenem, excluding ertapenem) first identified in urine, and not in a prior or simultaneous sterile site, between 2012 and 2015. Whole-genome sequencing (WGS) was performed on a convenience sample. We obtained epidemiologic and outcome data through chart review and Georgia Vital Statistics records (90-day mortality). Using WGS, we created a core-genome alignment-based phylogenetic tree of the *Klebsiella pneumoniae* isolates and calculated the SNP difference between each sample. Using SAS version 9.4 software, we performed the Fisher exact test and univariable odds ratios (OR) with 95% CI to compare patient isolates with and without a carbapenemase gene. **Results:** Among 81 patients included, the median age was 68 (IQR, 57–74) years, and most were female (58%), black (60%), and resided in a long-term care facility 4 days prior to culture isolation (53%). Organisms isolated were *K. pneumoniae* (84%), *Escherichia coli* (7%), *Enterobacter cloacae* (7%), and *Klebsiella oxytoca* (1%). WGS identified at least 1 β-lactamase gene in 91% of the isolates; 85% contained a carbapenemase gene, the most frequent of which was *bla*KPC-3 (94%). Patients with CRE containing a carbapenemase gene were more likely to be black (OR, 3.7; 95% CI, 1.0–13.8) and to have *K. pneumoniae* (OR, 8.9; 95% CI, 2.2–35.0). Using a core-genome alignment of 3,708 genes (~63% of the complete genome), we identified a median of 67 (IQR, 23–3,881) SNP differences between each *K. pneumoniae* isolate. A phylogenetic tree identified clustering around carbapenemase gene and multilocus sequence type (84% were ST 258) but not based on referring laboratory or county of residence (Fig. 1). Although 7% of patients developed an invasive CRE infection within 1 year and 21% died within 90 days, having a

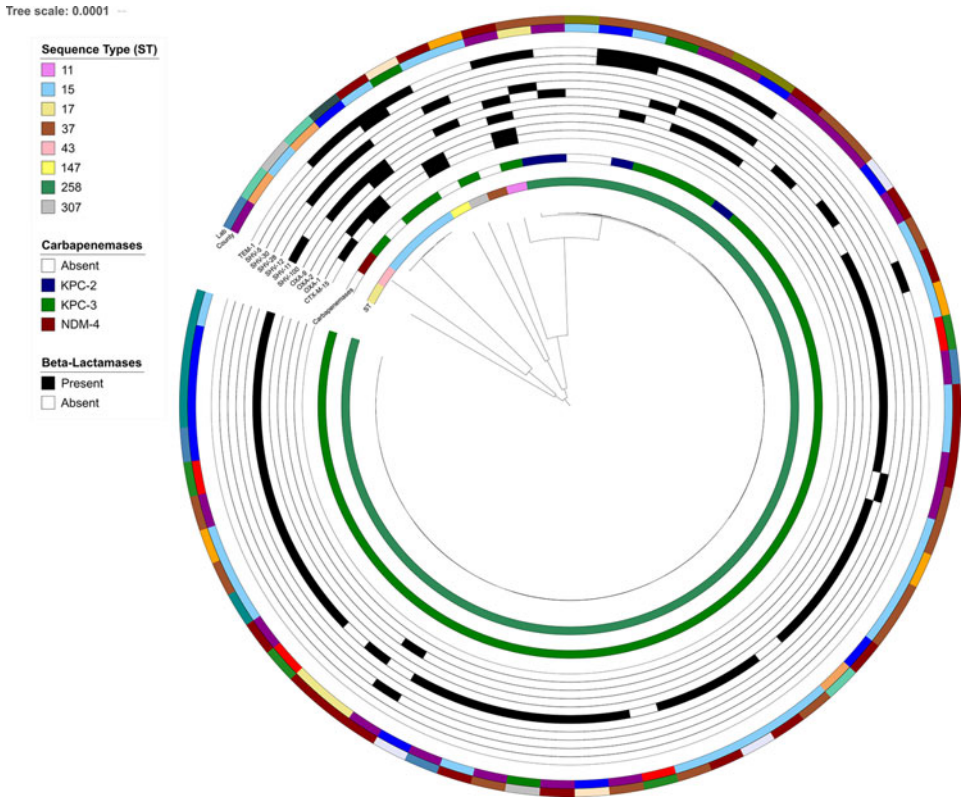

Fig. 1

carbapenemase gene was not associated with these outcomes. **Conclusions:** Molecular sequencing of a convenience sample of CRE bacteriuria support *K. pneumoniae* ST258 harboring *bla*KPC-3 being distributed throughout the Atlanta area, across the healthcare continuum. Overall mortality was high in this population, but the presence of carbapenemase genes was not associated with worse outcomes.

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Neonatal Exposure to *Staphylococcus aureus* in the Neonatal Intensive Care Unit: Identifying Reservoirs Among Colonized Healthcare Workers and Parents

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Background: *Staphylococcus aureus* (*S. aureus*) is the second most common cause of healthcare-acquired infections in neonates. *S. aureus* colonization is a known risk factor for invasive disease. Aside from healthcare workers (HCWs), recent data suggest that parents are important reservoirs of *S. aureus* in the neonatal intensive care unit (NICU). *S. aureus* typically colonizes the nares, but it can also colonize other anatomic locations such as the throat. **Objective:** Our objectives were to identify and compare *S. aureus* colonization among HCWs and parents and to identify and compare different sites of *S. aureus* colonization. **Methods:** Between April 2015 and July 2016, we performed 4 point-prevalence surveys and collected nares and throat swabs from HCWs (nurses, respiratory therapists, nurse practitioners, and physicians) at a quaternary-care NICU. During an overlapping period, we screened parents of neonates in the NICU for *S. aureus* colonization using nares, throat, groin, and perianal cultures as a part of an ongoing randomized control trial. Cultures from both studies were collected using standardized methods. ESwabs were used to collect samples, which were inoculated into broth for enrichment and subsequently cultured onto chromogenic agar to differentiate between MSSA and MRSA. **Results:** The prevalence of methicillin susceptible S. aureus (MSSA) colonization was 46% (105/226) in HCWs and 28% (239/842) in parents. The prevalence of methicillin resistant S. aureus (MRSA) colonization was 2.2% (5/226) in HCWs and 2.2% (19/842) in parents. Of those who were colonized with S. aureus, 35% (79/226) of HCWs and 46.5% (160/344) of parents had nares and throat colonization while 11.5% (26/226) of HCWs and 12.2% (42/344) of parents had only throat colonization but not nares colonization. Of those who were MRSA colonized, 1.3% (3/226) of HCWs and 1.8% (15/842) of parents had a positive nares and throat culture as compared to 0.9% (2/226) of HCWs and 0.2% (2/842) of parents had only positive throat cultures. Additionally, 68% (175/257) were colonized with S. aureus at any swabbed site including nares, throat, groin, or perinanal areas. However, only 30% (77/257) of parents had only nares colonization as compared to 58.8% (151/257) had throat and nares colonization, 38.1% (98/257) had nares and groin colonization, and