

Taxonomic diversity, abundance of class 1 integron gene and diversity of quinolone resistance genes from raw sewage and activated sludge samples from a Wastewater Treatment Plant, Belo Horizonte – MG.

Magna C. Paiva ^{1,2}, Marcelo P. Ávila ¹, Mariana P. Reis ¹, Patrícia S. Costa ¹, Regina M. D. Nardi ¹, Andréa M. A. Nascimento ¹.

¹ UFMG - Universidade Federal de Minas Gerais (Avenida Antônio Carlos 6627 – Pampulha - 31.270.901 -Belo Horizonte – MG).

² UFSJ - Universidade Federal de São João del Rei - Campus Centro-Oeste Dona Lindú (Rua Sebastião Gonçalves Coelho 400 – Chanadour – 35.501.296 – Divinópolis – MG).

Currently the reuse of water has been a major concern around the world due to the scarcity of this natural resource. Thus, efforts should be made to preserve and reduce of pollution. Among the various forms of water recycling, stands out the use of bacteria which can efficiently remove both organic and inorganic pollutants in wastewater treatment plants. In these environments, a huge amount of bacteria exhibits strategies for adaptation and survival, including development of resistance mechanisms to antimicrobial substances. In this study, bacterial diversity and quinolone resistance genes (*qnA*, *qnrB*, *qnrS* and *aac(6')Ib-cr*) from raw sewage (RS) and activated sludge (AS) from the Wastewater Treatment Plant (WWTP), Belo Horizonte – MG were investigated. The high throughput sequencing of V6 hypervariable region of the 16S rRNA gene revealed distinct and complex bacterial communities in samples, with Proteobacteria (especially Gamma and Betaproteobacteria classes), Bacteroidetes and Firmicutes phyla dominating the environments. Interestingly potential pathogens were detected, despite a reduction of these in the AS sample. Regarding to the quinolone resistance genes, only the *qnrS* gene was detected. Although the *aac(6')Ib* gene has been detected, the *cr* variant, which encodes resistance to quinolones, was not found. The *qnrS* and *aac(6')Ib* genes showed low diversity in these environments. Class 1 integrons from the RS and AS samples were quantified by real time PCR and a reduction of these elements was observed in the AS sample. These data revealed the presence of quinolone and aminoglycoside resistance genes and class 1 integrons in the WWTPs. It should be noted that the latter are important in the spread of resistance genes to antibiotics. Moreover, the results reinforce the effectiveness of the sewage treatment by conventional activated sludge systems, revealing the reduction of both pathogens and integrons in the water, contributing to the release of a better quality effluent to the environment.

Keywords: 16S rRNA gene, raw sewage, activated sludge, integron, *qnrS* gene, *aac(6')Ib-cr* gene

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