5th World Congress on
Microbial Biotechnology & Vaccine Design
September 17-18, 2018 Lisbon, Portugal

# Quantification of functional genes associated with microbial transformations of mercury in Colombia Amazon ecosystems

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Methylmercury (CH3Hg) is a potent neurotoxin produced by methylation of mercury (Hg) by anaerobic bacteria, especially sulfate-reducing bacteria (SRB) that carriers the hgcA gene, and which is biomagnified through the trophic chain. Many aerobic bacteria resistant to Hg possess mer operons that allow the reduction of Hg2+ to Hg0, a less toxic form of the metal. The objective of this study was to evaluate the abundance of genes involved in the reduction and methylation of Hg in the bacterial communities of Amazonian ecosystems. To do this, DNA was extracted from sediments, forest soils and waters from two locations with different degrees of intervention of gold mining: Tarapaca-Amazonas (low intervention) and Tarair- Vaupés (high intervention). The genes were quantified by real-time PCR (qPCR) in standardized curves. Clone libraries were generated and sequenced for dsrA gene, which detects SRB, hgcA and merA. The primers for dsrA amplified Deltaproteobacteria; two sets of primers of the hgcA gene were used to quantify Deltaproteobacteria and Firmicutes, the primers of the merA gene detected Beta and Gammaproteobacteria. In general, the dsrA gene was the most abundant in all the samples of both localities, especially in samples of superficial and deep sediment, being in the order of 103-104 copies of the gene/ng of DNA. Only a proportion of the SRBs carried the hgcA gene, confirming that only a part of the population of these bacteria is capable of methylation. In Tarapaca, the highest number of copies of the hgcA gene was found in sediments (102 copies/ng) and in Taraira in forest soils (103 copies/ng), which in turn detected some of the highest concentrations of Hg (13-43 ppm) and CH3Hg (0.02-0.05 ppm). Regarding the merA gene, it was more abundant in waters (104) and sediments (103) of Taraira.

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