Conclusion. An MRSA surveillance and prevention strategy in VA may have prevented a substantial number of MRSA and GNR infections. The savings associated with the prevented infections helped to offset some but not all of the cost of the initiative. Economic evaluations of these interventions can help decision makers understand the trade offs between increased cost and improved health that can come from such interventions.

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

1210. Staphylococcal Acute Post-Operative Prosthetic Joint Infection (PJI) Treated With "DAIR" (Debridement and Implant Retention) and Impact of Rifampin: A Retrospective Cohort Study in France

Agathe Becker, MD[1]; Claire Triffault-Fillit, MD[1]; Emmanuel Forestier, MD[2]; Olivier Lesens, MD, PhD[3]; Bertrand Boyer, MD[4]; Stéphane Descamps, MD[5]; Christian Chidiac, MD, PhD[1]; Sébastien Lustig, MD, PhD[6]; Eric Montbarbon, MD[7]; Cécile Batailler, MD[8]; Celine Cazorla, MD[9] and Tristan Ferry, MD, PhD[10]; [1]ID Department, Regional Reference Center for Bji, Hospices Civils de Lyon, Lyon, France, [2]ID Department, Centre Hospitalier Métropole Savoie, Chambéry, France, [3]Maladies Infectieuses, CHU de Clermont-Ferrand, Clermont-Ferrand, France, [4]Chirurgie Orthopédique Et Traumatologique, CHU de Saint Etienne, Saint Etienne, France, [5]Chirurgie Orthopédique Et Traumatologique, CHU de Clermont Ferrand, Clermont Ferrand, France, [6]Orthopaedic Surgery, Regional Reference Center for Bji, Hospices Civils de Lyon, Lyon, France, [7]Chirurgie Orthopédique Et Traumatologique, CH de Chambéry, Chambéry, France, [8]Chirurgie Orthopédique Et Traumatologique, CHU de Lyon, Lyon, France, [9]CHU de Saint Etienne, Saint Etienne, France, [10]Inserm 1111, UCBL1, Hospices Civils de Lyon, Lyon, France

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

Friday, October 5, 2018: 12:30 PM

Background. Staphylococci are the most frequent bacteria in PJI. In patients with acute PJI (i.e., <1 month following the implantation), DAIR with exchange of removal components followed by a combination of antibiotics including rifampin (RMP) (particularly RMP + fluoroquinolone) are recommended. Unfortunately, some patients could not receive RMP due to drug–drug interaction or stopped it due to an adverse event. Finally, it is unclear whether the dose and the duration of RMP influenced the prognosis.

Methods. Retrospective cohort study in four hospitals including patients with staphylococcal acute post-operative PJI treated with DAIR in 2011–2016. Univariate and multivariate Cox analysis and Kaplan–Meier curves were used to determine the risk factors for treatment failure.

Results. Seventy-nine patients were included (median age: 71 years [IQR 53–89]; 55 men [69.6%]; median ASA score: 2 [IQR 2–3]). Cultures revealed 65 (82%) *S. aureus* and 15 (19%) coagulase negative staphylococci infections, including 14 methicillin-resistant strains (18%). Among all isolates, only two (3%) were resistant to RMP and 16 (20%) were resistant to fluoroquinolone. The median duration of antimicrobial therapy was 92 days (IQR 31–152). Only 59 patients received RMP (75%), and 35 (44%) the combination RMP + fluoroquinolone. Median duration of RMP was 57 days (IQR 16–86) and median dose 14.6 mg/kg/d (IQR 13–17). Forty patients (51%) received RMP in the first 2 weeks and 43 patients (54%) received at least 2 weeks of RMP. Six patients (8%) developed an adverse event leading to RMP interruption. During a median follow-up of 443 days (IQR 220–791), 21 patients (27%) experienced a treatment failure including 12 persistence of the initial pathogen (57%) and nine superinfections (43%). An ASA score >2 (OR 2.8; 95% CI 1.26–6.15), the use of RMP (OR 0.4; 95% CI 0.71–0.95) and the duration of RMP treatment (OR 0.83; 95% CI 0.75–0.92 per week of treatment) were significant determinants of the outcome (but not methicillin-resistance). Receiving >2 weeks of RMP prevented the failure, but an introduction during the first 2 weeks did not influence the outcome.

Conclusion. In patients with staphylococcal acute PJI, the use of RMP and its duration strongly influenced the prognosis. As 25% of patients could not receive RMP, new drugs with anti-biofilm activity are required.

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

1211. Increasing Incidence of Invasive Methicillin-Resistant and Methicillin-Sensitive *S. aureus* Infections Among Persons Who Inject Drugs, 2014–2017

Christina B. Felsen, MPH[1]; Anita Gellert, RN[1]; Isaac See, MD[2] and Ghinwa Dumyati, MD, FSHEA[1]; [1]NY Emerging Infections Program, Center for Community Health and Prevention, University of Rochester Medical Center, Rochester, New York, [2]Division of Healthcare Quality Promotion, 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. In 2011, persons who inject drugs (PWID) were estimated to be 2.6% of the US population 13 years of age and older. Infectious endocarditis (IE) and hepatitis C infections among PWID are increasing. We describe trends in invasive *Staphylococcus aureus* (iSA) infections among PWID.

Methods. Population-based surveillance for invasive (from normally sterile site) methicillin-resistant *S. aureus* (MRSA) and methicillin-sensitive *S. aureus* (MSSA) has been conducted in Monroe County, NY (2010 Census population: 744,344) as part of the CDC's Emerging Infections Program since September 2014. Cases are county residents with an iSA infection; iSA incidence was calculated as cases/100,000 census population.

Results. During September 2014–August 2017, 1,460 iSA cases were identified; 150 (10%) in PWID. The incidence of PWID-associated iSA doubled among 18–49 year olds during years 1–3 (Table 1). The proportion of cases occurring in PWID increased among both MRSA (7% to 20%) and MSSA (6% to 11%). PWID were significantly younger ($P < 0.0001$) than noninjection drug users, and more often White ($P = 0.003$) and non-Hispanic (p = 0.004). Among PWID with iSA, 45% had IE. Almost all PWID with iSA used other illicit drugs ($n = 112$, 91% of 123 unique cases); 89% (110) were smokers, and 46% (56) had chronic liver disease. PWID with iSA had a longer mean length of stay (26 days [SD 22] vs. 21 [37], $P = 0.01$); PWID with MRSA were more likely to have septic shock (22% vs. 8%, $P = 0.03$) and pneumonia (9% vs. 1%, $P = 0.04$) when compared with PWID with MSSA. Among iSA, a history of recurrent skin abscess/boil (24% vs. 8%, $P = 0.02$) was more common in PWID with MRSA; fewer PWID with MRSA were obese (2% vs. 15%, p = 0.02).

Conclusion. The increasing incidence of invasive MRSA/MSSA among PWID, frequently accompanied by concurrent chronic liver disease, polysubstance use, and need for extended hospital stays, poses an increasing challenge to the public health and clinical communities. This highlights the critical need to prevent worsening of the epidemic of injection drug use and provide comprehensive treatment for individuals engaging in highest risk drug-related behaviors.

Table 1. Incidence (per 100,000 County Residents) of PWID-Associated iSA by Age Group

Year	18–49 Years	50–64 Years	65–84 Years	Total
1 (September 1, 2014–August 31, 2015)	7.1	5.4	1.2	4.3
2 (September 1, 2015–August 1, 2016)	13.9	5.4	1.2	7.3
3 (September 1, 2016–August 31, 2017)	16.4	5.4	3.5	5.6

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

1212. Whole Genome Sequencing for High-Resolution Methicillin-Resistant *Staphylococcus aureus* Outbreaks Tracing in Neonatal Intensive Care Units and *In silico* Resistance and Virulence Markers Detection

Geraldine Durand, PharmD. PhD[1]; Fabien Javerliat, PhD[1]; Michele Bes, PhD[2]; Frédéric Laurent, PharmD, Professor[2]; Francois Vandenesch, MD, Professor[2] and Anne Tristan, PharmD. PhD[2]; [1]R&D Microbiology, bioMérieux, La Balme Les Grottes, France, [2]Hospices Civils De Lyon, French National Reference Center for Staphylococci, Lyon, France

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

Friday, October 5, 2018: 12:30 PM

Background. The French National Reference Center for Staphylococci used whole genome sequencing (WGS) to investigate outbreaks due to a virulent MRSA clone containing the toxic shock syndrome toxin-1 (TSST-1+, sequence type 5, Geraldine clone) increasingly reported in neonatal intensive care units (ICUs).

Methods. We analyzed 48 isolates previously characterized by *spa* typing: 31 isolates from outbreak 1 (infected or colonized patients, healthcare workers carriage and environment), 12 isolates from four distinct outbreaks (2, 3, 4, and 5) that occurred in geographically independent neonatal ICUs, and five sporadic strains. We performed WGS using a *de novo* assembly approach to perform comparisons between isolates (EpiSeq®, bioMérieux). A phylogenetic analysis was constructed by comparing single nucleotide variations (SNVs) in 2020 core-genes using a cutoff of 40 SNVs for defining isolates belonging to the same transmission cluster. We detected *in silico* resistance and virulence markers using the same bioinformatic pipeline.

Results. For outbreak 1, 25/31 isolates with two distinct but related *spa* types t002 and t111 were highly related (<13 SNVs), suggesting the transmission of the same strain; 6/31 isolates were genetically distinct (>80 SNVs) from the previous cluster of 25 isolates suggesting their origin from separate sources. Interestingly the three isolates of outbreak 2 with a *spa* t111 differed by less than 22 SNVs from the main cluster of the 25 isolates of outbreak 1. This suggested origin from the same transmission cluster. The other three outbreaks showing respectively a *spa* t002 for outbreak 3 and outbreak 4 and a *spa* t045 for outbreak 5 were not affiliated to the main cluster of outbreak 1. The isolates carry numerous virulence factors (including TSST-1) and resistance markers confering a peculiar antibiotic resistance profile to the Geraldine clone.

Conclusion. WGS provides the resolution power to reveal unsuspected transmission events not indicated by conventional methods (different *spa* type). Based on its high resolution WGS is an all in one tool for epidemiology, virulence and resistance analysis. It really transforms outbreak management and infection control practice for an early response and should replace conventional methods for detection of MRSA transmission.

Disclosures. **G. Durand**, bioMérieux: Employee, Salary. **F. Javerliat**, bioMérieux: Employee, Salary.

1213. Evaluation of an Alcohol-Based Antiseptic for Nasal Decolonization of Methicillin-Resistant *Staphylococcus aureus* (MRSA)

Anubhav Kanwar, MD[1], Jennifer L. Cadnum, BS[2], Thriveen Sankar Chittoor Mana, MS[3], Scott Gestrich, MD[4], Annette Jencson, BS, MT, CIC[5] and Curtis J. Donskey, MD[6]; [1]Infectious Diseases, Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio, [2]Geriatric Research Education and Clinical Center, Louis Stokes Cleveland VA

Medical Center, Cleveland, Ohio, [3]Case Western Reserve University, Cleveland, Ohio, [4]Research Service Cleveland VA Medical Center, Cleveland, Ohio, [5]Research Service, Cleveland VA Medical Center, Cleveland, Ohio and [6]Infectious Diseases, Case Western Reserve University, Cleveland, Ohio

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

Friday, October 5, 2018: 12:30 PM

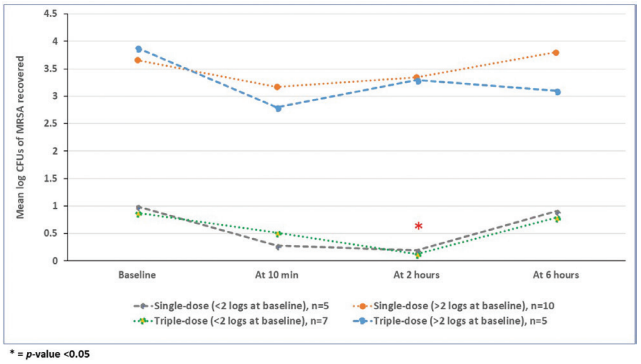
Background. Due to concerns for emergence of mupirocin resistance, there is an interest in use of topical antiseptics for nasal decolonization of *Staphylococcus aureus*. Alcohol-based nasal antiseptics have recently been developed as an alternative to mupirocin, but there is limited data on efficacy, particularly among patients where the burden of carriage is often high.

Methods. We evaluated the effectiveness of a one-time application of a commercial alcohol-based nasal sanitizer for reduction in nasal methicillin-resistant *Staphylococcus aureus* (MRSA) in MRSA-colonized patients. Patients received either a single dose or triple dose over 3 minutes; the triple dose is recommended for preoperative dosing. Swabs were used for quantitative culture of MRSA from the anterior nares and vestibule prior to and 10 minutes, 2 hours, and 6 hours after application. For a subset of patients, cultures for MRSA were collected from hands, clothing, groin, and chest/axilla.

Results. Of 34 MRSA carriers enrolled, 27 (79%) had MRSA detected in nares, 32 (94%) were male, and the mean age was 65. Of the 27 carriers positive for nasal MRSA, 15 (56%) received a single alcohol dose and 12 (44%) received a triple dose over 3 minutes. As shown in the figure, the single and triple dose applications significantly reduced MRSA concentrations at 2 hours post-treatment when the initial burden was low (i.e., <2 $\log_{10}$colonies per swab), but there was no significant reduction at 6 hours; there was no significant reduction with either dose when the initial burden was high (≥2 $\log_{10}$colonies per swab).

Conclusion. A single application of an alcohol nasal sanitizer significantly reduced nasal MRSA at 2 hours post-application when the initial burden of colonization was low, but not when a high burden of carriage was present. Additional studies are needed to determine whether higher alcohol doses or repeated applications might result in improved efficacy.

Figure. Efficacy of one-time application of a single- or triple-dose of alcohol-based nasal sanitizer on the burden of nasal MRSA.



* = *p*-value <0.05

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

1214. High Frequency of Genes Encoding Resistance to Heavy Metals in Methicillin-Resistant *Staphylococcus aureus* (MRSA) Endemic Lineages From South America

Lorena Diaz, PhD[1,2]; Juan Solano, MSc[1]; Rafael Rios, MSc[1]; Lina P Carvajal, BSc[1]; Jose M Munita, MD[2,3]; Sandra Rincon, MSc[1]; Cesar Arias, MD, PhD, FIDSA[1,2,4] and Jinnethe Reyes, 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]Genomics and Resistant Microbes (GeRM) Group, Clinica Alemana de Santiago, Universidad del Desarrollo School of Medicine, Santiago de Chile, Chile, [4]Microbiology and Molecular Genetics, University of Texas McGovern Medical School, Houston, Texas

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

Friday, October 5, 2018: 12:30 PM

Background. MRSA-USA300 is a community-associated clone that has spread worldwide, becoming the most successful clone in the USA. Since 2005, the MRSA-USA300 Latin-American Variant (USA300-LV) has disseminated in community and hospitals in Northern South America. Phylogenetic analysis revealed that USA300-LV is not derived from the USA300 (NA-USA300) but rather, the two clones diverged from a common ancestor. During their evolution, NA-USA300 strains incorporated the ACME element and USA300-LV acquired a copper and mercury resistance mobile element designated COMER. Interestingly, contamination by heavy metals in South American has been recently highlighted and could be driving the selection of resistant genetic lineages. We investigated the frequency of *merA, merB,* and *copB* in genomes of clinical isolates of *S. aureus* from Latin America (LA).

Methods. The presence of *merA*/*merB* and *copB* encoding mercury and copper resistance, respectively, were investigated in 515 *S. aureus* sequenced genomes recovered from bacteremic patients in hospitals from nine Latin American hospitals trough BLAST searches.

Results. The prevalence of *merAB* in *S. aureus* was 35% (181 out of 515 genomes). Interestingly, among 181 *merAB*-positive *S. aureus*, 174 were MRSA (96%). Moreover, 71%, 60%, 59%, and 51% of MRSA genomes from Peru, Ecuador, Colombia, and Venezuela, respectively, harbored mercury resistance genes. Similarly, 65%, 60%, and 22% of MRSA genomes from Ecuador, Colombia, and Venezuela, contained the *copB* gene. Among 174 MRSA harboring *merAB*, ST8 and ST5 were the most predominant lineages in (43% and 45% of genomes, respectively). In contrast, among 95 MRSA carrying *copB,* ST8 was the most frequent lineage (96% of isolates). MRSA from countries with high prevalence of mercury genes showed association with ST5 and ST8. 88% of Colombian and 87% of Ecuadorian MRSA harboring *merAB* belonged to ST8 lineage, whereas ST5 was predominant in 88% of Peruvian MRSA. In Venezuela, ST5 and ST8 were found in 44% and 33%, respectively, of MRSA positive for *merAB*.

Conclusion. High levels of mercury in rivers of Colombia, Ecuador and Peru has been reported. Thus, the prevalence of heavy metal resistance genes in MRSA clinical isolates suggest an adaptation of endemic genotypes to heavy metal contamination caused by activities like metal mining.

Disclosures. **J. M. 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.

1215. Geographic Distribution of *Staphylococcus aureus* With Reduced Sensitivity and Resistance to Vancomycin in the Dominican Republic

Alfredo J. Mena Lora, MD[1]; Patricia Gonzalez, MD[2]; Magnolia Lluberes, MS[2]; Gabriel Grau, MS[2] and Susan C. Bleasdale, MD[1]; [1]Division of Infectious Diseases, University of Illinois at Chicago, Chicago, Illinois, [2]Amadita Laboratorios, Santo Domingo, Dominican Republic

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

Friday, October 5, 2018: 12:30 PM

Background. Resistant *Staphylococcus aureus* (SA) poses a major challenge to clinicians. The prevalence of methicillin-resistant SA (MRSA) has increased over the past decades, while vancomycin resistance remains rare. Only 14 cases of vancomycin-resistant SA (VRSA) have been described in the United States since 2002. VRSA and SA with reduced susceptibility to vancomycin (VISA) cause high morbidity and mortality. There is a paucity of data on VRSA in developing nations. We seek to define the prevalence and resistance profile of SA in the Dominican Republic (DR).

Methods. This is a retrospective review of resistance patterns of SA isolates from a clinical laboratory in the DR (Amadita Laboratories). Amadita provides services nationwide. Data collected from 2016 to 2017 included SA phenotypic sensitivity patterns and geographic location and income level. VISA and VRSA were defined as having minimum inhibitory (MIC) concentrations between 4 and 8 and MIC >16.

Results. Of 5,372 SA samples, 2,735 (51%) were MRSA, 21 were VISA and 39 were VRSA. VRSA samples were more commonly from Santo Domingo (SD) (Figure 1). Communities in SD with mixed and low incomes had greater burden of VRSA (Figure 2). Antimicrobial susceptibilities are shown in Table 1.

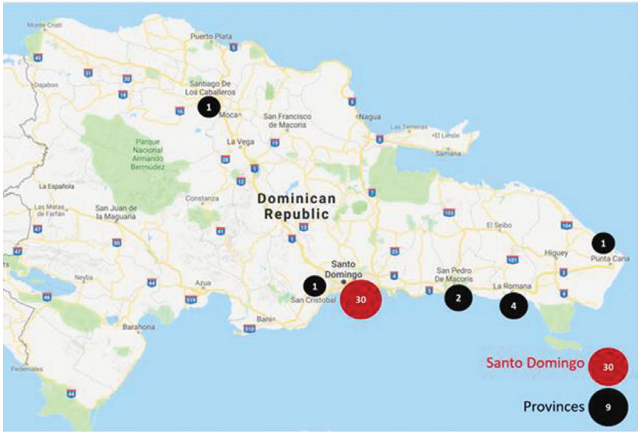


Figure 1. VRSA samples in the DR by location.