

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

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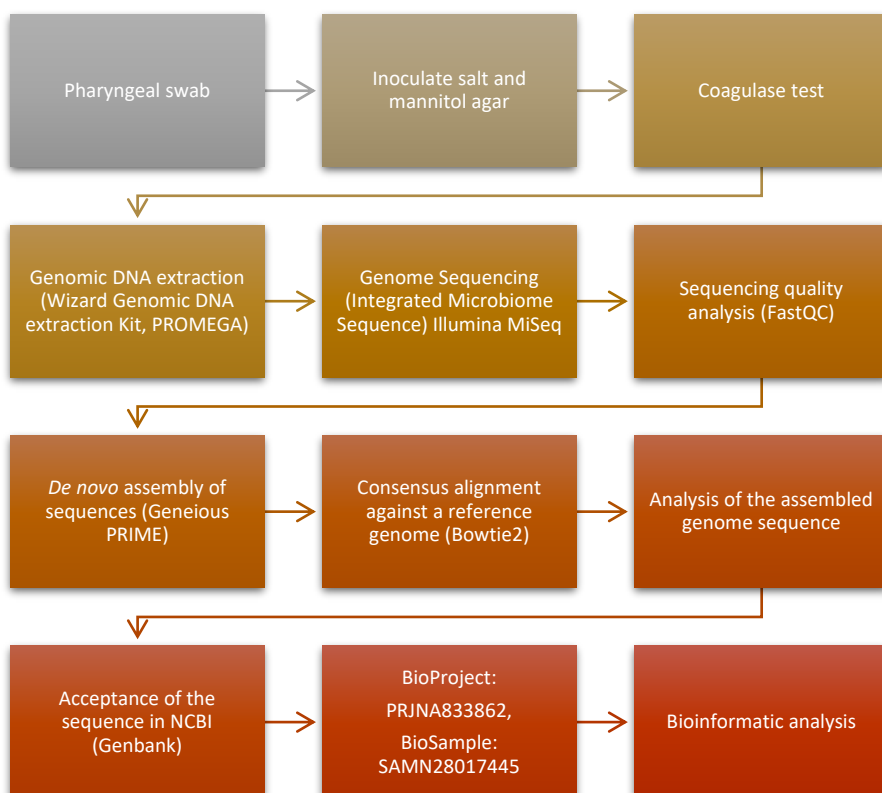
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Introduction

Staphylococcus aureus is a Gram positive bacteria that lives in symbiosis with humans, it is an opportunist and pathogen, potentially lethal [1, 2] of great clinical importance due to the different virulence, invasiveness and resistance factors that can possess [3]. In humans, it colonizes various tissues, forming part of the normal microbiota [3, 4]. The widespread use of antibiotics, particularly their inappropriate and excessive use, has favored the emergence and maintenance of *S. aureus* strains resistant to multiple antibiotics such as penicillin, methicillin (methicillin-resistant *S. aureus*; MRSA) [5, 6] or vancomycin which are associated with high rates of morbidity and mortality in many regions of the world [7]. Currently the study of Virulence factors are carried out through whole genome sequencing (WGS). Several investigations have been carried out with WGS data of *S. aureus* to predict susceptibility and resistance to antimicrobial drugs. The objective of the work was to assemble a genome of a strain of *S. aureus* resistant to methicillin isolated from persistent pharyngeal carrier.

Methods



Results

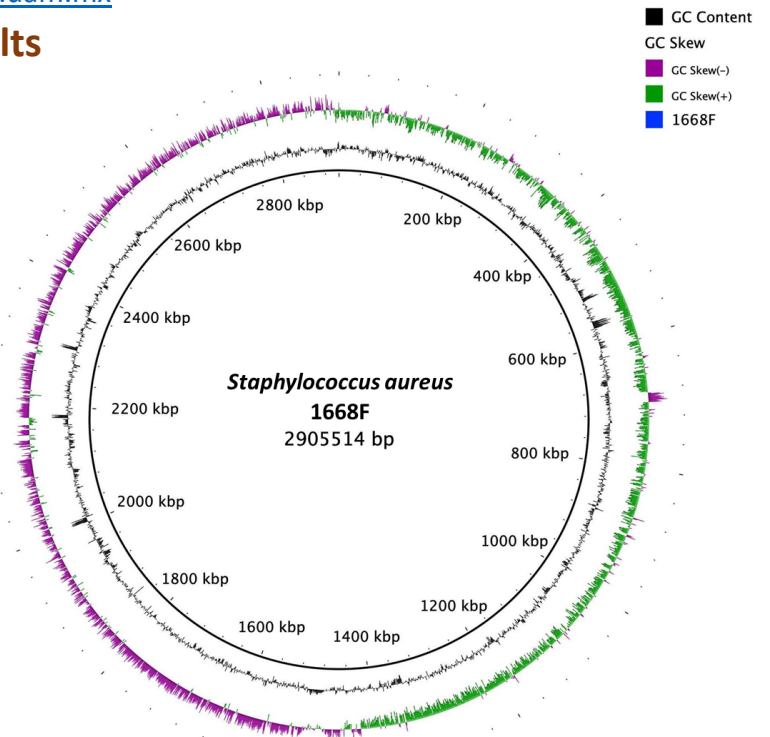


Figure 1. BRIG representation of the sequenced genome.

A genome of 2,905,514 bp and a plasmid of 26,428 bp were assembled. The chromosome has 2,887 genes and the plasmid has 34 genes, 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, it also has all the genes of the *ica* operon (*icaA*, *icaB*, *icaC*, *icaD* and *icaR*) and the *sdrC*, *sdrD* and *sdrE* that participate in biofilm formation.

Regarding the presence of antibiotic resistance genes, the sequence of the genome annotates the genes: *Aph(3')-III*, *mecA* (SCCmec IVa), *blaZ*, *mphC*, and *msrA* (aminoglycosides, methicillin, penicillin, macrolides and macrolide efflux pump) and the ACME gene. In the case of the toxin genes, the genome notes: the four hemolysin genes (*hla*, *hlb*, *hlc* and *hld*), the enterotoxins *selk* and *selq*, as well as 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 resistance genes to various types of antibiotics were found, the sequence typifies various genes for adhesins, biofilm formation and toxins, particularly the two subunits. of the Panton-Valentine leukocidin. With the characteristics found, it is concluded that it is a community-acquired methicillin-resistant strain (CA-MRSA).