Título: MERCURY RESISTANCE IN GRAM-NEGATIVE BACTERIA ISOLATED FROM BRAZILIAN AQUATIC ECOSYSTEMS

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Resumo

Mercury (Hg) is considered one of the most dangerous environmental pollutants, presenting a great risk to Public Health, due to its high toxicity, efficient atmospheric transport and its environmental persistence. The Hg biogeochemistry in aquatic environments is mainly controlled by bacteria mediated reactions. Hg(II) compounds can be converted to elemental mercury (Hg^0) by mercury resistant bacteria, who have *merA* gene in their genome. The objective of this study was to investigate the presence of *merA* gene and its expression in mercury resistant bacterial strains isolated from Brazilian aquatic systems. Specific primers (A1 and A5) were used in PCR reactions, in order to detect *merA* gene in 246 Gram-negative bacterial strains' genomes. Assays to quantify mercury bioavailability, using a bioluminescent bacterial biosensor, and mercury reduction, due to expression of *merA* gene, were performed also. *MerA* gene was detected in 75% of the studied bacteria, suggesting that mercury detoxification reaction codified by *merA* gene is the main Hg resistance mechanism among the bacterial strains analyzed. One sample, identified as *Leclercia adecarboxylata,* which was resistant to 25 μM Hg, was used to measure Hg reduction to Hg^0. In two hours of experiment, this strain was capable of reducing more than 80% of Hg added initially, while control system showed an Hg abiotic loss of less than 15%. The bioluminescent bacterial biosensor indicated a mercury bioavailability decrease of 65% during the assays (2 hours). Both assays' results were in agreement, and point to the potential use of this bacterial resistance mechanism to remove Hg(II) from aqueous solutions, and as a promising approach to bioremediate Hg pollution of aquatic ecosystems.

Palavras-chaves: bacteria, mercury, resistance, *merA* gene, bioavailability, bioremediation.

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