550. Carbapenem--Resistant *E. coli* and *A. baumannii* Among Catheter-Related Blood Stream Infection Patients in Egyptian ICUs

Arwa R. Elmanakhly, MSC[1] and Amani Kholy, MD, PhD[2]; [1]Dar Alfouad hospital, Giza, Al Qahirah, Egypt; [2]Cairo University, Egypt, Al Jizah, Egypt

Session: 60. HAI: MDRO – GNR Epidemiology, Acinetobacter
Thursday, October 3, 2019: 12:15 PM

Background. The spreading of *E. coli* and *A. baumannii* in hospitals is a growing concern due to increased resistance to carbapenems and Fluoroquinolones. The present study aimed to specifically evaluate the presence of mutations in the *gyrA* and *parC* genes in Egyptian ICU and their correlation with carbapenem-resistant genes *E. coli* and *A. baumannii* isolates from patients in 4 tertiary care hospital in Egypt.

Methods. A total of 120 *A. baumannii* and *E. coli* clinical isolates were isolated from ICU patients in 4 tertiary hospitals in Egypt. The bacterial isolates were identified by VITEK-2 (Bio Merieux, France). Antimicrobial susceptibility testing was performed according to CLSI guidelines. Phenotypic detection of carbapenemase activity was done by carba-NP test, followed by molecular identification of carbapenemase encoding genes bla_{NDM}, bla_{OXA-48} and bla_{KPC} by multiplex PCR. The quinolone resistance-determining regions (QRDRs) of *gyrA* and *parC* genes were amplified by singleplex PCR followed by reverse and forward sequencing to detect the gene mutation. The DNA sequences were compared with the sequences of wild type of these genes available in GenBank database. Then, the obtained DNA sequences and their amino acid sequences were analyzed using bioinformatics tools.

Results. *All isolates* showed a high level of resistance among tested antimicrobial agents (cephalosporins, aminoglycosides, carbapenems, penicillins) that ranged from 36% to 100%. Carba-NP detected 43.59% of the carbapenem-resistant isolates. Multiplex PCR detected that 17.95%, 46.15% and 2.56% of isolates were harboring bla_{KPC}, bla_{NDM} and bla_{OXA-48} respectively. PCR and sequencing technique showed combined gene mutation in 8 carbapenem-resistant *E. coli* and *A. baumannii* isolates. The specific substitutions observed in gyrA were Cys173Arg, Cys174 Gly, Asp80Val, Tyr178ASP, Tyr84Gly, Glu85Lys, Ser172Leu and Asp176Asn. While, the specific substitutions observed in parC were point mutation 62 Arg, Phe60Leu, Ils66Val, Gln76Lys. Point mutation 62 Arg was observed in two *A. baumannii* isolates, whereas Ser172Leu mutation was observed in two *E. coli* isolates.

Conclusion. The presence of carbapenem resistance genes in combination with single and multiple mutations in QRDR causes the presence of highly resistant *E. coli* and *A. baumannii* isolates in the Egyptian hospitals.

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

551. Burden of Illness in Carbapenem-Resistant *Acinetobacter baumannii* Infections in US Hospitals (2014 to 2018)

Jason M. Pogue, PharmD, BCPS, BCIDP[1]; Hemanth Kanakamedala, BS[2]; Yun Zhou, MS[3] and Bin Cai, MD, PhD[4]; [1]University of Michigan College of Pharmacy, Ann Arbor, Michigan; [2]Genesis Research Inc., Hoboken, New Jersey; [3]Genesis Research Inc., Hoboken, New Jersey; [4]Shionogi Inc., Florham Park, New Jersey

Session: 60. HAI: MDRO – GNR Epidemiology, Acinetobacter
Thursday, October 3, 2019: 12:15 PM

Background. Infections caused by *Acinetobacter baumannii* present a challenge for treating physicians due to the high level of antimicrobial resistance. The current analysis compared the burden of illness in patients infected with carbapenem-resistant (CR) vs. -susceptible (CS) strains of *A. baumannii*.

Methods. Hospitalized adult patients with microbiologically confirmed *A. baumannii* infections (defined as a positive culture and receipt of antibiotics between 2 days prior to 3 days after the culture) included in the Premier Healthcare Database were retrospectively evaluated. Patient characteristics including demographics, comorbidities, time of infection onset and site of infection were assessed. Comparative outcomes between CR and CS patients assessed included in-hospital mortality, length of hospital stay (LOS), ICU LOS, and discharge status. Outcomes were also stratified by site of infection.

Results. A total of 3,471 patients admitted between January 1, 2014 and June 30, 2018 were included. Patients with CR strains of *A. baumannii* were older (62 vs. 59 years), more likely to have Charlson Comorbidity Index ≥3 (63.4% vs. 56.1%), more likely admitted from a healthcare origin (30.3% vs. 11.4%) and less likely to have the onset of infection within first 48 hours of hospitalization (58% vs. 69%) than those with CS strains. CR patients had increased inpatient mortality compared with CS patients (16.3% vs. 11.0%), driven primarily by patients with bloodstream infections (42.6% vs. 12.4%, respectively, $P < 0.001$). CR patients had a non-significantly increased median overall LOS from the onset of infection (9 vs. 8 days, $P = 0.068$), were more likely to be admitted to the ICU, and were significantly less likely to be discharged home (16% vs. 47%, $P < 0.001$). Hospitalization charges were considerably higher for CR patients (table). Readmission rates were high among CR patients and were similar to patients with CS infections.

Conclusion. Patients with CR strains of *A. baumannii* face a greater burden of illness compared with CS patients, experiencing increased mortality, ICU admission and LOS, and incur higher hospitalization charges. Furthermore, CR patients were less likely to be discharged home after admission.

Table.

	CR N=1,592	CS N=1,879	P value
Age, years, Mean (SD)	62.1 (14.8)	58.9 (16.7)	<0.001
Charlson Comorbidity Index Score ≥3, N (%)	1,009 (63.4)	1,054 (56.1)	<0.001
Admission source, N (%)			
Non-healthcare facility point of origin	983. (61.8)	1,522 (81.0)	<0.001
Transferred from healthcare facility	483 (30.3)	215 (11.4)	
Onset of infection within 48 hours of admission, N (%)	917 (57.6)	1,300 (69.2)	<0.001
Site of index culture infection, N (%)			
Respiratory	691 (43.4)	516 (27.5)	<0.001
Urine	177 (11.1)	192 (10.2)	
Blood	122 (7.7)	346 (18.4)	
Other	602 (37.8)	825 (43.9)	
Total hospital charges, $, median (IQR)	96,795 (52,256 – 193,141)	62,860 (33,270 – 148,459)	<0.003
ICU admission, N (%)	1,017 (63.9)	864 (46.0)	<0.001
ICU at index culture, N (%)	749 (47.1)	622 (33.1)	<0.001
Infection-associated LOS, days, median (IQR)	9 (5 – 14)	8 (5 – 14)	0.068
Discharge status, N (%)			
Death	260 (16.3)	207 (11.0)	<0.001
Home	250 (15.7)	874 (46.5)	
Hospice	75 (4.7)	73 (3.9)	
Other healthcare facility	659 (41.4)	488 (26.0)	
Other	348 (21.9)	237 (12.6)	
Readmission rate by site of infection, N (%)			
Blood	44 (62.9)	174 (57.4)	0.406
Respiratory	286 (52.8)	176 (45.2)	0.024
Urine	97 (58.8)	122 (65.9)	0.167
Other	339 (61.1)	444 (55.8)	0.055

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

552. Within-Host Evaluation of Colonization During Active Methicillin-Resistant S. aureus Bacteremia

Ana B. Berbel Caban, MD[1]; Amy Dupper, MA, MPH[1]; Adriana Van de Guchte, M.S.[1]; Ajay Obla, PhD[2]; Marilyn Chung, BS[2]; Lindsey B. Gottlieb, MD[1]; Alexandra Mills, MD[1]; Lindsey Fox, MD[1]; Irina Oussenko, PhD[2]; Flora Samaroo[1]; Melissa L. Smith, PhD[1]; Jose Polanco, BS[2]; Gopi Patel, MD[1]; Melissa R. Gitman, MD[1]; Mitchell Sullivan, PhD[2]; Harm Van Bakel, PhD[2] and Deena R. Altman, MD MS [3]; [1]Icahn School of Medicine at Mount Sinai, New York, New York; [2]Department of Genetics and Genomics, Icahn School of Medicine at Mount Sinai, Bridgeport, Connecticut; [3]Icahn School of Medicine at Mount Sinai, New York, New York

Session: 61. HAI: MRSA Epidemiology
Thursday, October 3, 2019: 12:15 PM

Background. *Staphylococcus aureus* is a common commensal pathogen and a frequent cause of bacteremia, with nasal and blood isolates from single patients matching >80% of the time. Based on our prior work on paired single-patient isolates,[1] our aim was to collect a contemporary set of colonizing isolates from those with methicillin-resistant *S. aureus* (MRSA) bloodstream infections (BSIs), evaluate the within-host diversity by whole-genome sequencing (WGS), and detail the clinical features linked to colonization.

Methods. Adult patients with MRSA BSIs were screened for MRSA in the anterior nares from July 2018 to March 2019. Blood isolates underwent WGS, and spa and agr function screens were performed on three unique nasal isolates per patient. Clinical data from the electronic medical records underwent uni- and multivariate analyses on clinical features and outcomes.

Results. Of 55 unique patients with MRSA BSIs, screening of 45 subjects revealed that 67% were colonized with MRSA. The majority (64%) were males, 32% had prior colonization, and the most common infection sources were vascular access (27%), skin (24%), and unknown (24%). For those with nasal colonization, blood isolates were composed of 57% clonal complex (CC)5/t002, 33% CC8/t008, and 10% other. 81% of nasal isolates matched the blood, with 20% of nasal isolates harboring diverse spa types and 23% carried agr mutants. During this time frame, WGS found one transmission event involving a colonized subject. Colonization was associated with male gender (OR=4.52 95% CI [1.05–19.49]; $P = 0.04$) and prior hospital admission within the last 3 months (OR=6.12 95% CI [1.44–26.09]; $P = 0.01$) in multivariate analysis, with no differences in outcomes.

Conclusion. Colonization is an important component of invasive MRSA disease, and we found high rates of colonization with a predominance of the CC5. We also noted significant diversity and high proportion of agr mutants. At-risk groups included males and those with prior hospitalization. Combined molecular and clinical analyses can define the intrahost and interhost transmission dynamics of MRSA, and enables the development of targeted approaches in order to curtail disease.

1. Altman, D. R. et al. Genome Plasticity of agr-defective *Staphylococcus aureus* during clinical infection. *Infect. Immun.*(2018).

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

553. Outbreak of Methicillin-Resistant *Staphylococcus aureus* Associated with Hepatic Artery Infusion Pumps

Christopher Calero, BS[1]; Shauna Usiak, MPH, CIC[1];
Anoshé Aslam, MPH, CIC[1]; Margaret A. Palazzolo, MPH[1];
Tracy McMillen, M(ASCP)[1]; Esther Babady, PhD[1];
Rebecca Guest, MD, MPH[1]; Anabella Lucca Bianchi, MD[1];
Elizabeth Robilotti, MD MPH[2] and Mini Kamboj, MD [3]; [1]Memorial Sloan Kettering Cancer Center, New York, New York; [2]Memorial Sloan Kettering, New York, New York; [3]MSKCC, New York, New York

Session: 61. HAI: MRSA Epidemiology
Thursday, October 3, 2019: 12:15 PM

Background. Device-related infections account for a fourth of all HAIs. Hepatic artery infusion pump (HAIP) devices are used to deliver chemotherapy directly into the hepatic artery. This device is used primarily in patients with colorectal cancer for the management of unresectable hepatic metastases. We describe the infection rates and outbreak management of MRSA-related infections in newly placed HAIPs.

Methods. In December 2018, a cluster of 3 MRSA cases was identified within 15–26 days of HAIP insertion. From January 1, 2017 to December 31, 2018, patients with culture proven SSIs within 30 days of HAIP placement were identified through the infection control database to establish baseline rates. Procedural denominator data were found by querying CPT procedure codes. EMR was reviewed to extract clinical characteristics. In response to the cluster, healthcare personnel (HCP) were screened for MRSA by PCR and environmental cultures performed. PFGE and whole-genome sequencing (WGS) was performed to compare isolates recovered in culture and SNP analysis performed using the BioNumerics software v7.6.

Results. IIn December 2018, 3/15 patients with HAIP procedures developed MRSA infections within 30 days of the procedures (post-op days: 15,16,26). The baseline 30 day SSI rate for HAIP in 2017 was 1.3% (2/160). No infections, prior to the cluster, in 2017–18 were MRSA related. All patients were male, with a median age of 49 years (range: 45–54). Sixty HCP who provided direct care during the peri and early post-operative period for the 3 cases were screened for MRSA carriage; 2/60 (3.3%) were positive. All 56 environmental cultures were negative for MRSA. WGS of the 3 patient samples showed 2/3 samples were identical (1 SNP difference); confirming common source transmission. Only one HCP isolate was available for WGS and shown to be unrelated to the two patient isolates. Both employees underwent decolonization. Review of HAIP handling did not reveal obvious lapses, but mask use and strict hand hygiene were enforced with HCPs. No further infections have been identified in the 76 procedures since the cluster.

Conclusion. WGS confirmed common source transmission between two newly placed HAIP although the definitive source could not be identified. Surveillance and prevention efforts should extend to all types of vascular access devices.

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

554. The Changing Epidemiology of Methicillin-Resistant *Staphylococcus aureus* Causing Bacteremia in Hiroshima, Japan During 2008–2017

Hiroki Kitagawa, MD[1]; Junzo Hisatsune, PhD[2];
Hiroki Ohge, MD, PhD[3] and Motoyuki Sugai, DDS, PhD[2]; [1]Graduate School of Biomedical and Health Sciences, Hiroshima University, Hiroshima, Hiroshima, Japan; [2]Antimicrobial Resistance Research Center, National Institute of Infectious Diseases, Higashimurayama, Tokyo, Japan; [3]Hiroshima University Hospital, Hiroshima, Japan

Session: 61. HAI: MRSA Epidemiology
Thursday, October 3, 2019: 12:15 PM

Background. Recently, the Japanese intrinsic community-associated methicillin-resistant *Staphylococcus aureus* (CA-MRSA) clone (CA-MRSA/J), classified as sequence type (ST) 8 carrying staphylococcal cassette chromosome *mec* (SCC*mec*) type IVl (ST8-IVl), has been identified that causes invasive infections similar to those of USA300 clone. However, epidemiological information regarding epidemic CA-MRSA clones is limited in Japan. This study was performed to investigate the changing epidemiology of MRSA causing bacteremia in Japan.

Methods. We performed whole-genome sequencing of MRSA isolates causing bacteremia at Hiroshima University Hospital between January 2008 and December 2017. MRSA isolates were subjected to multilocus sequence typing, SCC*mec* typing and were analyzed for virulence factors. Clinical data of patients with MRSA bacteremia were analyzed.

Results. A total of 193 MRSA strains causing bacteremia were identified during the study period. Among these, most belonged to ST764-IIa (30%; 59 of 193) and ST5-IIa (26.9%; 52 of 193). The proportion of ST5-IIa MRSA decreased from 39.6% (42 of 106) in 2008–2012 to 11.5% (10 of 87) in 2013–2017, and that of ST764-IIa MRSA increased from 23.6% (25 of 106) to 39.1% (34 of 87) in the same time period. The proportion of CA-MRSA (MRSA carrying SCC*mec* type IV or V) increased from 28.3% (30 of 106) in 2008–2012 to 42.5% (37 of 87) in 2013–2017. In CA-MRSA strains, clonal complex (CC) 8-IV MRSA was predominant (76.1%; 51 of 67). Those belonging to CC8-IV MRSA isolates were ST380-IVc (18 of 51), ST8-IVl (CA-MRSA/J; 15 of 51), ST8-IVj (15 of 51), ST8-IVa (2 of 51), and ST4803-IVl (1 of 51). The rate of hospital-onset infections of ST380-IVc, ST8-IVl, and ST8-IVj were 83.3%, 46.7%, and 60%, respectively. In CA-MRSA/J strains, including their variants (e.g., ST4803-IVl), 14 of 16 strains (87.5%) carried genes for toxic shock syndrome toxin (*tst-1*), enterotoxin C (*sec*), and enterotoxin L (*sel*), while none of the ST380-IVc and ST8-IVj MRSA strains carried these genes.

Conclusion. During the study period of 10 years, predominant ST5-IIa MRSA causing hospital-onset infections was replaced by ST764-IIa MRSA. In CA-MRSA clone, ST380-IVc, ST8-IVl (CA-MRSA/J), and ST8-IVj were dominant and have already spread to the healthcare environment.

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

555. The Burden of Invasive *Staphylococcus Aureus* Disease Among Native Americans on the Navajo Nation

Catherine Sutcliffe, PhD ScM[1]; Lindsay Grant, PhD MPH[1];
Angelina Reid, Lab technician[2]; Grace K. Douglass, MPH[1];
Robert Weatherholtz, BS[3]; Robin Hubler, MS[4]; Alvaro Quintana, MD MSc[5];
Raymond Reid, MD MPH[6]; Del Yazzie, MPH[7];
Mathuram Santosham, MD MPH[6]; Katherine O'Brien, MD MPH[3] and Laura Hammitt, MD[3]; [1]Johns Hopkins Bloomberg School of Public Health/Center for American Indian Health, Baltimore, Maryland; [2]Johns Hopkins Center for American Indian Health, Whiteriver, Arizona; [3]Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland; [4]Pfizer, Collegeville, Pennsylvania; [5]Pfizer Inc., Collegeville, Pennsylvania; [6]Johns Hopkins Bloomberg School of Public Health, Baltim, Shiprock, New Mexico; [7]Navajo Epidemiology Center, Window Rock, Arizona

Session: 61. HAI: MRSA Epidemiology
Thursday, October 3, 2019: 12:15 PM

Background. Native Americans in the southwestern United States (US) may be at higher risk for invasive infections due to Staphylococcus aureus. The objective of this study was to determine the burden of invasive S. aureus among Native Americans on the Navajo Nation.

Methods. Prospective population and laboratory-based surveillance for invasive S. aureus infections was conducted from May 2016 through April 2018. A case was defined as a Native American individual living on or around the Navajo Nation with S. aureus isolated from a normally sterile body site. Incidence rates were calculated using the Indian Health Service User Population from 2016 and 2017 as the denominators for Years 1 and 2, respectively. Age-standardized incidence rates were calculated using US Census data from 2015 as the reference group.

Results. 363 cases were identified (Year 1: 159; Year 2: 204). Most cases were adults (96.9%; median age: 56.0 years) and had ≥1 underlying medical condition (94.5%), of which the most common were diabetes (63.2%), hypertension (39.1%), and obesity (37.2%). 38.0% of cases were categorized as community acquired and 28.7% of infections were methicillin-resistant (MRSA). 83.2% of cases were hospitalized, 10.7% required amputation, and 6.5% died within 30 days of the initial culture. The overall incidence of invasive S. aureus was 74.4 per 100,000 persons (95% confidence interval [CI]: 67.1, 82.4) with a significantly higher incidence in the second year (Year 1: 64.9; Year 2: 84.0; incidence rate ratio: 1.29; 95% CI: 1.05, 1.59). The overall incidence of invasive MRSA was 21.3 per 100,000 persons (95% CI: 17.6, 25.8) with no significant difference by year (Year 1: 21.2; Year 2: 21.4; incidence rate ratio: 1.01; 95% CI: 0.69, 1.48). The incidence of invasive S. aureus and MRSA increased with age and was highest among individuals ≥65 years of age. The overall age-standardized incidence of invasive MRSA was 25.9 per 100,000 persons (Year 1: 26.0; Year 2: 25.7; for comparison US 2015 general population: 18.8 per 100,000 persons).

Conclusion. The Navajo Nation has a higher burden of invasive MRSA than the general US population. Further research is needed to evaluate trends over time and identify prevention strategies and opportunities for intervention.

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

556. Phylogenomic Epidemiology of Methicillin-Resistant *Staphylococcus aureus* (MRSA) Chilean-Cordobes Clone in Latin America

Jose RW. Martínez, BSc, MSc[1]; Lorena Diaz, PhD[2]; Marcelo Rojas[3];
Rafael Rios, MSc[4]; Blake Hanson, PhD[5]; Lina M. Rivas, MS[1];
Maria Spencer, BSc, MSc[1]; Ahmed M. Moustafa, PhD[6];
Rafael Araos Bralic, MD, MMSc[1]; Anne Peters[1];
Jinnethe Reyes, MSc, PhD[7]; Lina P. Carvajal, PhD student [8];
Carlos Luna, MD[9]; Mauro Salles, MD, MSc, PhD[10];
Carlos Alvarez, MD, MSc, PhD[11]; Jaime Labarca, MD[12]; Carlos Seas, MD[13];
Carlos Seas, MD[13]; Manuel Guzmán, MD[14]; Paul J. Planet, MD, PhD[6];
Paul J. Planet, MD, PhD[6]; Cesar A. Arias, MD, MSc, PhD, FIDSA1[5] and
Jose Munita, MD[1]; [1]Genomics and Resistant Microbes (GeRM), Instituto de Ciencias e Innovación en Medicina, Facultad de Medicina Clínica Alemana, Universidad del Desarrollo, Chile; Millennium Initiative for Collaborative Research on Bacterial Resistance (MICROB-R), Santiago, Region Metropolitana, Chile; [2]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics,Universidad El Bosque,BOG, COL; MICROB-R, Bogota, Distrito Capital de Bogota, Colombia; [3]Centro de Genética y Genómica,