

TITLE: GENETIC CHARACTERIZATION OF *Klebsiella* sp., A MULTIRESISTANT ANTIBIOTIC STRAIN ISOLATED FROM ÁGUA PRETA LAKE, BELÉM, BRAZIL

AUTHORS: MORAES, C. N. S.¹; ARAÚJO, C. L. A.¹, ARAGÃO, A. O.¹, ALVES, J. T. C.¹, BARRETO, D. F.¹, DIAS, L. M.¹, BARAÚNA, R. A.¹, HENRIQUE, I.², SILVA, A.¹, FOLADOR, A. R. C.¹

INSTITUTION: ¹ UFPA – FEDERAL UNIVERSITY OF PARÁ (RUA AUGUSTO CORRÊA, 1, 66.075-110, BELÉM – PA, BRAZIL); ² BIOLOGY DEPARTMENT, CESAM, UNIVERSITY OF AVEIRO, AVEIRO, PORTUGAL

ABSTRACT:

Nowadays an increasing number of antibiotic-resistant bacteria have been observed due to anthropogenic interactions that provide environmental conditions when together, can promote selective pressure resulting in the selection of microorganisms with secondary resistance. Among them, the genus *Klebsiella* stands out, in which the related species are classified as Gram-negative bacilli, being able to be isolated from several environments. *K. pneumoniae* and *K. oxytoca*, for example, are important human pathogens associated with nosocomial infections. In this work, the strain APC28, belonging to the genus *Klebsiella*, was isolated from Água Preta lake, which supplies the metropolitan area of Belém - PA. The genome was sequenced by the Ion Proton™ platform, then the assembly was performed by the software MIRA 4.02 and Lasergene 11.2.1. The manual annotation of the predicted CDS' was performed using Artemis program. For *in silico* identification of antibiotic resistance and virulence-related genes the ResFinder and VirulenceFinder databases were used, respectively. The PathogenFinder platform was adopted for the prediction of pathogenic strains in human hosts. The BioEdit program was used to align the 16S rRNA gene markers of different representatives of *Klebsiella* spp.. Then, MEGA7 program was used to build the phylogenetic tree. Also, a phylogenomic analysis was performed based on the Gegenees program. Our results showed that four antibiotic resistance genes were predicted in the APC28 strain. The pathogenicity analysis showed that APC28 is pathogenic to humans, where the observed probability of this isolate being a human pathogen was 89.3%. In the phylogenetic analysis through the 16S rRNA genes of the APC28 and other *Klebsiella* species suggested that this strain may be a species not previously described in the literature. In the phylogenomic analysis through the Gegenees program, a close proximity of the lineage analyzed with the *K. pneumoniae* strains HS11286 and NTUH-K2044 was observed, with *hits* of 97.81 and 91.86%, respectively. Thus, this study contributes to future studies of environmental and clinical relevance in the field of multiresistant antibiotic strains.

Keywords: *Klebsiella*, antibiotics resistance, comparative genomics, phylogenetics.

Development Agency: CNPq and CAPES