1234. Racial Disparities in Invasive Staphylococcus aureus (iSA) Disease in Metropolitan Atlanta, a Population-Based Assessment, 2016

Rahsaan Overton, MPH1,2; Scott Fridkin, MD3; Amy Tunali, MPH4 and Susan M. Ray, MD, FIDSA5; 1Georgia Emerging Infections Program, Atlanta, Georgia, 2Atlanta Research and Education Foundation and Atlanta VA Medical Center, Atlanta, Georgia, 3Medicine, Emory University School of Medicine, Atlanta, Georgia, 4Division of Infectious Diseases, Emory University School of Medicine, Atlanta, Georgia

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Background. Disparities in incidence of invasive methicillin-resistant S. aureus (iMRSA) infections have been examined, suggesting that differences were in part driven by socio-economic factors. An analysis was conducted to determine whether similar disparities exist for invasive methicillin-susceptible S. aureus (i MSSA).

Methods. The Georgia Emerging Infections Program (GA EIP) conducts active, population-based surveillance for iSA within the 8-county area of Atlanta. Cases were defined as residents of the surveillance area with SA isolated from a normally sterile site, with cultures within a 30-day period considered a single case. Age- and race-specific incidence were calculated using 2016 US census data; other/unknown race were excluded from analysis (< 5% of cases). Incidence rate ratios (IRR) between stratum and summary adjusted rate ratios (aIRR) were calculated with the Mantel–Hanzel method.

Results. During 2016, 1,958 cases were identified (42% iMRSA and 58% iMSSA); crude incidence was 48.5/100,000. Rates were highest among those ≥ 65 years of age for both blacks and whites (Figure 1). When compared with iMSSA, iMRSA incidence was consistently lower across all age groups (aIRR: 0.7; 95% CI: 0.7–0.8) (Figure 2). However, the incidence of iMSSA among black cases was double that among white cases (aIRR: 2.0; CI: 1.7–2.3) across all age groups. This racial disparity was more extreme for iMRSA. Notably the racial disparity is not observed in cases age 65 and over.

Conclusion. In the Atlanta area, racial disparities in iSA were noted, with higher incidence among blacks than whites for both iMSSA and iMRSA. The racial disparity is more extreme for iMRSA. Notably the racial disparity is not observed in cases age 65 and over. Causes for these disparities should be investigated.

Figure 1. Age and Race Specific Rates for iSA, 2016, 8-county Atlanta

Figure 2. Age and Race Specific Rates by iSA type, 2016, 8-county Atlanta

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1235. Transmission of Genetically Related, Multidrug Resistant, and Invasive Vancomycin-resistant Enterococci (VRE) Between Patients and Rooms on the Stem Cell Transplant (SCT) and Leukemia (LKM) Units

Lynn El Haddad, PhD1; Blake Hanso, PhD2; Cesar Arias, MD, PhD, FIDSA3,4; Glen Otero, PhD5; Cynthia Harb, MSc1; Shashank S. Ghantoji, MD, PhD, MPH6; Marc Stambich, PhD1 and Roy F. Chemaly, MD, MPH, FIDSA, FACP7; 1Infectious Diseases, The University of Texas MD Anderson Cancer Center, Houston, Texas, 2Center for Infectious Diseases, UTHealth School of Public Health, Houston, Texas, 3Center for Antimicrobial Resistance and Microbial Genomics (CARMiG), UTHealth McGovern Medical School, Houston, Texas, 4Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogota, Colombia, 5Independent Researcher, San Diego, California, 6Department of Infections Diseases, Infection Control and Employee Health, The University of Texas MD Anderson Cancer Center, Houston, Texas

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Background. VRE are a major cause of morbidity and mortality in immunocompromised patients. Tracking the dissemination of VRE strains is crucial to understand the dynamics of infections, emergence, and spread of VRE in the hospital setting.

Methods. Whole-genome sequencing (WGS) and phylogenetic analyses were performed to identify dominant VRE strains and potential transmission networks between patients and their rooms on the leukemia (LKM) and the stem cell transplant (SCT) units, located on two consecutive floors. We included 35 VRE-positive rectal swabs from SCT and LKM patients, and 55 environmental swabs from the patients’ main rooms and bathrooms. Sequence types, drug resistance genes, virulence genes, and patients’ outcomes were also determined.

Results. We identified VRE strains with newly described sequence types (ST) such as ST736, ST494, and ST772 which were isolated from both floors. One VRE genetic lineage belonged to ST494 (only previously isolated in Peru and was the only VanB-type strain). All other strains harbored the vanA gene. We observed highly genetically related strains transmitted between distinct rooms, floors, and time periods within the hospital in a period of 1 month (figure). Of five VRE bacteremia events, three strains were lacking the pilus operon (fimL-fimL-17-13 (ST203) and the remaining two were resistant to daptomycin (ST736, ST664) (figure). Of 10 patients harboring daptomycin-resistant strains, only 3 (30%) were exposed to daptomycin within 18 months before strain recovery.

Conclusion. Our findings confirmed horizontal transfer of highly related genetic lineages of multidrug resistant and invasive VRE strains between SCT and LKM patients and their room environment. New STs were identified and some correlated with bacteremia events. The use of a routine real-time WGS can characterize VRE strains and identify potential reservoirs of transmission in the healthcare setting in order to design interventions to prevent and control the spread of opportunistic and highly resistant organisms.

Figure. Phylogenetic tree showing the genetic relatedness, features, and transmission networks of the 90 VRE isolates. Abbreviations: IA: hospital-acquired; CA: community-acquired; ST: sequence type; SCT: stem cell transplant; LKM: leukemia; DAP: daptomycin; vanA: vanA gene. We observed highly genetically related strains transmitted between distinct rooms, floors, and time periods within the hospital in a period of 1 month (figure). Of five VRE bacteremia events, three strains were lacking the pilus operon fimL-fimL-17-13 (ST203) and the remaining two were resistant to daptomycin (ST736, ST664) (figure). Of 10 patients harboring daptomycin-resistant strains, only 3 (30%) were exposed to daptomycin within 18 months before strain recovery.

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1236. Infection Control Risk Mitigation and Implementation of Best Practice Recommendations in Long-Term Care Facilities

Teresa Fitzgerald, RN, BSN, CIC1; Regina Naionl, RN, PhD2; Kate Tyner, RN, BSN, CIC3; Sue Beach, BA1; Margaret Drake, MT, ASCP, CIC2; Teresa Micheels, MSN, RN, CIC4; Mark E. Rupp, MD1; Michelle Schwedhelm, MSN, RN5; Maureen Tierney, MD, MSc6 and Muhammad Salman Ashraf, MBBS7; 1Nebraska Infection Control
Assessment and Promotion Program, Nebraska Medicine, Omaha, Nebraska, 3Nursing Research and Quality Outcomes, Nebraska Medicine, Omaha, Nebraska, 4Division of Epidemiology, Nebraska Department of Public Health, Lincoln, Nebraska, 5Infection Control and Epidemiology, Nebraska Medicine, Omaha, Nebraska, 6Infectious Diseases, University of Nebraska Medical Center, Omaha, Nebraska, 7Division of Infectious Diseases, University of Nebraska Medical Center, Omaha, Nebraska, 8Veterans Affairs: Investigator, Research grant.

Ampicillin/sulbactam

P < 0.001 for all comparisons.

Over 78,000 isolates were included (Table 1). The most prevalent isolates (11.9%), and E. coli (11.9%) were highly susceptible to ceftriaxone, ceftazidime, piperacillin/tazobactam, and ampicillin/subactam, piperacillin/tazobactam, and imipenem were compared. As guidelines discourage empiric use of antibiotics if susceptibility rates are < 80%, we assessed clinical discordance between each LTCF and affiliated VAMC antibiogram at a threshold of 80% susceptible. The proportions of concordant susceptibilities between LTCFs and VAMCs on the same campus vs. geographically distinct campuses were compared using Chi-square tests.

A total of 119 LTCFs and their affiliated VAMCs were included in this analysis with 80.6% (n = 94) of facilities located on the same campus and 20.4% (n = 35) on geographically distinct campuses. The table below shows the overall concordance (agreement) of LTCFs with their affiliated VAMC in regards to E. coli %S to the compared antibiotics. No significant differences were found when comparing LTCFs on the same campus vs. geographically distinct campuses.

Conclusion. Antibiotics between LTCFs and affiliated VAMCs had a high concordance, except for sulfa/thio/trimethoprim, cefazolin and ceftriaxone in regards to susceptibility rates of E. coli. Facilities on the same campus were found to have similar concordance rates to geographically distinct facilities. Future studies are needed to better understand the various approaches to creating LTCF-specific antibiograms that are associated with clinical outcomes.

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Table 1: Summary of Antimicrobial Susceptibilities

| Antibiogram | 0% | 10% | 20% | 40% | 50% | 60% | 70% | 80% | 90% | 100% |
|-------------|----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Piperacillin | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| Ceftriaxone  | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |
| Cefazolin    | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A | N/A |

Conclusion. NTF appears to be the best empiric choice for outpatient treatment of acute uncomplicated cystitis in New York State. TMP-SMX and ciprofloxaxin should be avoided empirically. These data also highlight the necessity to obtain uropathogen sensitivity data to confirm empiric therapy or make appropriate adjustments in the outpatient setting.

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