TITLE: EMERGENCE OF ACME AND PVL-POSITIVE USA300 *Staphylococcus aureus* ISOLATES FROM BLOODSTREAM INFECTIONS IN A BRAZILIAN TEACHING HOSPITAL

AUTHORS: AUGUSTO, M.F; OLIVEIRA, T.L.R; FERNANDES, D.C.S; FERREIRA, A.L.P; NOUÉR, S.A; CHAMON, R.C; SANTOS, K.R.N

INSTITUTION: INSTITUTO DE MICROBIOLOGIA PAULO DE GÓES, RIO DE JANEIRO, RJ (AV. CARLOS CHAGAS FILHO, 373, CCS, BLOCO I, SALA I2-010, CEP: 21941-902, CIDADE UNIVERSITÁRIA, RIO DE JANEIRO, RJ, BRASIL).

ABSTRACT:

Staphylococcus aureus is a versatile pathogen due to its virulence and ability to acquire antimicrobial resistance genes. *S. aureus* is the leading cause of nosocomial bloodstream infections (BSI), being methicillin-resistant *S. aureus* (MRSA) isolates related to high rates of morbidity and mortality. The present study analyzed characteristics related to antimicrobial resistance, virulence and genomic diversity of 123 consecutive *S. aureus* isolates from BSI in a Brazilian teaching hospital, between 2016 and 2018. The species was confirmed by MALDI-TOF/MS. Minimal inhibitory concentration (MIC) to daptomycin, linezolid, oxacillin and vancomycin was determined by broth microdilution method, and ceftaroline MIC was evaluated by E-Test. SCC*mec* typing as virulence genes (*pvl*, *tst*, *cna* and *fnbB*) were accessed by polymerase chain reaction (PCR), while the clonal lineage was determined by pulsed-field gel electrophoresis (PFGE) for MRSA isolates. Among the isolates, 30% (37/123) were characterized as MRSA. All isolates were susceptible to daptomycin, linezolid, and vancomycin. However, reduced susceptibility was detected for daptomycin in 14% (17 isolates) of isolates (MIC=2 mg/L), and for vancomycin (MIC_{50} and MIC_{90} = 2mg/L). Among MRSA isolates, the main clonal lineage identified was USA100/SCC*mec*II (52.6%) followed by USA800/SCC*mec*IV (18.4%), USA300/SCC*mec*IVa (15.8%), BEC/SCC*mec*III (5.3%) and USA1100/SCC*mec*IV (5.3%). MRSA isolates presented *pvl* (21.6%), *fnb*B (21.6%) and *cna* (5.4%) genes. Interestingly, six USA300/SCC*mec*IVa carried the ACME-I, *fnb*B and *pvl* genes. The adhesion gene *fnb*B was mostly found in BEC and USA300 lineages, while the USA300 and USA1100 clones were associated with the presence of the *pvl* genes (p value < 0.05). The results showed that *S. aureus* from ICS at the hospital studied presented reduced susceptibility to daptomycin and vancomycin over the years. Besides, highly virulent MRSA isolates were found causing BSI. The importance of epidemiological surveillance of *S. aureus* infections should be highlighted due to the constant clonal change that has been taking place in health institutions, evincing the emergence and spread of CA-MRSA clones which could lead to higher rates of morbidity and mortality in BSI.

Keywords: MRSA, BSI, antimicrobial resistance, virulence profile, clonal diversity, USA300

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