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Session: 137. Healthcare Epidemiology: MSSA, MRSA and Other Gram Positive Infections

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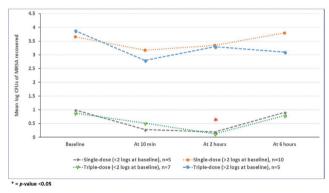
Background. Due to concerns for emergence of mupirocin resistance, there is an interest in use of topical antiseptics for nasal decolonization of *Staphylococcus aureus*. Alcohol-based nasal antiseptics have recently been developed as an alternative to mupirocin, but there is limited data on efficacy, particularly among patients where the burden of carriage is often high.

Methods. We evaluated the effectiveness of a one-time application of a commercial alcohol-based nasal sanitizer for reduction in nasal methicillin-resistant Staphylococcus aureus (MRSA) in MRSA-colonized patients. Patients received either a single dose or triple dose over 3 minutes; the triple dose is recommended for preoperative dosing. Swabs were used for quantitative culture of MRSA from the anterior nares and vestibule prior to and 10 minutes, 2 hours, and 6 hours after application. For a subset of patients, cultures for MRSA were collected from hands, clothing, groin, and chest/axilla.

Results. Of 34 MRSA carriers enrolled, 27 (79%) had MRSA detected in nares, 32 (94%) were male, and the mean age was 65. Of the 27 carriers positive for nasal MRSA, 15 (56%) received a single alcohol dose and 12 (44%) received a triple dose over 3 minutes. As shown in the figure, the single and triple dose applications significantly reduced MRSA concentrations at 2 hours post-treatment when the initial burden was low (i.e., <2 \log_{10} colonies per swab), but there was no significant reduction at 6 hours; there was no significant reduction with either dose when the initial burden was high ($\geq 2 \log_{10}$ colonies per swab).

Conclusion. A single application of an alcohol nasal sanitizer significantly reduced nasal MRSA at 2 hours post-application when the initial burden of colonization was low, but not when a high burden of carriage was present. Additional studies are needed to determine whether higher alcohol doses or repeated applications might result in improved efficacy.

Figure. Efficacy of one-time application of a single- or triple-dose of alcohol-based nasal sanitizer on the burden of nasal MRSA.



Disclosures. All authors: No reported disclosures.

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

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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 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 ACME element and USA300-LV acquired a copper and mercury resistance mobile element designated COMER. Interestingly, contamination by heavy metals in South American 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 trough BLAST searches.

Results. The prevalence of *merAB* in *S. aureus* was 35% (181 out of 515 genomes). Interestingly, among 181 *merAB*-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 *merAB*, 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 *merAB* 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.

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1215. Geographic Distribution of *Staphylococcus aureus* With Reduced Sensitivity and Resistance to Vancomycin in the Dominican Republic

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Background. Resistant Staphylococcus aureus (SA) poses a major challenge to clinicians. The prevalence of methicillin-resistant SA (MRSA) has increased over the past decades, while vancomycin resistance remains rare. Only 14 cases of vancomycin-resistant SA (VRSA) have been described in the United States since 2002. VRSA and SA with reduced susceptibility to vancomycin (VISA) cause high morbidity and mortality. There is a paucity of data on VRSA in developing nations. We seek to define the prevalence and resistance profile of SA in the Dominican Republic (DR).

Methods. This is a retrospective review of resistance patterns of SA isolates from a clinical laboratory in the DR (Amadita Laboratories). Amadita provides services nationwide. Data collected from 2016 to 2017 included SA phenotypic sensitivity patterns and geographic location and income level. VISA and VRSA were defined as having minimum inhibitory (MIC) concentrations between 4 and 8 and MIC >16.

Results. Of 5,372 SA samples, 2,735 (51%) were MRSA, 21 were VISA and 39 were VRSA. VRSA samples were more commonly from Santo Domingo (SD) (Figure 1). Communities in SD with mixed and low incomes had greater burden of VRSA (Figure 2). Antimicrobial susceptibilities are shown in Table 1.

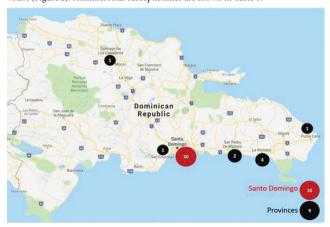


Figure 1. VRSA samples in the DR by location.