TITLE: GENOMIC CHARACTERIZATION OF AN ANTIBIOTIC MULTIRESISTANT *Enterobacter sp.* STRAIN ISOLATED FROM ÁGUA PRETA LAKE, BELÉM, PARÁ

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ABSTRACT: The excessive and incorrect antibiotics manipulation enables bacteria adaptation, which aggravates its resistance level through gene transfer mechanisms. Aquatic environments are the most common way of multiresistant bacteria dissemination between human and animal populations, modifying microbiota and representing a major threat to public health. The C6 strain used in this work was obtained from the Center of Genomics and System Biology's collection, which was isolated from the Água Preta lake, a particular relevant water supply to the city of Belém, Pará. To attain the lineage's resistance phenotypic characterization to numerous antibiotics, the disc diffusion method was utilized. Through application of the PCR technique, it was evaluated the presence of the beta-lactamase genes blaIMP, blaVIM, blaSHV, blaCTX and blaTEM, as well as integrons intl1 and intl2. The genome was sequenced through the Ion Torrent PGM[™] platform, and contigs were assembled using the MIRA 4.0 and SPAdes software, and afterwards applied to the Lasergene to obtain the scaffold. With the results achieved, it was performed automatic annotation on RAST web system, and then the results were observed on Artemis. RNAmmer and tRNAscan-SE were used to identify rRNA and tRNA. Gene abbreviations, product nomenclatures, conserved domains and motifs were identified by similarity search in public databases such as UniProt, Pfam and InterPro. The C6 bacterial lineage showed resistance to the antibiotics Amoxicillin, Amoxicillin + Clavulanic Acid, Ampicillin, Ceftazidime, Cephalothin, Cefotaxime, Ciprofloxacin, Gentamicin, Kanamycin, Aztreonam, Nalidixic Acid and Tetracycline. Resistance genes to beta-lactam antibiotics blaTEM, blaSHV and *blaVIM* were identified. The assembled genome showed a size of 6.574.221 bps and 8796 CDS's contained in 429 contigs, along with 133 RNAs, in which 114 tRNAs and 19 rRNAs. The BLAST results indicate a level of sequence similarity of about 99% with the Enterobacter genus group, with a closer phylogenetic proximity to the Enterobacter cloacae species. Therefore, despite being isolated from an aquatic environment used as an essential water resource, the Enterobacter sp. C6 bacterial strain consists of a multiresistant microorganism, emphasizing the relevance of more refined studies related to genomic analysis of this particular capacity.

Keywords: Bacterial resistance, *Enterobacter*, genome. Development agency: CNPq and CAPES