

TITLE: WHOLE GENOME SEQUENCING OF A MRSA STRAIN FROM A SELF-LIMITED ORTHOPEDIC SURGICAL SITE INFECTION PREVIOUSLY IDENTIFIED BY PREOPERATIVE SCREENING: DESCRIPTION AND COMPARATIVE GENOMIC WITH A HIGH PATHOGENIC STRAIN

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ABSTRACT:

Staphylococcus aureus is the main etiological agent of post-op infections in fractures of proximal femur, with a higher incidence in patients colonized in the nares by methicillin-resistant strains (MRSA). This higher incidence of infection, in patients with MRSA skin colonization only, has not been proved yet. We presented a MRSA post-op infection, in a non-institutionalized 86 y/o female, without other risk factors for MRSA colonization, with positive screening in the groin skin samples, and negative in nares. 23 days after osteosynthesis of the femur, she was diagnosed with a superficial infection of the surgical wound, treated with ciprofloxacin (CIP) for 21 days, with cure. Beside the positive screening sample, one obtained from needle puncture of the surgical wound was positive for MRSA, both identified by MALD-TOF, and exhibited resistance to CIP, by disk-diffusion and MIC determination (2 µg/mL). Moreover, using PCR, SCCmec IV, and PVL negative were observed. Both isolates belonged to ST 2594, CC 5 in MLST analysis. Whole genome sequencing of postoperative isolate revealed a genome size of 2,823,916 bp assembled in 91 contigs, with 2,624 coding sequences in RAST analyses. About antibiotic resistance, we highlight the presence of *mecA* and *blaZ* (beta-lactam resistance), a mutation in *grlA* gene (Ser-> Phe) and *norA* gene (CIP resistance); and genes *ant(6)-Ia* and *aph(3')-III* (aminoglycoside resistance). About biofilm production, we highlight the presence of the *icaABCD* operon, *tcaR*, *sarA*, *sigB*, *atl* and *rbf*; as well as *agr* type II, *fnbpA*, *fnbpB*, *spa*, *VWbp* and *sasG*. Other genes related to the production of adhesins were found, such as *isdA*, *ebpS*, *sdrC*, *coa*, *emp*, *efb*, *sasA*, *sasC*, *sasD*, *sasF* and *sasK*. Comparing the ST2594 and N315 annotated genomes, looking for genes related to adhesion, resistance, biofilm and toxin production, we identified nine ORFs presented only in ST2594 (resistance: *blaI*, *blaR1*, *blaZ*, Cadmium transporter, Cadmium efflux system accessory protein, Cation-efflux membrane protein, *acr3*, *qacJ*; adhesion and biofilm: *sdrC*), and nine only in N315 (resistance: *mecI*; adhesion and biofilm: *sdrD*, *bbp*, *clfA*, *clfB*, *sasG*; toxin: *seC*, *seL*, *tst*). The lack of *clfB* gene may justify the MRSA negative results in screening nares samples, which associated with the lack of *bbp*, *sdrD* and *tst* genes, may explain the low virulence of the isolate. We questioned the application of some prevention measures in patients colonized by low virulence MRSA.

Keywords: Methicillin-resistant *Staphylococcus aureus*; Surgical Wound Infection; Carrier State; Genome, Bacterial; Virulence.

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