Conclusion. Antibiotic resistance carriage is an under recognized problem in this setting. Resistance rates at 6 months of age are higher than expected, with surprisingly little variance explained by individual-level risk factors for resistance in this community.

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1207. Acquisition and Quantification of Antimicrobial Resistance Genes in the Gut Microbiome of Ugandan Women Exposed to Small-Scale Chicken Farming

Mert D, Debelis, BS; Daniel M, Muyanja, MBchb, MMed; Bernard Kakukhure, MRCPath, Infectious Diseases Division, Makerere University, Kampala, Uganda; David R. Bangsberg, MD, MPH, 1 Infectious Diseases Division, Massachusetts General Hospital, Boston, Massachusetts, 3Mbarara University of Science and Technology, Mbarara, Uganda, 4Oregon Health and Science University, Portland State University School of Public Health, Portland, Oregon, 5Harvard Medical School, Boston, Massachusetts, 6Harvard Center for Population and Development Studies, Cambridge, Massachusetts, 7Department of Psychiatry, Massachusetts General Hospital, Boston, Massachusetts, 8Division of Pulmonary and Critical Care, Massachusetts General Hospital, Boston, Massachusetts, 9Harvard T.H. Chan School of Public Health, Boston, Massachusetts

Session: 136. Healthcare Epidemiology: MDR-Gram Negative Infections
Friday, October 5, 2018: 12:30 PM

Background. Antibiotic use in livestock farming is thought to be a major contributor to the spread of antimicrobial resistance (AMR) genes in humans. However, quantitative data in this field are rare. To address this gap in the literature, we examined the prevalence of clinically important AMR genes before and after the introduction of chicken farming among women in rural Uganda.

Methods. We recruited a subset of women participating in a waitlist-randomized controlled trial of small-scale hybrid chicken farming in rural Uganda. Tetracycline is routinely administered to chicks during brooding. Stool samples before and one year after chick introduction were obtained from six women randomized to the control arm, from five women randomized to the intervention arm, and from chickens. Microbial DNA was extracted from chicken and human stool and screened for 87 genes conferring AMR to aminoglycosides, fluoroquinolones, macrolides, lincosamides, streptogramin B, Class A β-lactamases and tetracycline efflux pumps. Chickens harbored 23 AMR genes from the same classes as found in humans, and were also found to have vancomycin resistance genes (Van B and C) and Group D β-lactamases (OKA-58 and OKA-10). At one year, six new AMR genes emerged in chicken stool present in chicken stool in the intervention group, including four present in chickens: SHV, SHV(238G240E), (Class A β-lactamases) and QnrS, QnrB-5 (fluoroquinolone resistance genes). Two AMR genes gained by both control and intervention groups were not present in chickens.

Conclusion. Women exposed to small-scale chicken farming acquired more AMR genes compared with unexposed participants. Chickens harbored many of the genes that emerged in humans. Introduction of antibiotic-treated animals may result in the transfer of AMR genes from animals to humans, even among humans exposed to a wide range of animal agriculture baseline.

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1208. Impact of Admission to an Inpatient Infectious Disease Unit on Methicillin-Resistant Staphylococcus aureus Bloodstream Infections

Zainab Farooqui; Ana A. Weil, MD, MS; Alexander C. Tsai, MD, PhD; Ana W. Weil, MD, MPH; 1Peggy S. Lai, MD, MPH; 2Infectious Diseases Division, Massachusetts General Hospital, Boston, Massachusetts, 3Mbarara University of Science and Technology, Mbarara, Uganda, 4Oregon Health and Science University, Portland State University School of Public Health, Portland, Oregon, 5Harvard Medical School, Boston, Massachusetts, 6Harvard Center for Population and Development Studies, Cambridge, Massachusetts, Department of Psychiatry, Massachusetts General Hospital, Boston, Massachusetts, Division of Pulmonary and Critical Care, Massachusetts General Hospital, Boston, Massachusetts, 9Harvard T.H. Chan School of Public Health, Boston, Massachusetts

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Background. Methicillin-resistant Staphylococcus aureus (MRSA) bloodstream infection (BSI) remains a condition with high mortality. Despite the introduction of new antibiotics, the mortality in the past 10 years at our institution remains unchanged. To evaluate measures that improve outcomes in these patients (patients), we studied the impact of admission to an inpatient infectious disease (ID) unit.

Methods. We identified a retrospective cohort of patients with MRSA BSI at an 800-bed hospital in urban Detroit from January 2013 to February 2017. Patients were assigned to one of the three groups: group 1 was admission to inpatient ID unit where the ID doctors were the attending physicians, group 2 was ID consultation (without admission to ID unit), and group 3 was no ID consultation. Demographic data, clinical information, and 30 day mortality from index blood culture were collected. Source of BSI was classified into four categories: primary (endovascular infection); secondary (respiratory, skin, osteomyelitis, abdominal and genitourinary infections); central line associated; unknown. Unpaired t-test and Fisher's exact test were used to compare groups.

Results. A total of 477 patients were identified with MRSA BSI during the study period. 89 (18.7%) were in group 1, 299 (62%) in group 2 and 89 (18.7%) in group 3. Pt clinical characteristics and outcomes are shown in Table 1. Overall 30-day mortality was 21.4%. Comparison of mortality between groups is shown in Table 2.

Conclusion. While it is well established that ID consultation has improved outcomes in MRSA BSI, this is the first study that shows that admission to an inpatient ID unit decreases mortality even further.

Table 1: Patient Clinical Characteristics and Outcomes

|                      | Group 1 | Group 2 | Group 3 |
|----------------------|---------|---------|---------|
| N                     | 89 (%)  | 299 (%) | 89 (%)  |
| Age mean (±SD)        | 51.53 (75.16) | 62.86 (17.47) | 64.6 (17.60) |
| Male                  | 186 (62.2) | 106 (35.2) | 61 (69.5) |
| Mean duration of BSI  | 3.19 (2.502) | 3.09 (2.525) | 2.94 (2.503) |
| Source                | 31 (9.5) | 28 (9.1) | 7 (8.9) |
| Secondary             | 48 (55.2) | 138 (47.1) | 41 (46.1) |
| Central line associated| 10 (11.5) | 60 (20.5) | 14 (15.7) |
| Unknown               | 13 (11.8) | 69 (23.5) | 27 (30.3) |
| 30-day mortality      | 8 (9.0) | 54 (18.2) | 40 (44.9) |
| Recurrence            | 14 (16.7) | 42 (15.4) | 16 (18.0) |

Table 2: Comparison of 30-Day Mortality Between Groups

|                      | Group 1 vs. group 2 | Group 2 vs. group 3 |
|----------------------|---------------------|---------------------|
| P value              | 0.0083              | P <0.0001           |

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1209. Expanding an Economic Evaluation of the Veterans Affairs Initiative to Prevent Methicillin-Resistant Staphylococcus aureus Infections to Include Gram-Negative Bacteria

Richard E. Nelson, PhD; Michihiko Goto, MD, MSCF; Matthew Samore, MD, FSHEA; Makoto Jones, MD, MS; Vanessa Stevens, PhD; Martin Evans, MD; FIDSA, FSHEA; 1Marin Schweizer, PhD; Eli Perencovich, MD, MS, FIDSA, FSHEA 2and Michael Rubin, MD, PhD, FIDSA; 3Ideas Center, VA Salt Lake City Health Care System, Salt Lake City, Utah, Department of Internal Medicine, University of Iowa Carver College of Medicine, Iowa City, Iowa, 4University of Utah School of Medicine, Division of Epidemiology, Salt Lake City, Utah, 5Internal Medicine, VA Salt Lake City Health Care System, Salt Lake City, Utah, 6Ideas Center of Innovation, VA Salt Lake City Health Care System, Salt Lake City, Utah, Division of Infectious Diseases, Department of Internal Medicine, University of Kentucky College of Medicine, Lexington, Kentucky, 7Department of Epidemiology, University of Iowa College of Public Health, Iowa City, Iowa, 8Iowa VA Health Care System, Iowa City, Iowa and 9Internal Medicine, University of Utah School of Medicine, Salt Lake City, Utah

Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections
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Background. In October 2007, the Department of Veterans Affairs (VA) launched the National MRSA Prevention Initiative, a nationwide effort to reduce MRSA transmission through (1) universal screening, (2) contact isolation for MRSA+ patients, (3) institutional culture change that “infection prevention is everyone’s business,” (4) emphasis on hand hygiene, and (5) increased infection control resources. While the initiative focused on MRSA, recent evidence suggests that it also led to a significant decrease in hospital-onset (HO) Gram-negative rod (GNR) bacteremia. The objective of this analysis was to evaluate the cost-effectiveness and the budget impact of the initiative taking into account both MRSA and GNR infections.

Methods. We developed an economic model using published data on the rate of MRSA HAIs and HO-GNR bacteremia in the VA from October 2007 to September 2015, estimates of the attributable cost and mortality of these infections, and the costs associated with the intervention obtained through a microcosting approach. We explored several different assumptions for the rate of infections that would have occurred if the initiative had not been implemented. Effectiveness was measured in life-years (LYs) gained.

Results. We found that during fiscal years 2008–2015, the initiative resulted in an estimated 4,761–9,236 fewer MRSA HAIs and 1,447–2,159 fewer HO-GNR bacteremia. The initiative itself was estimated to cost $260 million over this 8-year period while the cost savings from prevented MRSA HAIs ranged from $75–165 million and from prevented HO-GNR bacteremia ranged from $42–62 million. The incremental cost-effectiveness of the initiative ranged from $12,146–$46,500/LY when just including MRSA HAIs and from $7,945–$24,387/LY when including HO-GNR bacteremia. The overall impact on the VA’s budget ranged from $202–$334 million.

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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, MD1; Claire Trifaut-Fillit, MD2; Emmanuel Forestier, MD2; Olivier Lesnai, MD, PhD2; Bertrand Boyer, MD3; Stéphane Descamps, MD2; Christian Chédier, MD2; Sébastien Lustig, MD, PhD1; Ervin Mondojohn, MD1; Cédile Batatalla, MD2; Celine Cazorla, MD3 and Tristan Ferry, MD, PhD1.

1ID Department, Regional Reference Center for Bji, Hospices Civils de Lyon, Lyon, France, 2ID Department, Centre Hospitalier Métropole Savoie, Chambéry, France, 3Maladie Infectieuse, CHU, de Chambéry, Chambéry, France, 4Chirurgie Orthopédique Et Traumatologique, CHU de Saint Etienne, Saint Etienne, France, 5Chirurgie Orthopédique Et Traumatologique, CHU de Clermont Ferrand, Clermont Ferrand, France, 6Orthopaedic Surgery, Regional Reference Center for Bji, Hospices Civils de Lyon, Lyon, France, 7Chirurgie Orthopédique Et Traumatologique, CH, de Lyon, Chambéry, France, 8Chirurgie Orthopédique Et Traumatologique, CHU de Lyon, Lyon, France, 9CHU de Saint Etienne, Saint Etienne, France, 10Inserm 1111, UCBII, 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 or subacute infection (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 [68.6%]; median ASA score: 2 [IQR 2–3]). Cultures revealed 65 (82%) S. aureus and 14 (18%) coagulase negatives. CHU de Clermont Ferrand, including 14 methicillin-resistant (MRSA) 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. The median duration of RMP was 57 days (IQR 16–86) and median dose 14.6 mg/kg (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 persisting at 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 0.17–0.95) 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-resistant, MRSA). Remaining 7 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.

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

Christina B. Felsen, MPH1; Anita Gellert, RN2; Isaac See, MD3; and Ghinwa Dumyat, MEd2, MPH1.

1Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, 2University of Rochester Medical Center, Rochester, New York, 3Division of Healthcare Quality Promotion, Centers for Disease Control and Prevention, Atlanta, Georgia

Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections
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Background. In 2011, persons who inject drugs (PWID) were estimated to be 2.6% of the US population (3 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 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 yr 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 < 0.0001) and non-Hispanic (P = 0.004). 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 with PWID with MSSA were obese (2% vs. 15%; P = 0.02).

Conclusion. The increasing incidence of invasive MSSA/MRSA among PWID, frequently accompanied by concurrent chronic liver disease, polysubstance use, and need for extended hospital stay, 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 | 50–64 | 65–84 | Total |
|----------|-------|-------|-------|-------|
| 1 (Sept 1, 2014–Aug 31, 2015) | 7.1   | 5.4   | 12    | 4.2   |
| 2 (Sept 1, 2015–Aug 31, 2016) | 13.9  | 5.4   | 12.7  | 7.3   |
| 3 (Sept 1, 2016–Aug 31, 2017) | 16.4  | 5.4   | 3.6   | 5.6   |

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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, PhD1; Fabien Javerliat, PhD1; Michele Bes, PhD2; Frederic Laurent, PharmD, Professor2, Francois Vandenesch, MD, Professor1 and Anne Tristan, PharmD, PhD2; RdD Microbiologie, bioMérieux, La Balme Les Grottes, France, 3Hospices Civils De Lyon, French National Reference Center for Staphylococcus, 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 2 with a spa t111 differed by less than 22 SNVs from the main cluster of the 25 isolates of outbreak 1. The isolates carry numerous virulence factors (including TSST-1) and resistance markers conferring 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 is an unalternate control practice for an early response and should replace conventional methods for detection of MRSA transmission.

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

Anubhav Kanwar, MD1, Jennifer L. Cadnum, BS2; Thriveen Sankar Chittoor Mana, MS3; Scott Gestrich, MD1; Annette Jenson, BS, MT, CLC4 and Curtiss J. Donskey, MD1.

1Infectious Diseases, Louis Stokes Cleveland V A Medical Center, Cleveland, Ohio, 2Geriatric Research Education and Clinical Center, Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio, 3Infectious Diseases, Louis Stokes Cleveland VA Medical Center, Cleveland, Ohio

Poster Abstracts • OFID 2018:5 (Suppl 1) • 5367