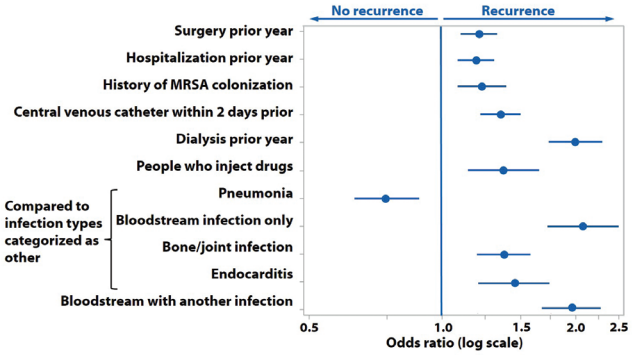

Disclosures. **All authors:** No reported disclosures.

1231. Patient-Level Factors Associated with Vancomycin-Resistant Enterococci Transmission to Healthcare Workers Gowns or Gloves

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Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections

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Background. Vancomycin-resistant *Enterococcus* (VRE) is transmitted from person-to-person, most commonly by healthcare workers (HCW) whose hands or attire have become contaminated while interacting with an infected or colonized patient. Our group recently found that VRE colonized patients transmitted this pathogen to HCW gowns or gloves 15% of the time. This study aims to describe patient-level factors associated with higher risk of transmission of VRE to HCW gowns or gloves and thus likely to subsequent patients.

Methods. We analyzed a prospective cohort that included 43 VRE-colonized patients and 215 HCW-patient interactions in medical or surgical intensive care units at the University of Maryland Medical Center. HCWs' gowns and gloves were cultured for VRE after performing patient care and before doffing. Univariate and multivariable logistic regression models, using generalized estimating equations to account for patient clustering, were used to estimate the odds ratios associated with specific patient-level factors (i.e., age, race, Elixhauser comorbidity score components obtained by ICD-10 codes, diarrhea, and devices). Multivariable models with and without stool VRE burden were created.

Results. In the initial multivariable model, having a nasogastric tube, diarrhea, complicated diabetes, rheumatoid arthritis/collagen vascular diseases, neurological disorders or psychoses doubled (OR greater than 2) the patient's risk of VRE transmission. After adjusting for VRE stool burden (OR 2.1 (95% CI 1.5–3.0)), having a nasogastric tube (OR 3.6 (95% CI 1.3–9.8)), diarrhea (OR 3.3 (95% CI 1.4–8.1)), or rheumatoid arthritis/collagen vascular diseases (OR 4.8 (95% CI 1.6–14.7)) remained significant in the model.

Conclusion. Patient-level factors associated with higher risk of VRE transmission to HCW gowns or gloves were identified even after adjusting for VRE stool burden, highlighting the importance of patient characteristics in VRE transmission. These patient-level factors may facilitate transmission by either increasing VRE stool shedding to the environment or the need for direct HCW-patient contact. These factors could be used to target more aggressive infection control interventions for these patients.

Disclosures. **All authors:** No reported disclosures.

1232. Phylogenomics of *Enterococcus faecium* From South America: Revisiting Worldwide VRE Population Structure

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Background. Previous studies have suggested that the population structure of *E. faecium* is composed of two main clades; a commensal clade (designated clade B) and a hospital-associated clade (Clade A) that encompass most of the clinical and animal isolates. The phylogenetic analyses leading to these results have been accomplished with the notable absence of isolates from diverse geographical regions (including South America). We aimed to refine the worldwide population structure of *E. faecium* by including 55 representative genomes from isolates obtained from five Latin American countries recovered between 1998 and 2014.

Methods. We sequenced our 55 representative isolates and selected other 285 genomes, from public databases, obtained across different regions (36 countries), different sources (animal, commensal, and clinical strains) and a wide range of dates of isolation (1946–2017). We characterized the genomes by presence/absence of resistance, virulence and mobile elements, and of CRISPR-*cas* systems. We analyzed the phylogeny of the entire population, selected the genomes belonging to clade A to examine recombination patterns and performed Bayesian molecular clock analysis excluding recombinant regions.

Results. Two major clades were identified, as previously reported. However, a higher degree of variation in clade A was found. Indeed, we identified a subclade (subclade I) that diverged ~894 years ago, and clearly distinguished clinical isolates from those of animal origin (distributed among a number of smaller early-branching subclades). A further split within the clinical subclade (subclade II) that diverged around ~371 years ago was also evident. Latin American isolates were distributed within subclades I (48%) and II (42%). Isolates in "animal" branches exhibited an average recombination of 34 Kbp, where it was 5 Kbp and 21 Kbp for subclades I and II, respectively. More resistance determinants were found in subclade II (62%), followed by I (54%) and absence of *cas* was the norm in the clinical subclades.

Conclusion. Inclusion of *E. faecium* isolates from diverse geographical region supports a continuous evolution of these organisms causing human infections. Important evolutionary events seem to favor emergence of novel subclades capable to cause important morbidity and mortality.

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1233. An Automated E-mail Notification Systemic to Infectious Disease Specialists and Effect on the Management of *Staphylococcal aureus* Bacteremia in a Community Hospital setting

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Background. *Staphylococcus aureus* is the leading cause of community and healthcare-associated bacteremia and carries a high burden with a substantial mortality, ranging from 20 to 40 %. Evidence suggests infectious disease (ID) consultation improves mortality and adherence to the Infectious Diseases Society of America (IDSA) guidelines. Due to complications from a lack of ID consultation, a notification system consisting of automated e-mails to ID providers was implemented. The objective of this study was to review the impact of the automatic notification to ID consultants with positive blood culture results in a community hospital system.

Methods. Cases of staphylococcus aureus bacteremia were identified from the microbiology database by at least one positive blood culture. The automated e-mail notification system was implemented in December 2014. ID providers were encouraged to verbally contact primary providers for positive results. Cases of bacteremia prior to implementation of the automated notification system were compared with those post-intervention. Patients under age 18 were excluded. Data gathered included mortality, re-admission rates, and compliance with IDSA guidelines.

Results. There were no significant differences in inpatient mortality (9 vs. 18%, $P = 0.180$). 30-day mortality between the two groups (18 vs. 20%, $P = 0.815$). The 30-day readmission rate among surviving patients was reduced by 50% (40% vs. 19%, $P = 0.014$). Compliance with antibiotic duration in complicated bacteremia increased post-intervention (57% vs. 85%, $P = 0.04$).

Conclusion. An automatic notification to ID specialists reporting patients with *Staphylococcus aureus* bacteremia led to improved compliance with IDSA guidelines regarding antibiotic duration and reduced re-admission rates. There was no effect on overall mortality.

Table 1: Patient Demographics

	Pre Intervention ($N = 57$)	Post Intervention ($N = 60$)	*P*-value
Average patient age (years)	64.4	62.2	0.448
Male	63%	63%	1
Immunosuppressed	16%	13%	0.80
Complicated bacteremia	70%	69%	1

Table 2: Patient Outcomes

	Preintervention ($N = 57$)	Postintervention ($N = 60$)	*P*-value
Inpatient mortality	9%	18%	0.180
30-day mortality (%)	18%	20%	0.815
Readmitted within 30 days	40%	19%	0.014
Bedside ID consult	75%	78%	0.888
Appropriate antibiotic duration -complicated bacteremia (>28 days)	57%	85%	0.04

All authors: No reported disclosures.

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

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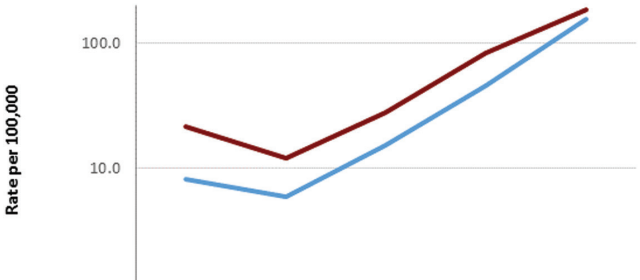
Background. Disparities in incidence of invasive methicillin-resistant *S. aureus* (iMRSA) infections have been examined, suggesting that differences were in part driven by socio-economic factors. An analysis was conducted to determine whether similar disparities exist for invasive methicillin-susceptible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

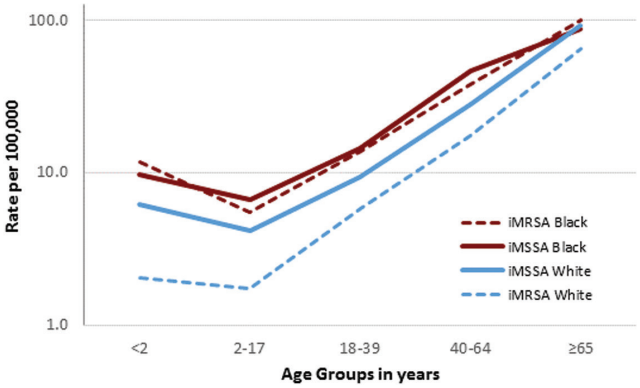
Conclusion. In the Atlanta area, racial disparities in iSA were noted, with higher incidence among blacks than whites for both iMSSA and iMRSA. The racial disparity is more extreme for iMRSA. Notably the racial disparity is not observed in cases age 65 and over. Causes for these disparities should be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



Disclosures. **S. Fridkin**, Pfizer Inc.: Grant Investigator, Research support.

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.

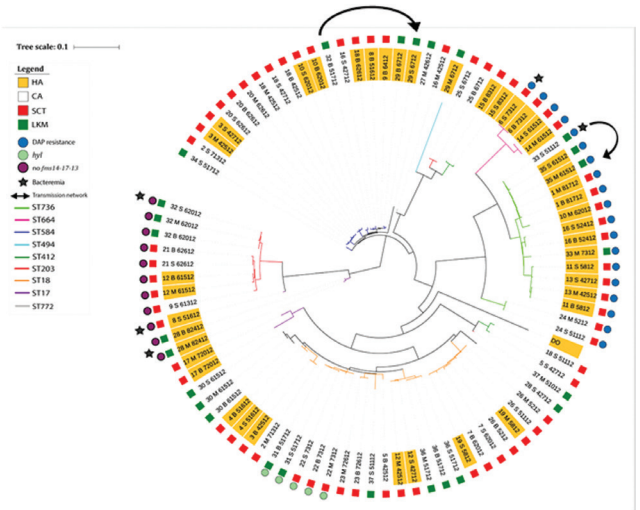

Figure. Phylogenetic tree showing the genetic relatedness, features, and transmission networks of the 90 VRE isolates. *Abbreviations: HA, hospital-acquired; CA, community-acquired; ST, sequence type; SCT, stem cell transplant; LKM, leukemia; DAP, daptomycin; hyl, hyaluronidase.*

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

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