

TITLE: PHENOTYPIC AND MOLECULAR CHARACTERIZATION OF NOSOCOMIAL STRAINS OF THE *SERRATIA MARCESCENS* HARBORING *bla*_{KPC} GENE

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ABSTRACT

Serratia marcescens is a Gram-negative bacillus and a member of *Enterobacteriaceae*, which is widely distributed in the environment, *Serratia marcescens* is a Gram-negative bacillus and a member of *Enterobacteriaceae*, which is widely distributed in the environment, , and is currently considered an emerging human microbial pathogen associated with nosocomial infections. The aim of this study was to analyze the antimicrobial susceptibility profile of *S. marcescens* strains isolated from clinical samples and to conduct a molecular characterization of strains carrying *Klebsiella pneumoniae* carbapenemase (*bla*_{KPC}). Twenty-two *S. marcescens* strains were isolated from blood cultures and respiratory samples of patients treated in an intensive care unit. The presence of the *bla*_{KPC} gene in the bacteria was determined by polymerase chain reaction (PCR) analysis. The presence of the *ShlA* and *ShlB* genes encoding serralyisin and its transporter, respectively, was determined by PCR. In addition, the minimum inhibitory concentrations (MICs) of antibiotics were determined using the VITEK 2 automated method. The genomes for *S. marcescens* strains harboring *bla*_{KPC} (SR3, SR5, SR7, SR8, and SR9) 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 22 strains of *S. marcescens* analyzed, 15 were carriers of the *bla*_{KPC} gene and showed resistance to the antibiotic meropenem. The MIC values ranged from 2 to 256 µg/mL. A partial genomic characterization performed for the SR3, SR5, SR7, SR8, and SR9 strains using *RAST* indicated a wide range of genes related to drug efflux pumps and biocidal agents. 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 *S. marcescens* strains confirmed the presence of the *bla*_{KPC-2} gene and other genes for β-lactamase resistance. The mobilome analysis of the *S. marcescens* strains showed a high concentration of insertion sequences associated with mobile genetic elements, and the existence of DNA from prophages inserted into the genomes, suggesting the existence of a flexible genome.

Keywords: *Serratia marcescens*.genomic sequencing. resistance genes. virulence.

Development Agencies: FAPEMA