

Complete genome of a methicillin-resistant *Staphylococcus aureus* strain isolated from the pharynx.

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INTRODUCTION: *Staphylococcus aureus* is a Gram positive bacterium that lives in symbiosis with humans, it is an opportunistic and potentially lethal pathogen of great clinical importance due to the different factors of virulence, invasiveness and resistance that it can possess. In humans, it colonizes various tissues, forming part of the normal microbiota. The widespread use of antibiotics, particularly their inappropriate and excessive use, has favored the emergence and maintenance of strains of *S. aureus* resistant to multiple antibiotics such as penicillin, methicillin (methicillin-resistant *S. aureus*; MRSA), or vancomycin. They are associated with high rates of morbidity and mortality in many regions of the world. *S. aureus* carriers have been found in the pharynx and have been reported with high variability in different populations from 4 to 64% in the pharynx. Some studies mention a higher rate of carriers in the pharynx than in the nose when samples are taken in parallel. Currently, the study of virulence factors is carried out through whole genome sequencing (WGS).

METHODS: DNA extraction was performed from a strain of *S. aureus* isolated from the pharynx of an apparently healthy deli meat worker. DNA was sequenced at IMR Sequencing, Canada, using Illumina MiSeq technology. The sequencing quality was analyzed with the FastQC software and the de novo assembly was performed with Geneious Prime, the generated contigs were aligned with the Bowtie2 software against the reference genome of the *S. aureus* NRS 384 and ATCC 1680 strains. analyzed the presence of virulence and resistance genes in the platforms of VFDB, CGE, MLST, etc.

RESULTS: A 2,879,076 bp long chromosome and a 26,428 bp plasmid were obtained. The chromosome has 2,887 genes and the plasmid 34, with 2,808 and 34 coding regions, 19 rRNA genes and 56 tRNA. The genome presents the adhesin genes: *atl*, *ebh*, *clfA*, *clfB*, *eap*, *fnbA*, *fnbB* and has the *spa*-type t008 and its MLST is 8, it also has all the *ica* operon genes (*icaA*, *icaB*, *icaC*, *icaD* and *icaR*) and the *sdrC*, *sdrD* and *sdrE* genes involved in biofilm formation. Regarding the presence of antibiotic resistance genes, the genome sequence annotates the genes: *Aph(3')-III*, *mecA*, *blaZ*, *mphC*, and *msrA* (aminoglycosides, methicillin, penicillin, macrolides, and macrolide efflux pump). In the case of toxin genes, the genome annotates: the four hemolysin genes (*hla*, *hlb*, *hlc*, and *hld*), the enterotoxins *selk* and *selq*, plus the Panton-Valentine leukocidin (*lukF-PV* and *lukS-PV*).

CONCLUSIONS: The assembly of a complete genome of *S. aureus* isolated from a persistent pharyngeal carrier was carried out, several genes of resistance to antibiotics were found, the sequence typifies various genes of adhesins, formation of biofilms and toxins, particularly the two subunits of Panton-Valentine leukocidin.