

TITLE: MOLECULAR CHARACTERIZATION OF THE PROVIDENCIA STUARTII HARBORING BL_{NDM} FROM CLINICAL SAMPLES

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ABSTRACT: *P. stuartii* has a highly dynamic genome, which contributes to its resistance to antimicrobials. The aim of this study was to analyze the antimicrobial susceptibility profile of *P. stuartii* strains isolated from clinical samples and to conduct a molecular characterization. Thirteen (13) *P. stuartii* strains were isolated from blood cultures samples of patients in an intensive care unit. The presence of the bla_{NDM} gene was determined by PCR analysis. In addition, the minimum inhibitory concentrations (MICs) of antimicrobials were determined using the VITEK and manual methods. The genome for *P. stuartii* PS1 strain harboring bla_{NDM-1} were sequenced with Illumina MiSeq, and preassembled genomic DNA sequences were annotated using Prokka software. A complementary analysis of the genome was performed using Rapid Annotation Subsystem Technology (RAST). Among the thirteen (13) of *P. stuartii* strains analyzed, 11 carriers of the bla_{NDM} gene and showed resistance to meropenem and imipenem. The MIC values ranged from 4-128 µg/mL. A partial genomic characterization for *P. stuartii* PS2 strain (resistant for 64 µg/mL, carbapenemic) using RAST indicated a wide range of genes related to drug efflux pumps and biocidal agents. A total of 73 genes were related to antimicrobial resistance and toxic compounds. The genetic systems were characterized, such as the multiple drug extrusion (MATE), family-division-nodulation (RND), and the major facilitator superfamily (MFS). Partial genomic analysis of the *P. stuartii* PS2 strain confirmed the presence of the bla_{NDM-1} and bla_{TEM} genes and other genes for β-lactamase resistance. The mobilome analysis of the PS2 strain showed a high concentration of insertion sequences associated with mobile genetic elements, and prophages inserted into the genomes, suggesting the existence of a flexible genome. These *P. stuartii* strains were highly diverse for antimicrobial resistance which may lead to a difficulty for therapies for infections caused by this bacterium.

Keywords: Providencia stuartii, genomic sequencing, mobilome, resistance genes

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