

TITLE: GENOME AND RESISTOME OF TWO MULTIDRUG-RESISTANT GRAM-NEGATIVE STRAINS ISOLATED FROM AN AMAZONIA LAKE

AUTHORS: CONCEIÇÃO, M.V.R.¹; COSTA, S.S.¹; ARAUJO, S.²; FOLADOR, A.R.C.¹; RAMOS, R.T.J.^{1,3}; SILVA, A.^{1,3}; AZEVEDO, J.S.N.⁴; TACÃO, M.²; HENRIQUES, I.²; BARAÚNA, R.A.^{1,3}

INSTITUTION: ¹CENTRO DE GENÔMICA E BIOLOGIA DE SISTEMAS UNIVERSIDADE FEDERAL DO PARÁ (AV PERIMETRAL, 66075-110, BRASIL); ²UNIVERSIDADE DE AVEIRO E CESAM (AVEIRO, PORTUGAL); ³LABORATÓRIO DE ENGENHARIA BIOLÓGICA, PARQUE DE CIÊNCIA E TECNOLOGIA GUAMÁ (AV PERIMETRAL, 66075-750, BELÉM, BRASIL); ⁴ UNIVERSIDADE FEDERAL RURAL DA AMAZÔNIA, CAMPUS CAPANEMA (CAPANEMA, BRASIL).

ABSTRACT:

The progressive insertion of antimicrobial agents into the environment has contributed to the dissemination of pathogenic and multidrug-resistant microorganisms. Aquatic environments are effective microhabitats for transmission of resistance genes through horizontal gene transfer. Impacted environments are even more important because they select resistant genotypes. We isolated two multidrug-resistant Gram-negative strains from an Amazonia lake near the city of Belém, Pará. The isolates were sequenced using Ion Proton platform. Reads were filtered and subsequently used to assembly in draft genomes using the software MIRA 4. The contigs were ordered using MAUVE. Automatic annotation was performed using RAST. Two databases were used to detect resistance genes: CARD and Resfinder. Plasmid sequences and virulence genes were detected using PlasmidFinder and VirulenceFinder, respectively. Resistance Islands (RIs) were predicted using GIPSy. The two strains were affiliated to the species *Escherichia coli* and *Acinetobacter baumannii*. *E. coli* showed 162 CDSs related to Virulence, Disease and Defense (3.2% of total genes) according to the RAST SEED server, among them 122 CDSs were related to antibiotic resistance and toxic compounds. Five RIs were identified in the genome. Two plasmids were detected: IncX4 and IncFIA. *E. coli* was classified as pathogenic by PathogenFinder since it carries six virulence genes (*gad*, *lpfA*, *ltaA*, *astA*, *cba* and *cma*). These genes are related to host-pathogen interaction during gastrointestinal infections. The clinically important extended-spectrum beta lactamase (ESBL) gene *bla*_{CTX-M-15} was found. An *ISEcp1* element was conserved 48 base pairs upstream of the ATG start codon of *bla*_{CTX-M-15} gene. *A. baumannii* showed 109 CDSs related to Virulence, Disease and Defense (2.6% of the total genes) being 83 related to resistance to antibiotics and toxic compounds. No plasmids were detected. Ten RIs were detected in the genome. Two ESBL genes were found: *bla*_{OXA-208} and *bla*_{ADC}-like. Lake Água Preta is a mesotrophic lake located near a densely populated area. The detection of clinically relevant *bla* genes in these two Gram-negative isolates emphasizes the importance of aquatic environments as potentially reservoirs of multidrug-resistant and pathogenic bacteria.

Keywords: Resistome, antibiotic resistance, Amazonia, genomic, comparative genomics.

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