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

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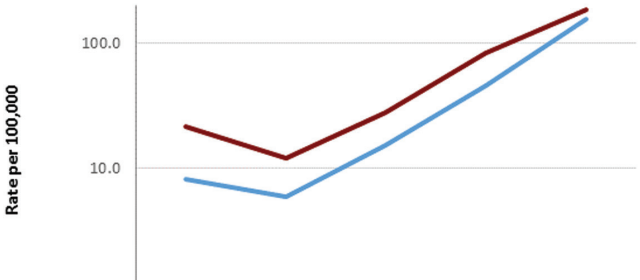
Background. Disparities in incidence of invasive methicillin-resistant *S. aureus* (iMRSA) infections have been examined, suggesting that differences were in part driven by socio-economic factors. An analysis was conducted to determine whether similar disparities exist for invasive methicillin-susceptible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

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 (RR) between stratum and summary adjusted rate ratios (aRR) 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 (aRR: 0.7; 95% CI: 0.7–0.8) (Figure 2). However, the incidence of iMRSA among black cases was double that among white cases (aRR: 2.0; CI: 1.7–2.3) across all age groups. This racial disparity was less pronounced in iMSSA: among younger cases (<65 years old), iMSSA incidence among blacks was significantly higher than whites (aRR: 1.6; CI: 1.4–2.0), while rates were similar in older blacks and whites (≥65 years old) (aRR: 0.9; CI: 0.8–1.2). Bloodstream infections were the most common presentation overall; however, for iMSSA infections, joint/synovial infections were significantly less common among black cases than white cases (RR: 0.3; CI: 0.1–0.7).

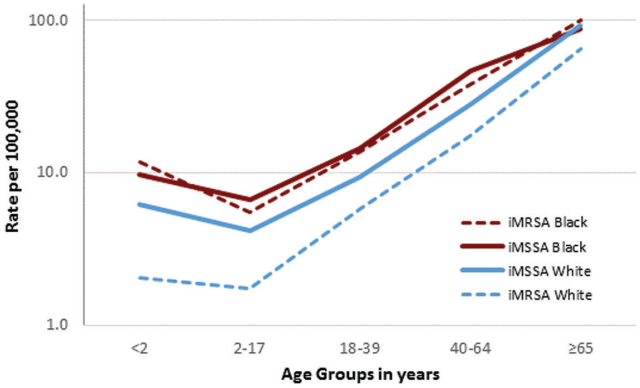
Conclusion. In the Atlanta area, racial disparities in iSA were noted, with higher incidence among blacks than whites for both iMSSA and iMRSA. The racial disparity is more extreme for iMRSA. Notably the racial disparity is not observed in cases age 65 and over. Causes for these disparities should be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

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



	<2	2-17	18-39	40-64	≥65
ALL iSA Black	21.5	12.1	28.1	84.0	186.4
ALL iSA White	8.2	5.9	15.1	45.4	156.6

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

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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 pili operon *fms14-17-13* (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.

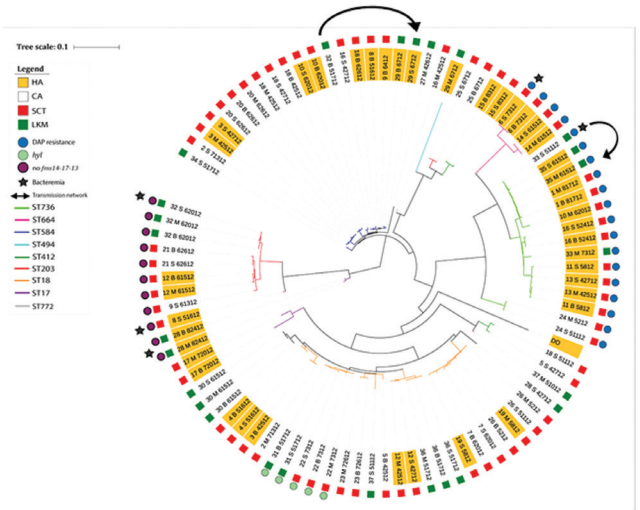

Figure. Phylogenetic tree showing the genetic relatedness, features, and transmission networks of the 90 VRE isolates. *Abbreviations: HA, hospital-acquired; CA, community-acquired; ST, sequence type; SCT, stem cell transplant; LKM, leukemia; DAP, daptomycin; hyl, hyaluronidase.*

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

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Background. Nebraska (NE) Infection Control Assessment and Promotion Program (ICAP) is a quality improvement initiative supported by the NE Department of Health and Human Services. This initiative utilizes subject matter experts (SMEs) including infectious diseases physicians and certified infection preventionists (IP) to assess and improve infection prevention and control programs (IPCP) in various healthcare settings. NE ICAP conducted on-site surveys and observations of IPCP in many volunteer facilities to include long-term care facilities (LTCF) between November 2015 and July 2017. SMEs provided on-site coaching and made best practice recommendations (BPR) for priority implementation. Impact of this intervention on LTCF IPCP was examined.

Methods. Using a standardized questionnaire, follow-up phone calls were made with LTCF to evaluate implementation of the BPR one-year post-assessment. Descriptive analyses were performed to examine BPR implementation in LTCF that had follow-up between 4/4/17 to 4/17/18 and to identify factors that promoted or impeded BPR implementation.

Results. Overall, 45 LTCF were assessed. The top 5 IC categories requiring improvement were audit and feedback practices (28 of 45, 62%), PPE supplies at point of use (62%), IC risk assessments (58%), TB risk assessments (56%), and supply and linen storage practices (56%). Follow-up assessments were completed for 270 recommendations in 25 LTCF. Recommendations reviewed ranged from three to 26 per LTCF (median = 15). The majority of the 270 recommendations (n = 162, 60%) had been either completely (35%) or partially (25%) implemented by the time of the follow-up calls. The ICAP visit itself was reported as the most helpful resource for BPR implementation (77 of 162). Lack of staffing was the most commonly mentioned barrier to implementation when LTCF implemented BPR partially or implementation was not planned (37 of 85). BPR Implementation most frequently involved additional staff training (64 of 162), review of policies and procedures (38 of 162), and implementing audit (34 of 162) and/or feedback (23 of 162) programs.

Conclusion. Numerous IC gaps exist in LTCF. Peer-to-peer feedback and coaching by SMEs facilitated implementation of many BPR directed toward mitigating identified IC gaps.

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1237. New York State Outpatient Regional Antibiogram for Urinary Pathogens: Have We Reached a Post Antibiotic Era for the Treatment of UTIs?

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Background. Outpatient prescribing for acute uncomplicated cystitis is a significant driver of antimicrobial use. Empiric therapy should be based on local susceptibility data. However, there is limited guidance on regional susceptibility trends in outpatient settings. This study describes the epidemiology and prevalence of antimicrobial resistance in uropathogens in New York State outpatient settings to help inform empiric treatment decisions.

Methods. Retrospective analysis of positive urine cultures sent to Quest Diagnostics in 2016 from outpatient settings. Cultures that grew $\geq 10^5$ CFU/mL were included from 17 NYS counties. Bacterial identification and antimicrobial sensitivities were determined on the Vitek-2 using CLSI M-100 S-25 breakpoints. Data were summarized as proportions and stratified by age (<17, 18–64, ≥65) and sex.

Results. Over 78,000 isolates were included (Table 1). The most prevalent isolates were *Escherichia coli* (65.2%), *Enterococcus* spp. (11.9%), and *Klebsiella pneumoniae* (9.9%). *E. coli* was highly susceptible to nitrofurantoin (NTF, 97.2%) and cefazolin (CFZ, 89.9%) and less susceptible to trimethoprim–sulfamethoxazole (TMP-SMX, 72.9%) and ciprofloxacin (CIP, 78.0%). *Enterococcus* spp. was highly susceptible to NTF (99.0%) and ampicillin (99.8%). *K. pneumoniae* was highly susceptible to TMP-SMX (90.0%) and CIP (95.2%) and markedly less susceptible to NTF (42.0%). *E. coli* was more prevalent in females (69.7% vs. 39.6%, $P < 0.001$). *Enterococcus* was more prevalent in males (39.6% vs. 10.1%, $P < 0.001$). The prevalence of *K. pneumoniae* was similar in men and women (9.6% vs. 10.1%, $P = 0.08$). Resistance was more prevalent in males (NTF: 6.3% vs. 4.2%; TMP-SMX: 26.3% vs. 22.7%; CIP: 35% vs. 17.3%) and for adults ≥65 (NTF: 6.2% vs. 3.6%; TMP-SMX: 25.1% vs. 22.1%; CIP: 30.0% vs. 14.0%) $P < 0.001$ for all comparisons.

Conclusion. NTF appears to be the best empiric choice for outpatient treatment of acute uncomplicated cystitis in New York State. TMP-SMX and ciprofloxacin 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.

Table 1. Summary of Antimicrobial Susceptibilities

Bacteria	N	Ampicillin	Cefotaxidime	Cefazolin	Ciprofloxacin	Nitrofurantoin	Gentamicin	Levofloxacin	Pip/Tazo	Tobramycin	TMP/SMX	Cefotaxime	Imipenem	Tetracycline	Oxacillin	Penicillin	Vancomycin
Gram negative																	
Citrobacter diversus	933	X	99.7	X	99.0	90.2	99.6	98.9	99.4	99.8	98.7	99.7	99.8	X	X	X	X
Citrobacter freundii	316	X	92.1	X	94.6	95.6	97.1	92.3	94.5	97.7	85.3	90.8	99.0	X	X	X	X
Enterobacter aerogenes	785	X	93.8	X	98.6	19.1	99.5	98.5	96.6	99.7	98.6	94.4	83.3	X	X	X	X
Enterobacter cloacae	604	X	91.1	X	94.6	44.8	96.5	95.0	X	96.0	86.1	87.6	99.3	X	X	X	X
Escherichia coli	54,533	54.3	94.9	89.9	78.0	97.2	89.8	77.8	96.8	90.0	72.9	92.5	99.9	X	X	X	X
Klebsiella pneumoniae	7734	X	95.7	93.2	95.2	42.0	96.9	95.2	94.8	95.9	90.0	95.0	99.8	X	X	X	X
Proteus mirabilis	3388	78.6	99.3	91.0	89.5	X	93.9	90.3	99.8	95.1	86.2	98.1	25.5	X	X	X	X
Providencia rettgeri	40	X	92.5	X	85.0	X	95.0	72.1	94.7	100.0	84.6	97.4	97.5	X	X	X	X
Pseudomonas aeruginosa	1105	X	89.2	X	75.8	X	87.8	67.6	91.9	95.3	X	X	88.3	X	X	X	X
Serratia marsescens	264	X	96.5	X	99.2	X	98.1	97.3	X	89.2	96.9	96.6	X	X	X	X	X
Stenotrophomonas maltophila	53	X	X	X	X	X	X	83.0	X	X	100.0	X	X	X	X	X	X
Gram Positive																	
Enterococcus spp.	9,222	99.8	X	X	X	99.0	X	X	X	X	X	X	X	X	X	99.6	100.0
Enterococcus faecium	35	94.3	X	X	X	97.1	X	X	X	X	X	X	X	X	X	91.2	0.0
Staphylococcus aureus	823	X	X	X	84.9	98.4	99.5	86.3	X	X	99.2	X	X	89.8	99.8	X	X
Staphylococcus epidermidis	1,107	X	X	X	43.6	99.6	92.7	44.3	X	X	84.6	X	X	82.6	98.8	X	X
Staphylococcus haemolyticus	337	X	X	X	45.4	99.7	90.9	47.8	X	X	89.3	X	X	69.1	97.0	X	X
Staphylococcus hominis spp hominis	53	X	X	X	47.2	96.2	100.0	47.2	X	X	93.1	X	X	62.8	100.0	X	X
Staphylococcus ludgunensis	84	X	X	X	95.2	100.0	98.8	95.2	X	X	97.6	X	X	95.1	28.0	X	X
Staphylococcus simulans	119	X	X	X	62.2	99.1	100.0	63.0	X	X	100.0	X	X	94.1	84.8	X	X

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1238. A National Comparison of Antibiograms Between Veterans Affairs Long-Term Care Facilities and Affiliated Hospitals

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Background. Long-term care facilities (LTCFs) face several barriers to creating antibiograms. Here, we evaluate if LTCFs can use antibiograms from affiliated hospitals as their own antibiogram.

Methods. Facility-specific antibiograms were created for all Veterans Affairs (VA) LTCFs and VA Medical Centers (VAMCs) for 2017. LTCFs and affiliated VAMCs were paired and classified as being on the same campus or geographically distinct campuses based on self-report. For each pair, *Escherichia coli* susceptibility rates (%S) to cefazolin, ceftriaxone, cefepime, ciprofloxacin, nitrofurantoin, sulfamethoxazole/trimethoprim, ampicillin/sulbactam, 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.

Results. A total of 119 LTCFs and their affiliated VAMCs were included in this analysis, with 70.6% (n = 84) of facilities located on the same campus and 29.4% (n = 35) on geographically distinct campuses. The table below shows the overall clinical 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.

Agreement Rates between LTCFs and Affiliated VAMCs	Antibiotics
90–100%	Ampicillin/sulbactam Imipenem Nitrofurantoin
80–89%	Cefepime Ciprofloxacin Piperacillin/tazobactam
70–79%	Sulfamethoxazole/trimethoprim
60–69%	Cefazolin Ceftriaxone

Conclusion. Antibiograms between LTCFs and affiliated VAMCs had a high concordance, except for sulfamethoxazole/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 investigate how the various approaches to creating LTCF-specific antibiograms are associated with clinical outcomes.

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