TITLE: GENOMIC ANALYSES OF A CLINICAL STAPHYLOCOCCUS HAEMOLYTICUS STRAIN WITH INCREASED VANCOMYCIN MIC RECOVERED FROM THE AMAZON BASIN

AUTHORS: FREITAS, F.S.[1]; FONSECA, E.L.[1]; CALDART, R.V.[1]; MORGADO, S.M.[1]; ROCHA, L.T[2]; VICENTE, A.C[1].

INSTITUTION: [1]INSTITUTO OSWALDO CRUZ, LAB. GENÉTICA MOLECULAR DE MICRORGANISMOS, FIOCRUZ, RIO DE JANEIRO – RJ, BRAZIL. [2] LABORATÓRIO CENTRAL DE SAÚDE PÚBLICA DE RORAIMA, BOA VISTA – RR, BRAZIL.

ABSTRACT:

Coagulase-negative *Staphylococcus haemolyticus* is an opportunistic pathogen frequently recovered from blood infections and implanted medical devices. Little is known about the pathogenicity determinants in this species, in spite of its importance in nosocomial infections. *S. haemolyticus* has the highest tendency for developing resistance to multiple antibiotics, which is associated with increased morbidity and mortality. This species is usually resistant to methicillin and other penicillins due to the presence of the *mecA* gene, which is embedded in the SCC*mec* region. This bacterium has been considered an important reservoir for resistance genes that can be transmitted to other staphylococcal species. The present study characterized nosocomial blood infections caused by Coagulase-negative *Staphylococcus sp.* in a hospital placed in the Amazon Basin. PCR and sequencing targeting the 16S rRNA gene revealed that these *Staphylococcus* isolates corresponded the *S. haemolyticus* (n=3) and *S. epidermidis* (n=2) species. The PFGE reaveald the non-clonal nature of these infections. Antimicrobial susceptibility tests demonstrated that, in general, the *S. haemolyticus* strains were more resistant than the *S. epidermidis*, presenting a MDR phenotype. All five strains from both species were resistant to penicillin and oxacillin, while only the *S. haemolyticus* strains were resistant to ciprofloxacin. All strains were susceptible to carbapenems and vancomycin, however, one *S. haemolyticus* strain presented an increased MIC (1.5 µg/mL) to this antibiotic. The complete genome sequence of this strain was obtained in order to perform phylogenomic analysis and to assess its resistome and virulome. *In silico* analyses for antimicrobial resistance gene prediction revealed that this *S. haemolyticus* strains harbored genes involved with resistance to penicillins (*mecA*, *blaZ*) ciprofloxacin (*norA*), teicoplanin and vancomycin (*tcABR* operon), explaining its resistance phenotype. The SCC*mec* was also assessed and classified. Several virulence determinants were also identified, such as *fbe*, *cap8D*, *sasH* and *sasA*, involved with adherence, invasion and pathogenecity. The epidemiology and resistance pattern of clinical *S. haemolyticus* in Brazil is scarce. Therefore, this study contributed to gain insights on the epidemiological context of clinical *S. Haemolyticus* in the North region of Brazil, unraveling the major antibiotic resistance and virulence traits.

Keywords: nosocomial infection, virulome, resistome, genomic epidemiology, *Staphylococcus haemolyticus*

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