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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

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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.

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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

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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.

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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

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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.

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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,

Instituto de Ciencias e Innovación en Medicina, Facultad de Medicina, Clínica Alemana Universidad del Desarrollo, , Santiago, Region Metropolitana, Chile; [4]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogota, Distrito Capital de Bogota, Colombia; [5]University of Texas Health Science Center School of Public Health, Houston, Texas; [6]Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, New York; The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania, Philadelphia, Pennsylvania; [7]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Colombia., Bogota, Distrito Capital de Bogota, Colombia; [8]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogota, Colombia, Bogota, Distrito Capital de Bogota, Colombia; [9]Pulmonary Division, Department of Medicine, Jose de San Martin Hospital, University of Buenos Aires, Buenos Aires, Buenos Aires, Argentina, [10]Division of Infectious Diseases, Department of Internal Medicine, Santa Casa de Sao Paulo School of Medicine, Sao Paulo, Brazil, [11]Unidad Infectologia, Departamento de Medicina Interna, Facultad de Medicina, Universidad Nacional de Colombia, Clinica Universitaria Colombia, Bogotá, Distrito Capital de Bogota, Colombia, [12]Department of Infectious Diseases, School of Medicine, Pontificia Universidad Catolica de Chile, Santiago, Region Metropolitana, Chile, [13]Universidad Peruana Cayetano Heredia, Lima, Peru, [14]Centro Medico de Caracas, Caracas, Miranda, Venezuela, [15]CARMiG, UTHealth and Center for Infectious Diseases, UTHealth School of Public Health, HOU, Texas; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, BOG, COL, Houston, Texas

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Background. The MRSA Chilean-Cordobes (ChC) clone belongs to the clonal complex 5 (CC5) and typically carries SCCmec I. The ChC clone predominated widely throughout several countries of Latin America (LA), but during the mid-2000s a CA-MRSA CC8 LA variant (USA300-LV) quickly replaced the ChC in Colombia and Ecuador. Most notably, this replacement was not observed in Peru or Chile. Here, we aimed to understand the phylogenomic relatedness of the CC5 ChC clone obtained from different countries of LA.

Methods. We sequenced and analyzed the genomes of 115 MRSA isolates obtained between 2011–2014 from bloodstream infections in 6 LA countries (Argentina, Brazil, Colombia, Chile, Peru, and Venezuela). All isolates were confirmed as ChC clone by pulsed-field gel electrophoresis (PFGE). We used core genome-based phylogenomic reconstructions and molecular clock analysis to infer the relationships and time of divergence between clades.

Results. Whole-genome-based multilocus sequence typing determined that 110/115 isolates belonged to ST5 and carried SCCmec I. The phylogenomic reconstruction showed ChC isolates clustered into 4 major clades distinctly segregated by country of origin (Figure 1). Interestingly, isolates recovered from Chile divided into 2 different clades that segregate according to the city of origin (Santiago [SCL] or Concepción [CON]), suggesting these clades evolved independently. Molecular clock analyses suggested all clades share a common ancestor with the divergence of the Chilean clades occurring earlier (Figure 2). Of note, analysis of heavy metal genes suggested the divergence between Chilean isolates was characterized by the loss of a mercury resistance gene cluster, which is present in an 88% of CON isolates, but only in 28% of SCL (Figure 2).

Conclusion. MRSA isolates belonging to the ChC clone from 6 LA countries clustered in 4 clades according to the geographical region of isolation. This segregation suggests divergent adaptations that may respond to different selective pressures. Heavy metal resistance could play a role in the ability of the MRSA ChC to disseminate in specific geographical locations.

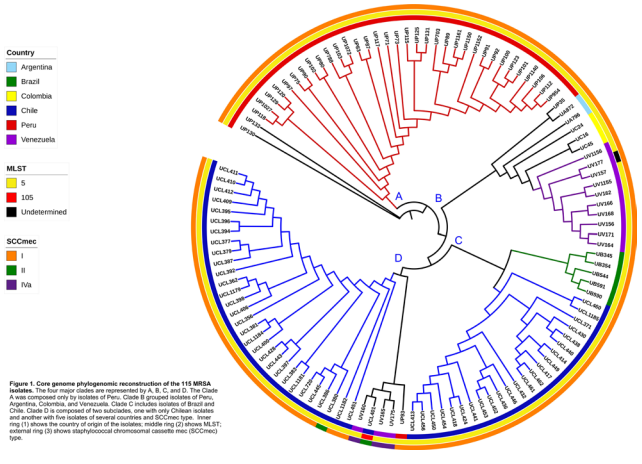

Figure 1. Core genome phylogenomic reconstruction of the 115 MRSA isolates. The four major clades are represented by A, B, C, and D. The Clade A was composed only by isolates of Peru. Clade B grouped isolates of Peru, Argentina, Colombia, and Venezuela. Clade C includes isolates of Brazil and Chile. Clade D is composed of two subclades, one with only Chilean isolates and another with five isolates of several countries and SCCmec type. Inner ring (1) shows the country of origin of the isolates; middle ring (2) shows MLST; external ring (3) shows staphylococcal chromosomal cassette mec (SCCmec) type.

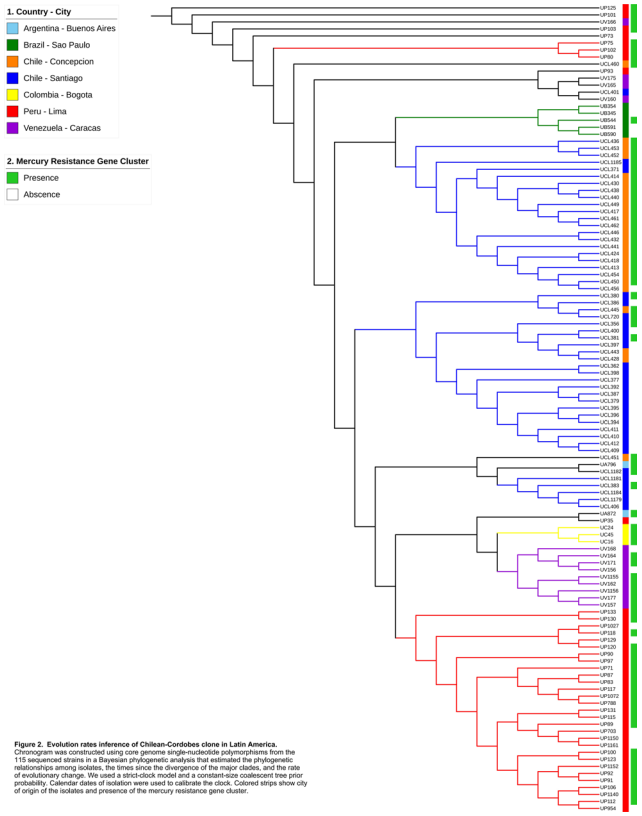

Figure 2. Evolution rates inference of Chilean-Cordobes clone in Latin America. Chronogram was constructed using core genome single-nucleotide polymorphisms from the 115 sequenced strains in a Bayesian phylogenetic analysis that estimated the phylogenetic relationships among isolates, the times since the divergence of the major clades, and the rate of evolutionary change. We used a strict-clock model and a constant-size coalescent tree prior probability. Calendar dates of isolation were used to calibrate the clock. Colored strips show city of origin of the isolates and presence of the mercury resistance gene cluster.

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557. Impact of Heavy Metal Exposure in the Transcriptional Response of Methicillin--Resistant *Staphylococcus aureus* (MRSA)-USA300 Latin-American Variant (USA300-LV)

Aura M. Echeverri, MSc[1]; Sandra Rincon, PhD[2]; Sebastian Solano, MSc[1]; Rafael Rios, MSc[1]; Lina P. Carvajal, PhD student [3]; Cesar A. Arias, MD, MSc, PhD, FIDSA[4]; Lorena Diaz, PhD[5] and Jinnethe Reyes, MSc, PhD[6]; [1]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Distrito Capital de Bogota, Colombia; [2]Molecular Genetics and Antimicrobial Resistance Unit and International Center of Microbial Genomics, Universidad El Bosque, Bogota, Distrito Capital de Bogota, Colombia; [3]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogota, Distrito Capital de Bogota, Colombia; [4]CARMiG, UTHealth and Center for Infectious Diseases, UTHealth School of Public Health, Hou, Texas; Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, BOG, COL, Houston, Texas; [5]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; [6]Molecular Genetics and Antimicrobial Resistance Unit and International Center for Microbial Genomics, Universidad El Bosque, Bogotá, Colombia., Bogota, Distrito Capital de Bogota, Colombia

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Background. USA 300-LV is the predominant MRSA clone in Colombia and contains a genomic island designated "COMER" with genes for copper (Cu) and mercury (Hg) resistance. HM environmental contamination is a serious threat to public health in Colombia and could also influence the selection and evolution of HM resistance genes in MRSA. Here, we investigate the global transcriptomic responses of USA300-LV after exposure to HM under the hypothesis that USA300-LV strains are highly capable of sustaining higher HM concentrations

Methods. We performed comparative RNAseq experiments in USA300-LV clinical strain (CA-MRSA12). Total RNA was isolated in exponential phase in the absence and presence of sub-inhibitory concentrations of Cu and Hg (3 replicates). cDNA libraries were prepared and sequenced on an Illumina platform. Differentially expressed genes (DEG) were calculated by DeSeq2 (p-adjusted value < 0.01) and results on 19 selected genes were confirmed by qRT-PCR.