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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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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 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 mining.

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