556. Phylogenomic Epidemiology of Methicillin-Resistant Staphylococcus aureus (MRSA) Chilean-Cordobes Clone in Latin America
Jose RW. Martinez, BSc, MSc; Lorena Diaz, PhD; Marcelo Rojas 1; Rafael Rios, MSc; Blake Haney, PhD; Lina M. Rivas, MS; Maria Spencer, BSc, MSc; Ahmed M. Moustafa, PhD; Rafael Araos Bralic, MD, MSc; Anne Peters; Janeth Reyes, MSc, PhD; Lisa P. Carvalho, PhD student 5; Carlos Luna, MD, Mauro Salles, MD, MSc, PhD; Carlos Alvarez, MD, MSc, PhD; Jaime Labarca, MD; Carlos Sea, MD; Manuel Guzman, MD; Paul J. Planet, MD, PhD; Paul J. Planet, MD, PhD; Cesar A. Arias, MD, MSc, PhD, FIDSA1; and Jose Munita, MD; 1Genomics and Resistant Microbes (GeRM), Instituto de Ciencias e Ingeniería, Facultad de Medicina y Ciencias de la Salud, Universidad de Chile; 2Microbiology and Immunology, University of Chile; 3Gender and Health, Faculty of Medicine, Universidad de Chile; 4Unidad de Genómica de Microorganismos, Universidad de Los Andes; 5Centro de Genética y Genómica, and 6Genome Institute, Universidad de Chile.

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

Disclosures. All authors: no reported disclosures.

555. The Burden of Invasive Staphylococcus aureus Disease Among Native Americans on the Navajo Nation
Catherine Succitche, PhD Scm; Lindsay Grant, PhD MPH;

Results. 363 cases were identified 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.

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.

554. The Changing Epidemiology of Methicillin-Resistant Staphylococcus aureus Causing Bacteremia in Hiroshima, Japan During 2008–2017
Hiroki Kitagawa, MD; Junzo Hisatune, PhD; Hiroki Obge, MD, PhD 1; Motoyuki Sugai, DDS, PhD; 2Graduate School of Biomedical and Health Sciences, Hiroshima University, Hiroshima, Hiroshima, Japan; 3Antimicrobial Resistance Research Center, National Institute of Infectious Diseases, Higashimurayama, Tokyo, Japan; 4Hiroshima University Hospital, Hiroshima, Japan

Session: 61. HA1: MRSA Epidemiology
Thursday, October 3, 2019: 12:15 PM

Background. The Japanese intrinsic community-associated methicillin-resistant Staphylococcus aureus (CA-MRSA) clone (CA-MRSA/J) 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, SCCmec 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 ST874-Ia (30%; 59 of 193) and ST5- Ia (26%; 52 of 193). The proportion of ST5-Ia MRSA decreased from 39.6% (42 of 106) in 2008–2012 to 11.5% (10 of 87) in 2013–2017, and that of ST874-Ia 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 SCCmec type IV or V) increased from 28.3% (30 of 106) in 2012–2015 to 42.5% (37 of 87) in 2013–2017. In CA-MRSA strains, the most common SCCmec elements were type IV (76.1%; 51 of 67). Those belonging to CC8-IV MRSA isolates were ST380-Ivc (15 of 51), ST7-IV (15 of 51), ST8-Iv (2 of 51), and ST4803-Iv (1 of 51). The rate of hospital-onset infections of ST380-Ivc, ST7-IV, and ST8-IV was 83.3%, 46.7%, and 60%, respectively. In CA-MRSA strains, including their variants (e.g., ST4803-Iv), 14 of 16 strains (87.5%) carried genes for toxic shock syndrome toxin (tst-I), enterotoxin C (sea), and enterotoxin L (sel), while none of the ST380-Ivc and ST8-IV MRSA strains carried these genes.

Conclusion. During the study period of 10 years, predominant ST-384-Ia MRSA causing hospital-onset infections was replaced by ST874-Ia MRSA. In CA-MRSA clone, ST380-Ivc, ST7-IV (CA-MRSA/J), and ST8-IV were dominant and have already spread to the healthcare environment.

Disclosures. All authors: no reported disclosures.
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 SCL isolates, but only in 28% of SCL (Figure 2).

Conclusion. MRSA isolates belonging to the ChC clone from 6 LA countries segregated into 4 clades according to 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.

Disclosures. All authors: No reported disclosures.