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

Lorena Diaz, PhD1,2; Juan Solano, MSc1; Rafael Rios, MSc1; Lima P Carvajal, BSc1; Jose M. Munita, MD1; Sandra Rincón, MSc2; Cesar Arias, MD, PhD, FIDSA1,2;3 and Jinnethe Reyes, PhD1,2,4

1Molecular Genetics and Antimicrobial Resistance Unit, International Center for Microbial Genomics, Universidad El Bosque, Bogota, Colombia
2Center for Antimicrobial Resistance and Microbial Genomics (CARMiG), University of Texas McGovern Medical School, Houston, Texas
3Genomics and Resistant Microbes (GrRM) Group, Clinica Alemana de Santiago, Universidad del Desarrollo School of Medicine, Santiago de Chile, Chile
4Microbiology 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 AGME element and USA300-LV acquired a copper and mercury resistance mobile element designated COMER. Interestingly, contamination by heavy metals in South America 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 through BLAST searches.

Results. The prevalence of merA in S. aureus was 35% (181 out of 515 genomes). Interestingly, among 181 merA-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 merA, 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 merA 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. All authors: No reported disclosures.
### Table 1: Antimicrobial Susceptibility for SA Isolates by Drug Resistance Category (%)

| Antimicrobial          | VISA   | VRSA   |
|------------------------|--------|--------|
| Ciprofloxacin          | 81     | 87     |
| Clindamycin            | 23     | 43     |
| Erythromycin           | 33     | 51     |
| Gentamicin             | 90     | 94     |
| Levofloxacin           | 80     | 87     |
| Linezolid              | 100    | 94     |
| Oracin                 | 52     | 64     |
| Quinupristin-Dalfopristin | 100 | 100   |
| Penicillin G           | 0      | 0      |
| Trimethoprim Sulfamethoxazole (TMP-SMX) | 100 | 100   |
| Rifampin               | 57     | 92     |
| Tetracyclines          | 33     | 97     |
| Tigecycline            | 100    | 71     |

**Conclusion.** In this nationwide sample, we found an alarming number of VISA and VRSA. Most cases were in metropolitan SD, with lower income communities carrying a higher case burden. Linezolid and TMP-SMX retain activity against VISA and VRSA in the DR. The rise of vancomycin resistance in developing countries and the disproportionate burden on communities of low income is concerning and requires further study. Infection control measures and antimicrobial stewardship interventions may help prevent further spread of resistant strains.

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

---

1216. Cost-Effectiveness of Penicillin Skin Allergy Testing in Methillin-Sensitive Staphylococcus aureus (MSSA) Bacteremia

**Background.** β-Lactams remain the gold standard for treatment of MSSA bacteremia due to superior outcomes compared with vancomycin. Approximately nine in 10 patients receiving penicillin skin testing (PST) will be de-labeled of a penicillin allergy and able to receive a β-lactam antibiotic. The study aims to evaluate the cost-effectiveness of penicillin allergy confirmation during acute care admission for methillin-sensitive staphylococcus aureus (MSSA) bacteremia through a PST service.

**Methods.** A decision tree analysis was used to compare a PST intervention in patients with a registered penicillin allergy during an inpatient admission for MSSA bacteremia vs. usual care (No PST). The model was created from the health sector perspective with a 1-year time horizon. Patients with a penicillin allergy label were expected to receive vancomycin while patients with no penicillin allergy were expected to receive cefazolin. Potential inpatient, outpatient, and adverse reaction costs were considered in all arms of the model. The effects were measured in quality adjusted life years (QALY) and were calculated for patients who were cured, hospitalized, experienced severe adverse events, or died from MSSA infection.

**Results.** Patients who received PST services had a mean yearly cost of $12,802, mean quality adjusted life years (QALY) of 0.70, and mean cost/QALY of $18,311. The comparator group not receiving PST services had a mean yearly cost of $12,264, mean quality adjusted life years (QALY) of 0.64, and mean cost/QALY of $19,192. The model produced a final base case ICER of $8,966/QALY for receiving a PST during a hospital admission for the treatment of methillin-sensitive staphylococcus aureus (MSSA) bacteremia.

**Conclusion.** Penicillin allergy confirmation through PST services was cost-effective for patients with a reported penicillin allergy admitted for MSSA bacteremia. Additional research to determine potential benefits of PST services beyond one year could further improve the cost-effectiveness of this intervention.

**Disclosures.** S. Meninger, ALK-Abelló: Grant Investigator, Research grant. E. Heil, ALK-Abelló: Grant Investigator, Research grant. T. J. Mattingly II, ALK-Abelló: Grant Investigator, Research grant.

---

1217. Staphylococcus Protein A (spa) Typing Demonstrates Genetic Heterogeneity of Methillin-Susceptible Staphylococcus aureus (MSSA) in a Neonatal Intensive Care Unit (NICU)

**Background.** Protein A (spa) typing is a reliable method for tracking MSSA within NICUs. We characterized spa typing in the NICU setting to evaluate potential genetic heterogeneity and to identify potential sources of transmission.

**Methods.** All infants in the NICU were screened twice monthly. Spa typing was performed to genetically characterize isolates.

**Results.** Spa typing demonstrated that MSSA isolates in our NICU exhibited substantial genetic heterogeneity. While these data do not elucidate acquisition routes, they suggest infants are acquiring MSSA from multiple sources, likely including family members and the local community. Ongoing sequencing studies are examining common spa types to further understand transmission dynamics.

**Disclosures.** A. C. Uhleman, Merck: Investigator, Grant recipient.