Figure 1. Overall *S. aureus* Incidence Rates After Elective Surgeries by Infection Timing among Adults 18+ Years

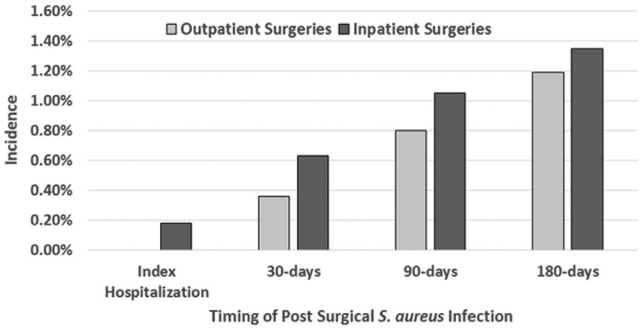
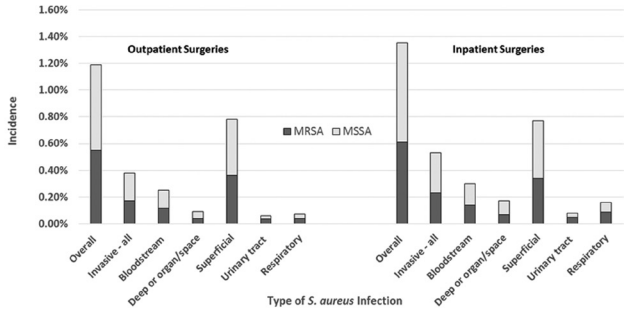


Figure 2. Incidence by Type of *S. aureus* Infection at 180-Days after Elective Surgeries among Adults 18+ Years*



*Not mutually exclusive categories (patients might have more than one type of infection)

Disclosures. **J. Dreyfus**, Premier, Inc.: Employee and Shareholder, Salary. **E. Begier**, Pfizer, Inc.: Employee and Shareholder, Salary. **H. Yu**, Pfizer, Inc.: Employee and Shareholder, Salary. **A. Quintana**, Pfizer, Inc.: Employee and Shareholder, Salary. **J. Gayle**, Premier, Inc.: Employee, Salary. **M. A. Olsen**, Pfizer: Consultant, Consulting fee.

1229. Prevalence and Acquisition of MRSA in Females During Incarceration at a Large Inner-City Jail

Kyle J. Popovich, MD MS FIDSA[1,2]; Chad Zawitz, MD[1,2,3]; Alla Aroutcheva, MD, PhD[1,2]; Darjai Payne, BS, MPH[2]; Michael Schoeny, PhD[4]; Lisa Diep, MPH[1]; Bala Hota, MD, MPH[2]; Mary K. Hayden, MD, FIDSA, FSHEA[2] and Robert A. Weinstein, MD[1,2]; [1]Stroger Hospital of Cook County, Chicago, Illinois, [2]Rush University Medical Center, Chicago, Illinois, [3]Cermak Health Services, Chicago, Illinois, [4]Department of Nursing, Rush University Medical Center, Chicago, Illinois

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

Friday, October 5, 2018: 12:30 PM

Background. USA300 MRSA is endemic in the community, with congregate settings such as urban jails potentially facilitating spread. It has been reported previously that males have a higher risk for MRSA carriage and bacteremia than females. However, it is unclear if there is differential risk for MRSA based on gender in high-risk populations. We determined the prevalence of MRSA colonization at jail entrance in females and defined an acquisition rate during incarceration.

Methods. Females incarcerated at the Cook County Jail, one of the largest US single-site jails, were enrolled within 72 hours of intake. Surveillance cultures (nares, throat, groin) were collected to determine prevalence of MRSA colonization. A survey was administered to identify predictors of colonization. Detainees in jail at Day30 had cultures repeated to determine MRSA acquisition. Univariate and multivariate analyses were performed to identify predictors of MRSA colonization.

Results. 250 women were enrolled (70% AA, 15% Hispanic) with 70% previously in jail (21% in the past 6 months). The prevalence of MRSA colonization at intake was 20% (50/250), with 42% of those colonized solely in the throat or groin. This intake prevalence is comparable to the 19% for male detainees in a parallel study. 9% (2/23) of initially negative women who remained in jail for 30 days acquired MRSA; five remained colonized and no one lost colonization. Univariate predictors (table) of MRSA at entrance to the jail were: illicit drug use (including using needles), unstable housing, engaging in anal sex, and recent exchange of sex for drugs/money. Women who exchange sex for drugs/money (vs. not) reported higher rates of needle use (35% vs. 4%, $P < 0.001$) and unstable housing (80% vs. 20%, $P < 0.001$). With multivariate adjustment for race/ethnicity, needles for illicit drugs was a significant predictor of MRSA (OR 5.89, 95% CI, 1.66, 20.94, $P = 0.006$).

Conclusion. We found that a high proportion (20%) of females entered jail colonized with MRSA, comparable to rates in males, suggesting that previously reported gender disparities in MRSA may not exist in high-risk populations. Entrance colonization risk factors suggest high-risk activities or venues in the community, with potential for directing gender-specific interventions.

Table. Predictors of MRSA Colonization in Females at Entrance to a Large Inner-City Jail

	Univariate			Multivariate		
Epidemiologic Factor						
	OR	**95% CI**	**p value**	**OR**	**95% CI**	**p value**
Race/Ethnicity						
Black/African-American	0.79	(0.51-1.23)	0.293	1.01	(0.60-1.69)	0.981
Latino	0.99	(0.55-1.78)	0.968	1.27	(0.66-2.45)	0.467
Non-Hispanic White	reference					
Cocaine use in past year	1.93	(1.01-3.71)	0.047			
Heroin use in past year	2.18	(1.07-4.46)	0.032			
Other Narcotic use in past year	2.30	(0.96-5.52)	0.063			
Benzodiazepine past year	2.79	(1.34-5.79)	0.006			
Prescription drugs to get high in past year	2.82	(0.95-8.33)	0.061			
Used needle for illicit drugs in past year	5.13	(1.87-14.10)	0.002	5.89	(1.66-20.94)	0.006
Released from jail in past 6 months	1.89	(0.94-3.83)	0.076			
Homeless or unstable housing in past year	2.11	(1.11-4.00)	0.023			
Substance abuse center in past year	2.72	(1.00-7.43)	0.051			
Ever diagnosed with Gonorrhea	1.88	(0.88-4.04)	0.104	2.01	(0.90-4.46)	0.087

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

1230. Epidemiology and Risk Factors for Recurrent Invasive Methicillin-Resistant *Staphylococcus aureus* Infection: nine US States, 2006–2013

Ian Kracalik, PhD, MPH[1]; Kelly Jackson, MPH[1]; Joelle Nadle, MPH[2]; Wendy Bamberg, MD[3]; Susan Petit, MPH[4]; Susan M. Ray, MD[5]; Ruth Lynfield, MD, FIDSA[6]; Lee H. Harrison, MD[7]; John M. Townes, MD[8]; Ghinwa Dumyati, MD, FSHEA[9]; William Schaffner, MD, FIDSA, FSHEA[10]; Jason Lake, MD[11] and Isaac See, MD[1]; [1]Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia, [2]California Emerging Infections Program, Oakland, California, [3]Colorado Department of Public Health and Environment, Denver, Colorado, [4]Connecticut Department of Public Health, New Haven, Connecticut, [5]Emory University School of Medicine, Atlanta, Georgia, [6]State Epidemiologist and Medical Director for Infectious Diseases, Epidemiology and Community Health, Minnesota Department of Health, St. Paul, Minnesota, [7]University of Pittsburgh, Pittsburgh, Pennsylvania, [8]Infectious Diseases, Oregon Health and Science University, Portland, Oregon, [9]NY Emerging Infections Program, Center for Community Health and Prevention, University of Rochester Medical Center, Rochester, New York, [10]Vanderbilt University School of Medicine, Nashville, Tennessee, [11]Centers For Disease Control and Prevention, Atlanta, Georgia

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

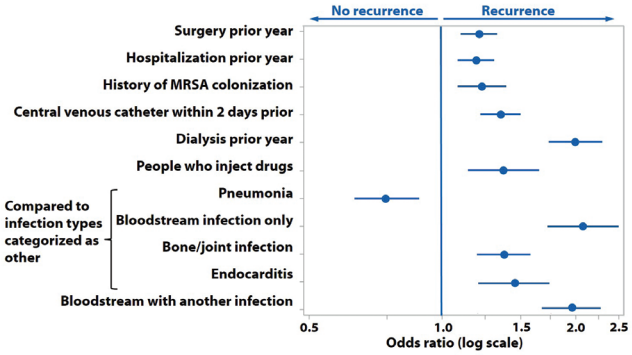
Friday, October 5, 2018: 12:30 PM

Background. Methicillin-resistant *Staphylococcus aureus* (MRSA) causes >70,000 invasive infections annually in the United States, and recurrent infections pose a major clinical challenge. We examined risk factors for recurrent MRSA infections.

Methods. We identified patients with an initial invasive MRSA infection (isolation from a normally sterile body site) from 2006 to 2013, through active, population-based surveillance in selected counties in nine states through the Emerging Infections Program. Recurrence was defined as invasive MRSA isolation >30 days after initial isolation. We used logistic regression with backwards selection to evaluate adjusted odds ratios (aOR) associated with recurrence within 180 days, prior healthcare exposures, and initial infection type, controlling for patient demographics and comorbidities.

Results. Among 24,478 patients with invasive MRSA, 3,976 (16%) experienced a recurrence, including 61% (2,438) within 180 days. Risk factors for recurrence were: injection drug use (IDU) (aOR; 1.38, 95% confidence interval [CI]: 1.15–1.65), central venous catheters (aOR; 1.35, 95% CI: 1.22–1.51), dialysis (aOR; 2.00, 95% CI: 1.74–2.31), and history of MRSA colonization (aOR; 1.35, 95% CI: 1.22–1.51) (figure). Recurrence was more likely for bloodstream infections (BSI) without another infection (aOR; 2.08, 95% CI: 1.74–2.48), endocarditis (aOR; 1.46, 95% CI: 1.16–1.55), and bone/joint infections (aOR; 1.38, 95% CI: 1.20–1.59), and less likely for pneumonia (aOR: 0.75, 95% CI: 0.64–0.89), compared with other initial infection types. When assessed separately, the presence of a secondary BSI with another infection increased the odds of recurrence over that infection without a BSI (aOR: 1.96, 95% CI: 1.68–2.30).

Conclusion. Approximately one in six persons with invasive MRSA infection had recurrence. We identified potential opportunities to prevent recurrence through infection control (e.g., management and early removal of central catheters). Other possible areas for preventing recurrence include improving the management of patients with BSI and bone/joint infections (including both during and after antibiotic treatment) and mitigating risk of infection from IDU.



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

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

Natalia Blanco, PhD; Sarah S. Jackson, PhD; Lisa Pineles, MA; Kerri A. Thom, MD and Anthony D. Harris, MD, MPH[1]; Department of Epidemiology and Public Health, University of Maryland School of Medicine, Baltimore, Maryland

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

Friday, October 5, 2018: 12:30 PM

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

Rafael Rios, MSc[1]; Jinnethe Reyes, PhD[1,2]; Lina P Carvajal, BSc[1]; Sergios-Orestis Kolokotronis, PhD[3,4]; Paul Planet, MD PhD[4,5]; Apurva Narechania, MA[4]; Jose Munita, MD[2,6]; Cesar Arias, MD, PhD, FIDSA[1,2] and Lorena Diaz, PhD[1,2]; [1]Molecular Genetics and Antimicrobial Resistance Unit – International Center for Microbial Genomics, Universidad El Bosque, Bogota, Colombia, [2]Center for Antimicrobial Resistance and Microbial Genomics (CARMiG), University of Texas McGovern Medical School, Houston, Texas, [3]Department of Epidemiology and Biostatistics, School of Public Health, SUNY Downstate Medical Center, Brooklyn, New York, [4]Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, New York, [5]Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, [6]Genomics and Resistant Microbes (GeRM) Group, Clinica Alemana de Santiago, Universidad del Desarrollo School of Medicine, Santiago de Chile, Chile

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

Friday, October 5, 2018: 12:30 PM

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.

Disclosures. **J. Munita**, Pfizer: Grant Investigator, Research grant. **C. Arias**, Merck & Co., Inc.: Grant Investigator, Research support. MeMed: Grant Investigator, Research support. Allergan: Grant Investigator, Research support.

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

Nicole Roe, DO[1,2]; Michael Wang, MD[1,2] and Richard Douce, MD[1,2]; [1]Medicine, Lakeland Health, Saint Joseph, Michigan, [2]Medicine, Michigan State University College of Osteopathic Medicine, East Lansing, Michigan

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

Friday, October 5, 2018: 12:30 PM

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.