**TITLE:** CHARACTERIZATION OF THE RESISTOME OF LAKE BOLONHA BY METAGENOMIC APPROACH

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**ABSTRACT:**

Among AR dissemination vehicles, aquatic environments are the main receptacles for antibiotic resistance genes (ARGs) and antibiotic resistant strains. Resistant antibiotics and bacteria are released into the environment through wastewater effluents and agricultural and livestock flows, altering natural ecosystems, altering the population dynamics of microorganisms and introducing a selective pressure of the environment contributes to the diversity of the set of ARGs. The resistome consists in a set of ARGs that can be transferred to pathogens, especially in aquatic environments. The presence of ARGs in these environments can be harmful to health. Lake Bolonha is one of the main sources of water for public supply in the metropolitan region of Belém, supplying about 75% of the population. As the lake is located in the metropolitan region, growing and disorderly urbanization and deforestation that reach the springs and the lake surroundings lead to anthropic problems that can affect the quality of the water supply, which may contribute to the spread of resistant bacteria antibiotics. Thus, the present work aims to analyze the resistance present in Lake Bolonha through the metagenomic approach. Therefore, a liter of water was collected from three different points (P1, P2, and P3) in the lake. The samples were filtered on 0.22 µm membranes and stored in STE solution. DNA extraction was through the MOBIO PowerSoil® DNA Isolation kit, and the sequencing was performed by the Ion Torrent™ platform. The raw data were analyzed for quality of reads using the FastQC tool. The GCSplit tool was used for generate the contigs, and the Prodical software was used for predicted ORFs. The contigs was submitted to CARD for identification to the antibiotic resistance genes. In point P1, the most abundance drug classes were: aminoglycoside (16.9%), penam/cephalosporin (9.4%) and tetracycline antibiotic (6.4%). Tetracycline (10.3%), aminoglycoside (10.3%), and carbapenem (8.6%) were more abundant in P2, and aminoglycoside antibiotic (12.9%), glycopeptide (5.6%), and penam/ cephalosporin (5.6%) in P3. This study identified the presence of genes that participate in mechanisms of resistance to various classes of drugs, emphasizing the importance of clarification on the dissemination of ARGs in aquatic environments.

**Key-words:** Lake Bolonha, Metagenomic, Resistome, Antibiotic resistance genes.